5'-most EST

```
5792
Seq. No.
                   5434 2.R1040
Contig ID
5'-most EST
                   sat7\overline{0}1015329.h1
                   BLASTX
Method
                   q3850582
NCBI GI
                   249
BLAST score
                   4.0e-21
E value
                   55
Match length
                   84
% identity
                   (AC005278) F15K9.14 [Arabidopsis thaliana]
NCBI Description
                   5793
Seq. No.
                   5435 1.R1040
Contig ID
                   wvk700685378.hl
5'-most EST
                   BLASTX
Method
                   q1706476
NCBI GI
                   199
BLAST score
                   3.0e-15
E value
                   71
Match length
                   55
% identity
                   DNAJ-LIKE PROTEIN SLR0093 >gi_1001729_dbj_BAA10566_
NCBI Description
                   (D64004) DnaJ [Synechocystis sp.]
                   5794
Seq. No.
                   5438 1.R1040
Contig ID
                   LIB3028-001-Q1-B1-F7
5'-most EST
                   BLASTX
Method
                   g3892054
NCBI GI
                   536
BLAST score
                   6.0e-55
E value
                   133
Match length
% identity
                   (AC002330) putative glycosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   5795
Seq. No.
                   5439 1.R1040
Contig ID
                   LIB3028-001-Q1-B1-G1
5'-most EST
                   5796
Seq. No.
                   5442 1.R1040
Contig ID
                   uxk7\overline{0}0671601.h1
5'-most EST
                   BLASTX
Method
                   g4538964
NCBI GI
                   148
BLAST score
                   3.0e-09
E value
                   58
Match length
                    47
% identity
                    (AL049488) NAM/NAP like protein [Arabidopsis thaliana]
NCBI Description
                    5797
Seq. No.
                    5442 2.R1040
Contig ID
5'-most EST
                    zhf700956093.hl
                    5798
Seq. No.
                    5445 1.R1040
Contig ID
```

LIB3051-101-Q1-K1-F3

```
Seq. No.
                   5799
                   5445 2.R1040
Contig ID
5'-most EST
                   LIB3050-012-Q1-E1-G5
Seq. No.
                   5445 3.R1040
Contig ID
5'-most EST
                   pxt700942928.hl
                   5801
Seq. No.
Contig ID
                   5445 4.R1040
5'-most EST
                   uxk700668613.hl
                   5802
Seq. No.
Contig ID
                   5447 1.R1040
5'-most EST
                   LIB3028-001-Q1-B1-D8
                  -5803
Seq. No.
                   5448 1.R1040
Contig ID
5'-most EST
                   fC-gmse7000756618r1
Method
                   BLASTX
NCBI GI
                   g4006924
BLAST score
                   267
                   4.0e-23
E value
Match length
                   60
                   75
% identity
                   (Z99708) beta-galactosidase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   5804
Seq. No.
                   5448 2.R1040
Contig ID
                   fC-gmse700756174a2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2580440
BLAST score
                   293
                   4.0e-26
E value
Match length
                   81
% identity
                   72
                   (D87261) PCF2 [Oryza sativa]
NCBI Description
                   5805
Seq. No.
                   5448 3.R1040
Contig ID
5'-most EST
                   uC-gmropic030d07b1
                   BLASTN
Method
                   g2580437
NCBI GI
BLAST score
                   68
                   9.0e-30
E value
Match length
                   164
                   85
% identity
                   Oryza sativa mRNA for PCF1, complete cds
NCBI Description
                   5806
· Seq. No.
Contig ID
                   5448 4.R1040
5'-most EST
                   g5753241
                   5807
Seq. No.
```

5448 5.R1040

Contig ID

```
5'-most EST
                   fC-gmse7000756174f1
                  BLASTX
Method
NCBI GI
                  q2979559
BLAST score
                   145
                   9.0e-21
E value
                  171
Match length
% identity
                   40
                   (AC003680) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                   5808
Seq. No.
Contig ID
                   5448 6.R1040
                  LIB3170-017-Q1-K1-H11
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2580440
BLAST score
                   300
                   4.0e-27
E value
Match length
                  74
% identity
                   74
                   (D87261) PCF2 [Oryza sativa]
NCBI Description
                   5809
Seq. No.
Contig ID
                   5449 1.R1040
5'-most EST
                  LIB3028-001-Q1-B1-E11
Method
                  BLASTX
NCBI GI
                   g2245108
BLAST score
                   382
E value
                   1.0e-36
Match length
                   157
% identity
                   52
                   (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
NCBI Description
                   5810
Seq. No.
Contig ID
                   5451 1.R1040
                   ssr700559029.h1
5'-most EST
                   5811
Seq. No.
                   5451 2.R1040
Contig' ID
5'-most EST
                   LIB3028-001-Q1-B1-B6
                   5812
Seq. No.
                   5452 1.R1040
Contig ID
                   LIB3030-005-Q1-B1-C12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2661840
                   1216
BLAST score
                   1.0e-134
E value
                   340
Match length
                   66
% identity
                   (Y15430) adenosine kinase [Physcomitrella patens]
NCBI Description
                   5813
Seq. No.
                   5452 2.R1040
Contig ID
                   xpa700797523.h1
5'-most EST
                   BLASTX
Method
                   g2244759
NCBI GI
```

BLAST score

NCBI Description

E value 0.0e + 00Match length 489 % identity 79 (Z97335) selenium-binding protein [Arabidopsis thaliana] NCBI Description Seq. No. 5814 Contig ID 5452 6.R1040 $asn7\overline{0}1131792.h1$ 5'-most EST Method BLASTX NCBI GI g2244760 BLAST score 616 E value 4.0e-64 Match length 151 73 % identity NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana] Seq. No. 5815 Contig ID 5452 7.R1040 5'-most EST hyd700729029.h1 BLASTX Method NCBI GI q2661840 BLAST score 329 E value 1.0e-30 Match length 98 59 % identity NCBI Description (Y15430) adenosine kinase [Physcomitrella patens] Seq. No. Contig ID 5454 1.R1040 5'-most EST dpv701099580.h1 5817 Seq. No. Contig ID 5454 2.R1040 5'-most EST LIB3028-001-Q1-B1-C1 5818 Seq. No. Contig ID 5454 3.R1040 5'-most EST zzp700835538.h1 Seq. No. 5819 Contig ID 5455 1.R1040 5'-most EST LIB3049-055-Q1-E1-B8 Method BLASTX NCBI GI g3876299 BLAST score 325 7.0e-30 E value Match length 135 % identity

(Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabdi... >gi_3880760_emb_CAA16311_ (AL021474) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhab

```
5820
  Seq. No.
                     5456 1.R1040
  Contig ID
                     leu701156483.hl
  5'-most EST
                     BLASTX
  Method
                     g3928090
  NCBI GI
  BLAST score
                     318
                     2.0e-29
  E value
                     104
  Match length
                     60
  % identity
                     (ACO05770) putative MTN3 protein [Arabidopsis thaliana]
  NCBI Description
                     5821
  Seq. No.
                     5458 1.R1040
  Contig ID
                     zhf700958912.h1
  5'-most EST
  Method
                     BLASTX
                     q3420055
  NCBI GI
  BLAST score
                     864
                     8.0e-93
  E value
                     184
  Match length
                     88
  % identity
                     (AC004680) cyclophilin [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                     5822
                     5460 1.R1040
  Contig ID
                     kmv700738102.h1
  5'-most EST
  Seq. No.
                     5823
  Contig ID
                     5460 2.R1040
                     LIB3051-083-Q1-K1-F6
  5'-most EST
  Method
                     BLASTX
                     g1488647
  NCBI GI
                     2033
  BLAST score
  E value
                     0.0e + 00
                     609
  Match length
  % identity
                     (X99937) RNA helicase [Spinacia oleracea]
  NCBI Description
  Seq. No.
                     5824
  Contig ID
                     5460 3.R1040
  5'-most EST
                     uC-gmropic096e01b1
                     5825
  Seq. No.
                     5467 1.R1040
🤝 Contig ID
                     LIB3049-003-Q1-E1-B10
  5'-most EST
                     BLASTN
  Method
                     g458337
  NCBI GI
                     539
  BLAST score
                     0.0e+00
  E value
                     1127
  Match length
                     89
  % identity
  NCBI Description
                     Vigna radiata clone pVR-ACO1
                     1-aminocyclopropane-1-carboxylate oxidase homolog mRNA,
                     complete cds
  Seq. No.
                     5826
```

5467 2.R1040

Contig ID

E value

Match length

268

```
5'-most EST
                   leu701146339.h1
Method
                   BLASTN
NCBI GI
                   q458337
BLAST score
                   256
                   1.0e-142
E value
Match length
                   442
                   90
% identity
NCBI Description
                  Vigna radiata clone pVR-ACO1
                   1-aminocyclopropane-1-carboxylate oxidase homolog mRNA,
                   complete cds
Seq. No.
                   5827
                   5468 1.R1040
Contig ID
                   ssr700555552.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3785983
BLAST score
                   401
E value
                   6.0e-39
Match length
                   117
% identity
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5828
Contig ID
                   5469 1.R1040
5'-most EST
                   jC-qmst02400032b01a1
Method
                   BLASTX
NCBI GI
                   g2623296
BLAST score
                   677
E value
                   4.0e-71
Match length
                   232
% identity
NCBI Description
                   (AC002409) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   5829
                   5469 3.R1040
Contig ID
5'-most EST
                   LIB3106-100-Q1-K1-B8
Seq. No.
                   5830
Contig ID
                   5471 1.R1040
5'-most EST
                   LIB3051-063-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   g2462762
BLAST score
                   959
                   1.0e-104
E value
Match length
                   288
% identity
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                   5831
                   5472 1.R1040
Contig ID
5'-most EST
                   LIB3028-001-Q1-B1-A11
Method
                   BLASTX
NCBI GI
                   g4262149
BLAST score
                   1131
                   1.0e-124
```

```
% identity
                   73
NCBI Description
                   (AC005275) putative xyloglucan endotransglycosylase
                   [Arabidopsis thaliana]
                   5832
Seq. No.
                  5472 2.R1040
Contig ID
5'-most EST
                  g4260368
                  BLASTX
Method
NCBI GI
                  g4262149
BLAST score
                   311
E value
                   2.0e-28
Match length
                  93
% identity
                  57
                   (AC005275) putative xyloglucan endotransglycosylase
NCBI Description
                   [Arabidopsis thaliana]
                  5833
Seq. No.
                   5472 3.R1040
Contig ID
                  zhf700953943.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4262149
BLAST score
                  543
E value
                   9.0e-56
Match length
                  170
                  59
% identity
                  (AC005275) putative xyloglucan endotransglycosylase
NCBI Description
                   [Arabidopsis thaliana]
                  5834
Seq. No.
                  5473 1.R1040
Contig ID
                  LIB3028-001-Q1-B1-B10
5'-most EST
                  BLASTX
Method
                  g2654559
NCBI GI
BLAST score
                  314
                  1.0e-28
E value
Match length
                  152
                  39
% identity
NCBI Description
                  (AF006621) embryonic lung protein [Homo sapiens]
                  5835
Seq. No.
                  5475 1.R1040
Contig ID
5'-most EST
                  zsq701119377.hl
Seq. No.
                  5836
                  5480 1.R1040
Contig ID
5'-most EST
                  LIB3028-001-Q1-B1-E10
                  BLASTX
Method
NCBI GI
                  g4539422
BLAST score
                  581
E value
                  6.0e-60
                  134
Match length
% identity
                  (AL049171) putative protein [Arabidopsis thaliana]
NCBI Description
                  5837
Seq. No.
                  5480 2.R1040
Contig ID
```

LIB3049-013-Q1-E1-G1

5'-most EST

Seq. No.

5842

```
Method
                   BLASTX
NCBI GI
                   q4539422
BLAST score
                   535
E value
                   5.0e-55
Match length
                   110
                   83
 % identity
                   (AL049171) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5838
                   5481 1.R1040
Contig ID
 5'-most EST
                   LIB3028-001-Q1-B1-E12
Method
                   BLASTX
                   g1213629
NCBI GI
                   771
BLAST score
E value
                   4.0e-82
                   238
Match length
                   60
 % identity
                   (X95991) pectinesterase [Prunus persica]
NCBI Description
                   5839
Seq. No.
Contig ID
                   5482_1.R1040
                   jC-gmst02400072a09d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2108252
BLAST score
                   317
E value
                   3.0e-29
Match length
                   102
                   34
 % identity
                    (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
                   >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
                   [Arabidopsis thaliana] >gi 4538925 emb CAB39661.1
                    (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                   5840
Seq. No.
                   5486_1.R1040
Contig ID
 5'-most EST
                   LIB3028-001-Q1-B1-G10
Method
                   BLASTX
                   g132724
NCBI GI
BLAST score
                   305
                   2.0e-27
E value
                   118
Match length
                   54
 % identity
                   50S RIBOSOMAL PROTEIN L18 >gi_71259_pir__R5BS8F ribosomal
NCBI Description
                   protein L18 - Bacillus stearothermophilus
                   5841
 Seq. No.
                   5487 1.R1040
Contig ID
                   gsv701056432.hl
 5'-most EST
                   BLASTN
Method
                   g20866
NCBI GI
BLAST score
                   196
                   1.0e-105
E value
Match length
                   585
 % identity
                   85
                   P.sativum mRNA for plastid ribosomal protein CL15
NCBI Description
```

```
5487 2.R1040
Contig ID
                    LIB3028-001-Q1-B1-G11
5'-most EST
Seq. No.
                    5843
                    5487 3.R1040
Contig ID
                    pcp700991074.hl
5'-most EST
                    BLASTN
Method
NCBI GI
                    g20866
BLAST score
                    53
                    4.0e-21
E value
Match length
                    161
% identity
                    83
                   P.sativum mRNA for plastid ribosomal protein CL15
NCBI Description
                    5844
Seq. No.
                    5497 1.R1040
Contig ID
                    jC-qmro02910072a11d1
5'-most EST
                    BLASTX
Method
                    q4204294
NCBI GI
BLAST score
                    240
                    4.0e-20
E value
                    82
Match length
                    62
% identity
                    (AC003027) lcl prt_seq No definition line found
NCBI Description
                     [Arabidopsis thaliana]
                    5845
Seq. No.
                    5498 1.R1040
Contig ID
5'-most EST
                    LIB3049-011-Q1-E1-D3
                    5846
Seq. No.
                    5499 1.R1040
Contig ID
                    LIB3109-056-Q1-K1-E12
5'-most EST
                    BLASTX
Method
                    q1709358
NCBI GI
BLAST score
                    1489
E value
                    1.0e-166
                     441
Match length
                     64
% identity
                    NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE
NCBI Description
                     PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__S48859
                     nucleoside triphosphatase - garden pea
                     >gi_2129890_pir__S65147 nucleoside triphosphatase
                    precursor, chromatin-associated - garden pea >gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase [Pisum sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319)
                     nucleoside triphosphatase (NTPase) [Pisum sativum]
                     5847
Seq. No.
                     5501_1.R1040
Contig ID
                     ncj7\overline{0}0975782.h1
5'-most EST
                     BLASTX
Method
NCBI GI
                     q2982303
                     387
BLAST score
                     2.0e-37
E value
Match length
                     83
```

% identity

5'-most EST

```
NCBI Description (AF051236) hypothetical protein [Picea mariana]
                   5848
Seq. No.
Contig ID
                   5508 1.R1040
5'-most EST
                   LIB3028-005-Q1-B1-C12
                   BLASTX
Method
                   g2398829
NCBI GI
BLAST score
                   640
E value
                   1.0e-66
                              A. . . .
                   239
Match length
% identity
                   29
                   (Y11220) mitochondrial uncoupling protein [Solanum
NCBI Description
                   tuberosum]
                   5849
Seq. No.
Contig ID
                   5508 2.R1040
                   LIB3040-031-Q1-E2-H5
5'-most EST
                   BLASTX
Method.
                   g2398829
NCBI GI
BLAST score
                   418
E value
                   7.0e-41
Match length
                   111
                   42
% identity
                   (Y11220) mitochondrial uncoupling protein [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   5850
                   5510 1.R1040
Contig ID
                   LIB3028-005-Q1-B1-D4
5'-most EST
                   BLASTX
Method
                   g2583112
NCBI GI
BLAST score
                   315
                   9.0e-29
E value
                   142
Match length
                   44
% identity
                   (AC002387) putative PD1-like DNA-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   5851
Seq. No.
                   5510 2.R1040
Contig ID
                   hyd7\overline{0}0726712.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3668079
                   177
BLAST score
                   8.0e-13
E value
Match length
                   62
                   50
% identity
                   (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5852
                   5512 1.R1040
Contig ID
                   LIB3092-055-Q1-K1-G10
5'-most EST
                   5853
Seq. No.
                   5517 1.R1040
Contig ID
```

LIB3028-006-Q1-B1-D5

```
5854
Seq. No.
                   5520 1.R1040
Contig ID
                   q5605979
5'-most EST
Method
                   BLASTX
                   q4006829
NCBI GI
                   675
BLAST score
                   1.0e-70
E value
                   304
Match length
                   56
% identity
                   (AC005970) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5520 2.R1040
Contig ID
5'-most EST
                   jC-qmro02800037a12a1
                   BLASTX
Method
                   g3461835
NCBI GI
                   856
BLAST score
                   6.0e-92
E value
                   218
Match length
                   74
% identity
                   (AC005315) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi_3927840 (AC005727) putative protein kinase [Arabidopsis
                   thaliana]
                   5856
Seq. No.
                   5520_3.R1040
smc700746635.h1
Contig ID
5'-most EST
                   5857
Seq. No.
                   5521 1.R1040
Contig ID
                   trc700563573.hl
5'-most EST
                   BLASTX
Method
                   g2191150
NCBI GI
                   173
BLAST score
                    4.0e-12
E value
                    98
Match length
                    14
% identity
                    (AF007269) similar to mitochondrial carrier family
NCBI Description
                    [Arabidopsis thaliana]
                    5858
Seq. No.
                    5523 1.R1040
Contig ID
                    LIB3028-007-Q1-B1-F11
5'-most EST
                    5859
Seq. No.
                    5528 1.R1040
Contig ID
                    LIB3106-101-Q1-K1-E2
5'-most EST
                    5860
Seq. No.
                    5528 2.R1040
Contig ID
                    1eu7\overline{0}1152989.h1
 5'-most EST
                    5861
Seq. No.
                    5529 1.R1040
Contig ID
                    LIB3072-012-Q1-E1-G3
 5'-most EST
                    BLASTX
Method
```

g548774

NCBI GI

```
1028
BLAST score
                  1.0e-112
E value
Match length
                  240
% identity
                  82
                  60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal
NCBI Description
                  protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
                  ribosomal protein L7A [Oryza sativa]
Seq. No.
                   5862
                   5536 1.R1040
Contig ID
                   asn701135418.h1
5'-most EST
                  BLASTX
Method
                   q4234941
NCBI GI
                   848
BLAST score
E value
                   7.0e-99
                   210
Match length
% identity
                   (AF097938) cytosolic phosphoglucomutase [Populus tremula x
NCBI Description
                   Populus tremuloides]
                   5863
Seq. No.
                   5540 1.R1040
Contig ID
                   jC-gmf102220094d09a1
5'-most EST
                   BLASTX
Method
                   q2102691
NCBI GI
BLAST score
                   412
                   4.0e-40
E value
                   125
Match length
                   65
% identity
                   (U64817) fructokinase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   5864
                   5543_1.R1040
Contig ID
                   jC-gmst02400041g07a1
5'-most EST
                   BLASTX
Method
                   g123601
NCBI GI
BLAST score
                   766
                   2.0e-81
E value
                   242
Match length
                   62
% identity
                   HEAT SHOCK 70 KD PROTEIN >gi_99913_pir__S14992 heat shock
NCBI Description
                   protein, 70K - soybean >gi_18663_emb_CAA44620_ (X62799)
                   Heat Shock 70kD protein [Glycine max]
                   5865
Seq. No.
                   5547 1.R1040
Contig ID
                   LIB3028-009-Q1-B1-B4
5'-most EST
                   BLASTX
Method
                   g2827704
NCBI GI
BLAST score
                   218
                   2.0e-17
E value
                   82
Match length
                   54
% identity
                   (AL021684) LRR-like protein [Arabidopsis thaliana]
NCBI Description
```

5548_1.R1040

Seq. No.

Contig ID

```
5'-most EST
                  uC-gmropic012c05b1
                  BLASTX
Method
                  q2464905
NCBI GI
                  295
BLAST score
                  2.0e-26
E value
Match length
                  148
                  47
% identity
                   (Z99708) minor allergen [Arabidopsis thaliana]
NCBI Description
                  5867
Seq. No.
Contig ID
                  5548 2.R1040
5'-most EST
                  LIB3028-009-Q1-B1-C1
Method
                  BLASTN
                  g4006885
NCBI GI
BLAST score
                  34
                  1.0e-09
E value
                  78
Match length
% identity
                  92
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                  fragment No
                  5868
Seq. No.
Contig ID
                  5550 1.R1040
5'-most EST
                  uxk700667830.h1
Method
                  BLASTX
NCBI GI
                  q3834322
BLAST score
                  274
E value
                  8.0e-24
Match length
                  189
% identity
                   (AC005679) EST qb R30300 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  5869
Contig ID
                  5550 2.R1040
5'-most EST
                  LIB3049-009-Q1-E1-A1
                  BLASTN
Method
NCBI GI
                  q4006885
BLAST score
                  62
E value
                  5.0e-26
Match length
                  150
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  5870
Contig ID
                  5552 1.R1040
5'-most EST
                  LIB3051-006-Q1-E1-F9
Method
                  BLASTX
NCBI GI
                  q4006867
BLAST score
                  214
E value
                  5.0e-17
Match length
                  53
% identity
                  (299707) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

```
Contig ID
                   5552 2.R1040
5'-most EST
                  LIB3051-091-Q1-K1-E9
                  5872
Seq. No.
                  5554 1.R1040
Contig ID
                  LIB3028-009-Q1-B1-E4
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4469003
BLAST score
                  367
                  2.0e-34
E value
Match length
                  102
% identity
                   63
NCBI Description
                   (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   5873
Contig ID
                  5554 2.R1040
5'-most EST
                  wrq700788935.h2
Seq. No.
                   5874
Contig ID
                  5556 1.R1040
5'-most EST
                  q4291358
                  BLASTX
Method
NCBI GI
                  g2462837
BLAST score
                  262
E value
                  2.0e-22
Match length
                  184
                  36
% identity
NCBI Description
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  5875
Contig ID
                  5557 1.R1040
5'-most EST
                  LIB3138-044-Q1-N1-A10
                  BLASTX
Method
NCBI GI
                  q3913711
BLAST score
                  2382
E value
                  0.0e+00
Match length
                  495
                  93
% identity
NCBI Description
                  NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
                   (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE
                  DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
                   (NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE)
                  >gi 4379384 emb CAA53076 (X75327)
                  glyceraldehyde-3-phosphate dehydrogenase
                   (nonphosphorylating, NADP+) [Pisum sativum]
                  5876
Seq. No.
                  5557 5.R1040
Contig ID
5'-most EST
                  hyd700726390.h1
Method
                  BLASTN
NCBI GI
                  g496493
BLAST score
                  73
E value
                  5.0e-33
                  226
Match length
                  88
% identity
NCBI Description
                  P.sativum (Rosakrone) mRNA for nonphosphorylating,
                  NADP-specific, glyceraldehyde-3-phosphate dehydrogenase
```

```
5877
Seq. No.
                   5562 1.R1040
Contig ID
                   LIB3039-040-Q1-E1-C8
5'-most EST
                   BLASTN
Method
NCBI GI
                   q3776081
                   217
BLAST score
                   1.0e-118
E value
                   353
Match length
                   90
% identity
                  Medicago truncatula mRNA for MtN30 gene, partial
NCBI Description
                   5878
Seq. No.
                   5562 4.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy104b02b1
Method
                   BLASTX
                   g3892712
NCBI GI
BLAST score
                   338
E value
                   1.0e-31
Match length
                   76
% identity
                   84
                   (AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7) -
NCBI Description
                   like protein [Arabidopsis thaliana]
Seq. No.
                   5879
                   5562 5.R1040
Contig ID
5'-most EST
                   LIB3028-009-Q1-B1-H2
Method
                   BLASTN
NCBI GI
                   q3776081
BLAST score
                   147
E value
                   5.0e-77
Match length
                   231
                   91
% identity
NCBI Description
                  Medicago truncatula mRNA for MtN30 gene, partial
Seq. No.
                   5880
Contig ID
                   5564 1.R1040
5'-most EST
                   jC-qmf102220051h02a1
                   BLASTX
Method
NCBI GI
                   q3759184
BLAST score
                   651
E value
                   4.0e-68
Match length
                   198
% identity
NCBI Description
                   (AB018441) phi-1 [Nicotiana tabacum]
                   5881
Seq. No.
                   5568 1.R1040
Contig ID
5'-most EST
                   LIB3028-010-Q1-B1-B2
                   5882
Seq. No.
Contig ID
                   5570 1.R1040
5'-most EST
                   LIB3028-010-Q1-B1-B4
Method
                   BLASTX
                   g1168750
NCBI GI
BLAST score
                   269
```

2.0e-23

E value

```
157
Match length
                    38
% identity
                    CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY
NCBI Description
                    SUBUNIT) >gi 458230 (U04380) calcineurin B [Naegleria
                    gruberi]
                    5883
Seq. No.
                    5573 1.R1040
Contig ID
5'-most EST
                    ncj7\overline{0}0983528.h1
Method
                    BLASTX
                    q557882
NCBI GI
BLAST score
                    361
                    5.0e-34
E value
                    183
Match length
                    45
% identity
                    (U13923) putative serine/threonine protein kinase; similar
NCBI Description
                    to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of
                     the Pto gene family [Solanum pimpinellifolium] >gi_1809263
                     (U59317) serine/threonine protein kinase Fen [Lycopersicon
                    pimpinellifolium] >gi_1096880_prf__2112354B Fen gene [Lycopersicon esculentum] >gi_1098334_prf__2115395A Fen
                     gene [Lycopersicon esculentum]
                     5884
Seq. No.
                     5573 2.R1040
Contig ID
5'-most EST
                     zsq7\overline{0}1127563.h1
                     5885
Seq. No.
                     5575 1.R1040
Contig ID
                     uC-qmropic090e01b1
5'-most EST
                     5886
Seq. No.
                     5576 1.R1040
Contig ID
                     zzp700831186.hl
5'-most EST
                     BLASTX
Method
                     g2501102
NCBI GI
BLAST score
                     212
                     6.0e-17
E value
                     100
Match length
                     49
% identity
                     SYNTAXIN-RELATED PROTEIN KNOLLE >gi_1184165 (U39451)
NCBI Description
                     syntaxin-related [Arabidopsis thaliana] >gi_1184167
                     (U39452) syntaxin-related [Arabidopsis thaliana]
                     >gi_3063443 (AC003981) F22013.4 [Arabidopsis thaliana]
                     >gi_1587182_prf__2206310A syntaxin-related protein
                     [Arabidopsis thaliana]
                     5887
Seq. No.
                     5577 1.R1040
Contig ID
                     LIB3\overline{0}28-010-Q1-B1-E1
5'-most EST
                     BLASTX
Method
                     q4204315
NCBI GI
BLAST score
                     404
E value
                     9.0e-42
                     148
Match length
                     59
% identity
```

Contig ID

```
NCBI Description
                  (AC003027) Unknown protein [Arabidopsis thaliana]
                  5888
Seq. No.
                  5577 2.R1040
Contig ID
5'-most EST
                  LIB3138-015-Q1-N2-F2
                  BLASTX
Method
                  q4204315
NCBI GI
BLAST score
                  402
                  3.0e-39
E value
                  130
Match length
                                 潮凉。 。.
                  56
% identity
                  (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  5889
                  5577 3.R1040
Contig ID
5'-most EST
                  bth700848565.h1
                  BLASTX
Method
                  g4204315
NCBI GI
BLAST score
                  425
E value
                  7.0e-42
Match length
                  138
% identity
                  (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  5890
Seq. No.
                  5581 1.R1040
Contig ID
5'-most EST
                  LIB3106-063-Q1-K1-B8
                  BLASTX
Method
NCBI GI
                  g3323581
BLAST score
                  409
E value
                  6.0e-40
Match length
                  101
                  83
% identity
                   (AF057281) two-component response regulator homolog
NCBI Description
                   [Arabidopsis thaliana]
                  5891
Seq. No.
                  5581 3.R1040
Contig ID
5'-most EST
                  LIB3028-010-Q1-B1-E5
                  5892
Seq. No.
                  5586 1.R1040
Contig ID
5'-most EST
                  LIB3028-010-Q1-B1-G1
Method
                  BLASTX
NCBI GI
                  g4006827
BLAST score
                  433
E value
                  4.0e-43
Match length
                  193
                  47
% identity
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  5893
                  5588 1.R1040
Contig ID
5'-most EST
                  LIB3028-010-Q1-B1-G4
                  5894
Seq. No.
```

5589 1.R1040

```
LIB3028-010-Q1-B1-H1
5'-most EST
Method
                  BLASTX
                  g710626
NCBI GI
BLAST score
                  303
                  4.0e-27
E value
                  87
Match length
                  72
% identity
                  (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
NCBI Description
                  (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                  thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                  thaliana]
                  5895
Seq. No.
                  5591 1.R1040
Contig ID
                  LIB3094-054-Q1-K1-A3
5'-most EST
Method
                  BLASTX
                  q2764941
NCBI GI
BLAST score
                  323
                  1.0e-29
E value
                  89
Match length
                  61
% identity
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  5896
Seq. No.
                  5591 2.R1040
Contig ID
5'-most EST
                  LIB3094-078-Q1-K1-E1
Method
                  BLASTX
                  g2764941
NCBI GI
                  374
BLAST score
                  8.0e-36
E value
                  89
Match length
% identity
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
Seq. No.
                  5897
                  5592 1.R1040
Contig ID
                  LIB3028-010-Q1-B1-H4
5'-most EST
                  5898
Seq. No.
                  5593 1.R1040
Contig ID
                  LIB3028-011-Q1-B1-A1
5'-most EST
                  BLASTX
Method
                  g2244971
NCBI GI
                  166
BLAST score
                  3.0e-11
E value
                  39
Match length
                  77
% identity
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  5899
Seq. No.
```

5594 1.R1040

LIB3049-011-Q1-E1-B2

Contig ID

5'-most EST

```
5900
Seq. No.
                  5595 1.R1040
Contig ID
                  LIB3052-007-Q1-B1-A2
5'-most EST
                  5901
Seq. No.
                  5597 1.R1040
Contig ID
                  LIB3072-012-Q1-E1-G8
5'-most EST
                  BLASTX
Method
                  g2047324
NCBI GI
                  696
BLAST score
                  3.0e-73
E value
                  157
Match length
                  78
% identity
                 (U80192) HAL3 homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  5902
                  5597 2.R1040
Contig ID
                  LIB3051-028-Q1-K1-D1
5'-most EST
                  BLASTX
Method
                  q4106515
NCBI GI
                  648
BLAST score
                  1.0e-80
E value
Match length
                  183
% identity
                   (AF092743) CAK associated cyclinH homolog [Populus tremula
NCBI Description
                   x Populus tremuloides]
                   5903
Seq. No.
                   5597 3.R1040
Contig ID
                   LIB3093-058-Q1-K1-A11
5'-most EST
                   5904
Seq. No.
                   5597 4.R1040
Contig ID
                   LIB3109-047-Q1-K1-A10
5'-most EST
Seq. No.
                   5905
                   5597 5.R1040
Contig ID
                                                 g5126313
5'-most EST
Seq. No.
                   5906
                   5597 6.R1040
Contig ID
                   leu701147304.h1
5'-most EST
                   5907
Seq. No.
                   5597 7.R1040
Contig ID
                   LIB3093-012-Q1-K1-D9
5'-most EST
                   BLASTX
Method
                   g549706
NCBI GI
                   193
BLAST score
                   2.0e-14
E value
                   113
Match length
                   36
% identity
                   KTI12 PROTEIN >gi 539197 pir__S37937 KTI12 protein - yeast
NCBI Description
                   (Saccharomyces cerevisiae) >gi_486185_emb_CAA81950_
                   (Z28110) ORF YKL110c [Saccharomyces cerevisiae]
                   >gi_536816_emb_CAA54646_ (X77511) KTI12 [Saccharomyces
```

cerevisiae]

```
5908
Seq. No.
                   5597 8.R1040
Contig ID
                   yza700764032.h1
5'-most EST
                   5909
Seq. No.
                   5597 9.R1040
Contig ID
                   zsg701129470.hl
5'-most EST
                   BLASTN
Method
                   g4519195
NCBI GI
BLAST score
                   36
                   2.0e-10
E value
                   172
Match length
                   85
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MQC12, complete sequence
                   5910
Seq. No.
                   5597 11.R1040
Contig ID
                   LIB3050-020-Q1-K1-C4
5'-most EST
                   5911
Seq. No.
                   5597_12.R1040
Contig ID
                   uC-gmrominsoy201a07b1
5'-most EST
                   5912
Seq. No.
                   5597 14.R1040
Contig ID
                   uaw700661065.hl
5'-most EST
                   5913
Seq. No.
                   5597 20.R1040
Contig ID
                   dpv701098531.h1
5'-most EST
                   5914
Seq. No.
                   5597 21.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0979023.h1
Seq. No.
                   5915
Contig ID
                   5603 1.R1040
                   gsv701055160.hl
5'-most EST
                   5916
Seq. No.
                   5605 1.R1040
Contig ID
                   LIB3028-012-Q1-B1-A1
5'-most EST
                   5917
Seq. No.
                   5608 1.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0981742.h1
Method
                   BLASTX
NCBI GI
                   g2497702
                   137
BLAST score
                   8.0e-15
E value
                   118
Match length
                   47
% identity
                   OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR
NCBI Description
                   >gi_2121019_pir__I40710 outer membrane lipoprotein -
```

Citrobacter freundii >gi_717136 (U21727) lipocalin

precursor [Citrobacter freundii] 5918 Seq. No. 5611 1.R1040 Contig ID $ncj7\overline{0}0988402.h1$ 5'-most EST BLASTX Method g3115204 NCBI GI 334 BLAST score 2.0e-30 E value 304 Match length 22 % identity (Y12059) strong homology to human RING3 sequence [Homo NCBI Description sapiens] 5919 Seq. No. 5611 2.R1040 Contig ID q5677950 5'-most EST 5920 Seq. No. 5611 3.R1040 Contig ID LIB3092-030-Q1-K1-G11 5'-most EST 5921 Seq. No. 5612 1.R1040 Contig ID zhf700958085.h1 5'-most EST 5922 Seq. No. Contig ID 5613 1.R1040 LIB3028-013-Q1-B1-B7 5'-most EST BLASTX Method g4467146 NCBI GI 679 BLAST score 3.0e-71 E value Match length 254 53 % identity (AL035540) galactosidase like protein [Arabidopsis NCBI Description thaliana] 5923 Seq. No. 5615 1.R1040 Contig ID $k117\overline{0}1215452.h1$ 5'-most EST BLASTX Method q3334320 NCBI GI. 1131 BLAST score 1.0e-124 E value 273 Match length 80 % identity 40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) NCBI Description ribosome-associated protein p40 [GTycine max] 5924 Seq. No. 5617 1.R1040 Contig ID jC-gmro02910065c04d1 5'-most EST BLASTX Method

g4572673

2.0e-56

551

NCBI GI

E value

BLAST score

5'-most EST

```
Match length
                  182
                  54
% identity
                  (AC006954) putative sarcosine oxidase [Arabidopsis
NCBI Description
                 thaliana]
                  5925
Seq. No.
                  5618 1.R1040
Contig ID
                 rry700808482.h1
5'-most EST
                 BLASTX
Method
                  g4263787
NCBI GI
BLAST score
                  405
                  2.0e-39
E value
                  120
Match length
                  72
% identity
                  (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
                . 5926
Seq. No.
                  5623 1.R1040
Contig ID
                  uaw700661344.h1
5'-most EST
                  BLASTX
Method
                  g4098678
NCBI GI
                  300
BLAST score
E value
                  2.0e-26
                  305
Match length
                  19
% identity
                  (U80821) C1 transcription factor [Mus musculus]
NCBI Description
Seq. No.
                  5927
Contig ID
                  5624 1.R1040
                  art700605411.h2
5'-most EST
                  BLASTX
Method
                  q730165
NCBI GI
                  248
BLAST score
                  8.0e-21
E value
                  80
Match length
                  60
% identity
                  EARLY NODULIN 93 (N-93) >gi_486679_pir__S34801 nodulin
NCBI Description
                  (clone GmN93) - soybean >gi_218262_dbj_BAA02724_ (D13506)
                  early nodulin [Glycine max] >gi_3763851_dbj_BAA33816_
                  (AB018378) early nodulin [Glycine max]
                  5928
Seq. No.
Contig ID
                  5628 1.R1040
                  LIB3028-014-Q1-B1-C4
5'-most EST
                  BLASTX
Method
                  g418754
NCBI GI
                  224
BLAST score
E value
                  4.0e-18
                  110
Match length
                  48
% identity
                  catechol oxidase (EC 1.10.3.1) precursor - fava bean
NCBI Description
                  5929
Seq. No.
                  5629 1.R1040
Contig ID
```

LIB3028-014-Q1-B1-D12

```
5930
Seq. No.
                   5629 2.R1040
Contig ID
                   sat701014978.hl
5'-most EST
                   5931
Seq. No.
                   5633 1.R1040
Contig ID
                  LIB3028-014-Q1-B1-F12
5'-most EST
                   BLASTX
Method
                   g4336205
NCBI GI
                  . 359
BLAST score
                   9.0e-34
E value
Match length
                   191
                   42
% identity
                   (AF077372) cytochrome b5 reductase [Zea mays]
NCBI Description
                   5932
Seq. No.
                   5633 2.R1040
Contig ID
5'-most EST
                   LIB3040-020-Q1-E1-H2
Seq. No.
                   5933
                   5641 1.R1040
Contig ID
                   kl1701209531.hl
5'-most EST
                   5934
Seq. No.
                   5641 2.R1040
Contig ID
                   LIB3028-016-Q1-B1-D4
5'-most EST
                   5935
Seq. No.
Contig ID
                   5641 3.R1040
                   sat701002867.h1
5'-most EST
                   5936
Seq. No.
                   5641 4.R1040
Contig ID
5'-most EST
                   epx701109189.h1
                   5937
Seq. No.
                   5642 1.R1040
Contig ID
                   pmv700892068.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4056432
BLAST score
                   714
                   3.0e-75
E value
Match length
                   221
% identity
                   (AC005990) Similar to gi 2245014 glucosyltransferase
NCBI Description
                   homolog from Arabidopsis thaliana chromosome 4 contig
                   gb\_Z97341. ESTs gb\_T20778 and gb\_AA586281 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   5938
                   5642 2.R1040
Contig ID
                   hyd700726120.h1
5'-most EST
Method
                   BLASTX
                   g4263795
NCBI GI
                   389
BLAST score
                   1.0e-37
E value
```

Match length

Method

NCBI GI

BLASTX

q3885338

```
59
% identity
                  (AC006068) putative glucosyltransferase [Arabidopsis
NCBI Description
                  5939
Seq. No.
                  5644 1.R1040
Contig ID
                  LIB3028-016-Q1-B1-H3
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3123295
                  383
BLAST score
                  1.0e-36
E value
                  136
Match length
                  39
% identity
                  CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169
NCBI Description
                   (AF026473) calmodulin-related protein [Arabidopsis
                  thaliana]
                  5940
Seq. No.
                  5648 1.R1040
Contig ID
5'-most EST
                  LIB3028-047-Q1-B1-G10
                  BLASTX
Method
                  g4567260
NCBI GI
                  740
BLAST score
                  1.0e-78
E value
Match length
                  166
% identity
                   (AC006841) putative NADPH dependent mannose 6-phosphate
NCBI Description
                  reductase [Arabidopsis thaliana]
                  5941
Seq. No.
                  5648 2.R1040
Contig ID
                  LIB3167-049-P1-K1-H1
5'-most EST
                  BLASTX
Method
                  g4567260
NCBI GI
                  383
BLAST score
                   2.0e-65
E value
Match length
                  163
% identity
                   (AC006841) putative NADPH dependent mannose 6-phosphate
NCBI Description
                   reductase [Arabidopsis thaliana]
                   5942
Seq. No.
                   5649 1.R1040
Contig ID
                   pmv700894289.h1
5'-most EST
                   BLASTN
Method
                   g3021347
NCBI GI
BLAST score
                   160
                   2.0e-84
E value
                   555
Match length
                   83
% identity
                  Cicer arietinum mRNA for cytoplasmic ribosomal protein L18
NCBI Description
                   5943
Seq. No.
Contig ID
                   5651 1.R1040
                   q4395973
5'-most EST
```

5'-most EST

```
BLAST score
                  179
                   1.0e-12
E value
Match length
                   168
% identity
                   27
                   (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   5944
                   5651 2.R1040
Contig ID
                   LIB3051-025-Q1-K1-D8
5'-most EST
                   5945
Seq. No.
Contig ID
                   5652 1.R1040
                   LIB3028-018-Q1-B1-A11
5'-most EST
Seq. No.
                   5946
Contig ID
                   5653 1.R1040
                   jC-gmro02800031d05d1
5'-most EST
                   5947
Seq. No.
Contig ID
                   5657 1.R1040
5'-most EST
                   LIB3107-079-Q1-K1-F10
                   BLASTX
Method
NCBI GI
                   g2388585
BLAST score
                   521
E value
                   7.0e-53
Match length
                   127
                   80
% identity
                   (AC000098) Similar to Caenorhabditis unknown protein
NCBI Description
                   T03F1.1 (gb U88169). [Arabidopsis thaliana]
Seq. No.
                   5948
                   5658 1.R1040
Contig ID
5'-most EST
                   epx701105396.h1
                   BLASTX
Method
NCBI GI
                   g1762945
BLAST score
                   389
E value
                   3.0e-37
Match length
                   138
% identity
                   54
NCBI Description
                   (U66269) ORF;
                                  able to induce HR-like lesions [Nicotiana
                   tabacum]
                   5949
Seq. No.
                   5658 2.R1040
Contig ID
5'-most EST
                   q5677292
Method
                   BLASTX
                   g1762945
NCBI GI
BLAST score
                   209
E value
                   5.0e-35
Match length
                   107
                   70
% identity
                   (U66269) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                   tabacum]
                   5950
Seq. No.
Contig ID
                   5659 1.R1040
```

LIB3106-037-Q1-K1-C9

```
BLASTX
Method
                   g2499966
NCBI GI
                   347
BLAST score
                   2.0e-32
E value
Match length
                   123
                   65
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E
NCBI Description
                   A) >gi 632722 bbs_151001 (S72356) photosystem I subunit
                   PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,
 C. 36. 3.
                   141 aa] [Nicotiana sylvestris]
                   5951
Seq. No.
                   5659 2.R1040
Contig ID
                   LIB3028-047-Q1-B1-A12
5'-most EST
                   5952
Seq. No.
                   5666 1.R1040
Contig ID
                   LIB3\overline{0}51-077-Q1-K1-F6
5'-most EST
                   BLASTX
Method
                   q1808656
NCBI GI
                   1298
BLAST score
                   1.0e-143
E value
                   285
Match length
% identity
                   (Y10804) Ubiquitin activating enzyme El [Nicotiana tabacum]
NCBI Description
                   5953
Seq. No.
                   5666 2.R1040
Contig ID
                   pmv7\overline{0}0892693.h1
5'-most EST
                   BLASTX
Method
                   g1808656
NCBI GI
BLAST score
                   654
E value
                   1.0e-112
                   247
Match length
                   80
% identity
                   (Y10804) Ubiquitin activating enzyme El [Nicotiana tabacum]
NCBI Description
                   5954
Seq. No.
                   5669 1.R1040
Contig ID
5'-most EST
                   LIB3170-043-Q1-J1-B10
Method
                   BLASTX
                   q2739370
NCBI GI
BLAST score
                   538
                   6.0e-55
E value
                   163
Match length
% identity
                   (AC002505) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                   5955
Seq. No.
Contig ID
                   5671_1.R1040
                   LIB3065-022-Q1-N1-H5
5'-most EST
                   BLASTX
Method
                   g4539459
NCBI GI
                   658
BLAST score
                   2.0e-68
E value
```

44

Match length % identity

```
(AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                  5956
Seq. No.
Contig ID
                  5673 1.R1040
                  q4286504
5'-most EST
Method
                  BLASTX
                  g2494222
NCBI GI
                  344
BLAST score
E value
                  5.0e-32
                  83
Match length
                  72
% identity
                  PROBABLE DYNEIN LIGHT CHAIN 1; CYTOPLASMIC >gi_470344
NCBI Description
                   (U00043) No definition line found [Caenorhabditis elegans]
Seq. No.
                  5957
                  5673 3.R1040
Contig ID
5'-most EST
                  jC-gmst02400073g05a1
                  BLASTX
Method
NCBI GI
                  g2494222
BLAST score
                  240
E value
                  2.0e-20
                  60
Match length
                  70
% identity
                  PROBABLE DYNEIN LIGHT CHAIN 1, CYTOPLASMIC >gi_470344
NCBI Description
                   (U00043) No definition line found [Caenorhabditis elegans]
Seq. No.
                  5958
                  5674 1.R1040
Contig ID
                  LIB3107-021-Q1-K1-D6
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4432857
BLAST score
                   380
                   3.0e-36
E value
                  141
Match length
                  52
% identity
                  (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  5959
                  5674 2.R1040
Contig ID
5'-most EST
                  fde700876268.hl
                  5960
Seq. No.
Contig ID
                  5675 1.R1040
5'-most EST
                  jC-gmf102220080b08d1
                   5961
Seq. No.
                   5679_1.R1040
Contig ID
5'-most EST
                  uC-gmropic047h01b1
                  BLASTX
Method
                  g4567247
NCBI GI
BLAST score
                   727
E value
                  1.0e-76
Match length
                  335
% identity
                   42
                   (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

```
5679 3.R1040
Contig ID
                   leu7\overline{0}1150389.h1
5'-most EST
                  5963
Seq. No.
                  5680 1.R1040
Contig ID
                  ssr700554933.hl
5'-most EST
                   5964
Seq. No.
                   5684 1.R1040
Contig ID
                  LIB3030-009-Q1-B1-H11
5'-most EST
                  BLASTX
Method
                   g2914700
NCBI GI
                   786
BLAST score
                   1.0e-83
E value
Match length
                   277
% identity
                   (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                   thaliana]
                   5965
Seq. No.
                   5685 1.R1040
Contig ID
                   LIB3170-070-Q1-J1-H10
5'-most EST
                   5966
Seq. No.
                   5686 1.R1040
Contig ID
                   txt700736063.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q118507
BLAST score
                   699
                   2.0e-73
E value
                   309
Match length
                   46
% identity
                   ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (CLASS 3)
NCBI Description
                   (TUMOR-ASSOCIATED ALDEHYDE DEHYDROGENASE) (HTC-ALDH)
                   >gi_91936_pir__A30149 aldehyde dehydrogenase (NADP+) (EC
                   1.2.1.4) 3, tumor-associated - rat >gi_202833 (J03637)
                   aldehyde dehydrogenase [Rattus norvegicus]
                   5967
Seq. No.
                   5688 1.R1040
Contig ID
                   LIB3028-021-Q1-B1-H4
5'-most EST
                   5968
Seq. No.
                   5696 1.R1040
Contig ID
                   leu701152149.h1
5'-most EST
                   BLASTX
Method
                   g2739044
NCBI GI
BLAST score
                   1226
                   1.0e-135
E value
Match length
                   321
                   70
% identity
                   (AF024651) polyphosphoinositide binding protein Ssh1p
NCBI Description
                   [Glycine max]
                   5969
Seq. No.
                   5696 2.R1040
Contig ID
```

g5753550

5'-most EST

```
BLASTX
Method
                   g2739044
NCBI GI
BLAST score
                   373
                   1.0e-35
E value
Match length
                   108
% identity
                   65
                   (AF024651) polyphosphoinositide binding protein Sshlp
NCBI Description
                   [Glycine max]
                   5970
Seq. No.
                   5697 1.R1040
Contig ID
5'-most EST
                   vwf700678766.hl
                   5971
Seq. No.
                   5698 1.R1040
Contig ID
                   LIB3049-019-Q1-E1-A6
5'-most EST
                   BLASTX
Method
                   g1001607
NCBI GI
                   290
BLAST score
                   2.0e-25
E value
Match length
                   136
                   39
% identity
                  (D64000) hypothetical protein [Synechocystis sp.]
NCBI Description
                   5972
Seq. No.
                   5698 2.R1040
Contig ID
                   LIB3139-033-P1-N1-D8
5'-most EST
                   5973
Seq. No.
                   5700 1.R1040
Contig ID
                   LIB3028-023-Q1-B1-E8
5'-most EST
                   5974.
Seq. No.
Contig ID
                   5704 1.R1040
                   LIB3\overline{0}56-009-Q1-N1-B6
5'-most EST
                   BLASTX
Method
                   g1916613
NCBI GI
BLAST score
                   232
E value
                   8.0e-19
Match length
                   175
% identity
                   37
                   (U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]
NCBI Description
                   5975
Seq. No.
                   5710 1.R1040
Contig ID
                   LIB3028-025-Q1-B1-B11
5'-most EST
                   5976
Seq. No.
Contig ID
                   5718 1.R1040
                   jC-gmf102220130d06d1
5'-most EST
                   5977
Seq. No.
                   5729 1.R1040
Contig ID
                   fde7\overline{0}0876539.h1
5'-most EST
                   BLASTX
Method
                   g2271477
NCBI GI
```

BLAST score

Contig ID

```
2.0e-42
E value
Match length
                   85
                   95
% identity
NCBI Description
                   (AF009631) AP47/50p [Arabidopsis thaliana]
Seq. No.
                   5732 1.R1040
Contig ID
5'-most EST
                   LIB3170-042-Q1-J1-C10
                   BLASTN
Method
                   g4263694
NCBI GI
                   51
BLAST score
                   9.0e-20
E value
Match length
                   135
% identity
                   Arabidopsis thaliana chromosome II BAC F22D22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
Contig ID
                   5732 2.R1040
                   taw700658026.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4263711
                   522
BLAST score
E value
                   3.0e-53
Match length
                   114
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   5980
Seq. No.
                   5735 1.R1040
Contig ID
5'-most EST
                   wvk700683896.h1
                   BLASTX
Method
                   q1076579
NCBI GI
BLAST score
                   676
                   3.0e-71
E value
                   167
Match length
% identity
                   alcohol dehydrogenase homolog ADH3a - tomato
NCBI Description
                   5981
Seq. No.
Contig ID
                   5736 1.R1040
                   dpv701102630.h1
5'-most EST
                   BLASTX
Method
                   q2245127
NCBI GI
BLAST score
                   166
                   1.0e-11
E value
                   74
Match length
                   47
% identity
                   (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   5982
Seq. No.
                   5740 1.R1040
Contig ID
                   vwf700676662.h1
5'-most EST
                   5983
Seq. No.
```

5752 1.R1040

% identity

32

```
5'-most EST
                  LIB3170-076-Q1-J1-A10
                  5984
Seq. No.
Contig ID
                  5755 1.R1040
5'-most EST
                  uC-gmflminsoy076f04b1
                  BLASTX
Method
                  g4508068
NCBI GI
BLAST score
                  250
                  1.0e-20
E value
                  151
Match length
                  42
% identity
                  (AC005882) 3063 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  5756 1.R1040
Contig ID
                  jC-gmf102220075f08d1
5'-most EST
                  BLASTN
Method
                  g1841474
NCBI GI
BLAST score
                  38
                  6.0e-12
E value
                  64
Match length
                  91
% identity
                  P.sativum mRNA for Myb-like protein (Myb26)
NCBI Description
                  5986
Seq. No.
                  5763 1.R1040
Contig ID
                  LIB3028-039-Q1-B1-B5
5'-most EST
Seq. No.
                  5987
Contig ID
                  5763 2.R1040
                  LIB3107-080-Q1-K1-D1
5'-most EST
                  5988
Seq. No.
                   5763 3.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy115g03b1
                   5989
Seq. No.
                   5777 1.R1040
Contig ID
                  LIB3028-040-Q1-B1-H4
5'-most EST
                  BLASTX
Method
                  g4490752
NCBI GI
BLAST score
                   580
                   8.0e-60
E value
                   134
Match length
% identity
                   78
                   (AL035708) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   5990
Seq. No.
                   5780 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir015c09b1
                   BLASTX
Method
NCBI GI
                   q4512625
BLAST score
                   293
E value
                   5.0e-26
Match length
                   236
```

estate.

```
(AC004793) ESTs qb T20423, qb AA712864, gb H76323 and
NCBI Description
                   gb Z25560 come from this gene. [Arabidopsis thaliana]
Seq. No.
Contig ID
                   5784 1.R1040
                   LIB3028-041-Q1-B1-F12
5'-most EST
                   BLASTX
Method
                   q3258637
NCBI GI
BLAST score
                   537
                   7.0e-55
E value
Match length
                   145
% identity
                   70
                   (AF041050) 4-coumarate:CoA ligase [Populus tremuloides]
NCBI Description
                   5992
Seq. No.
                   5786 1.R1040
Contig ID
                   zpv700763688.hl
5'-most EST
                   5993
Seq. No.
                   5787 1.R1040
Contig ID
                   trc700562171.hl .
5'-most EST
                   BLASTX
Method
                   g4544389
NCBI GI
                   708
BLAST score
                   2.0e-74
E value
                   381
Match length
% identity
                   46
                   (AC007047) putative homeodomain protein [Arabidopsis
NCBI Description
                   thaliana]
                   5994
Seq. No.
                   5791 1.R1040
Contig ID
                   zzp700832642.h1
5'-most EST
                   BLASTX
Method
                   g1085002
NCBI GI
BLAST score
                   552
                   4.0e-56
E value
Match length
                   295
                   42
% identity
                   mitochondrial carrier protein DIF-1 homolog -
NCBI Description
                   Caenorhabditis elegans >gi_472902_emb_CAA53721_ (X76115)
                   carrier protein (c1) [Caenorhabditis elegans]
                   >gi 829102 emb_CAA88283_ (Z48240) DIF-1 [Caenorhabditis
                   elegans]
                   5995
Seq. No.
                   5791 2.R1040
Contig ID
                   LIB3\overline{1}07-061-Q1-K1-G9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1085002
                   179
BLAST score
                   6.0e-13
E value
                   58
Match length
                   53
% identity
                   mitochondrial carrier protein DIF-1 homolog -
NCBI Description '
                   Caenorhabditis elegans >gi_472902_emb_CAA53721_ (X76115)
```

carrier protein (c1) [Caenorhabditis elegans]

```
elegans]
Seq. No.
                   5996
Contig ID
                   5791 4.R1040
5'-most EST
                  rlr700895682.h1
Seq. No.
                   5997
                   5791 5.R1040
Contig ID
                  bth700849349.h1
5'-most EST
                   5998
Seq. No.
Contig ID
                   5792 1.R1040
5'-most EST
                  LIB3028-042-Q1-B1-H12
                   5999
Seq. No.
Contig ID
                   5795 1.R1040
5'-most EST
                   ssr700555019.hl
                   6000
Seq. No.
                   5797 1.R1040
Contig ID
5'-most EST
                   hyd7\overline{0}0726496.h1
                   BLASTX
Method
NCBI GI
                   g3831441
BLAST score
                   179
                   3.0e-12
E value
                   47
Match length
% identity
NCBI Description
                   (AC005819) hypothetical protein [Arabidopsis thaliana]
                   6001
Seq. No.
                   5797 2.R1040
Contig ID
5'-most EST
                   jC-qmf102220073f08d1
Seq. No.
                   6002
                   5798 1.R1040
Contig ID
5'-most EST
                   g4291359
                   BLASTX
Method
NCBI GI
                   q3335375
BLAST score
                   222
E value
                   1.0e-17
Match length
                   89
% identity
                   (AC003028) putative amidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6003
                   5804 1.R1040
Contig ID
                   LIB3074-028-Q1-K1-F10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4104816
                   505
BLAST score
                   6.0e-51
E value
Match length
                   136
% identity
                   (AF039662) ferredoxin-like protein [Capsicum annuum]
NCBI Description
                   6004
Seq. No.
```

>gi 829102 emb CAA88283 (Z48240) DIF-1 [Caenorhabditis

% identity

```
5804 2.R1040
Contig ID
                   LIB3106-014-Q1-K1-B6
5'-most EST
                   BLASTX
Method
                   g4104816
NCBI GI
BLAST score
                   473
                   2.0e-47
E value
                   130
Match length
                   68
% identity
                  (AF039662) ferredoxin-like protein [Capsicum annuum]
NCBI Description
                   6005
Seq. No.
                   5804 3.R1040
Contig ID
                   LIB3106-092-Q1-K1-B12
5'-most EST
                   BLASTX
Method
                   g3023752
NCBI GI
                   437
BLAST score
                   3.0e-43
E value
Match length
                   114
                   71
% identity
                   FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520)
NCBI Description
                   ferredoxin-I [Lycopersicon esculentum]
                   6006
Seq. No.
                   5804 4.R1040
Contig ID
                   LIB3\overline{0}93-006-Q1-K1-A2
5'-most EST
                   BLASTX
Method
                   q1834353
NCBI GI
BLAST score
                   213
                   9.0e-17
E value
Match length
                   67
                   57
% identity
                   (Y10986) hypothetical protein 194 [Arabidopsis thaliana]
NCBI Description
                   6007
Seq. No.
                   5804 6.R1040
Contig ID
                   LIB3051-014-Q1-E1-F9
5'-most EST
                   BLASTX
Method
                   g1834353
NCBI GI
BLAST score
                   215
                   6.0e-17
E value
                   245
Match length
                   29
% identity
                   (Y10986) hypothetical protein 194 [Arabidopsis thaliana]
NCBI Description
                   6008
Seq. No.
                   5808 1.R1040
Contig ID
                   LIB3028-045-Q1-B1-D2
5'-most EST
                   6009
Seq. No.
                   5809 1.R1040
Contig ID
5'-most EST
                   LIB3092-037-Q1-K1-D11
                   BLASTX
Method
                   g2829897
NCBI GI
BLAST score
                   201
E value
                   3.0e-15
                   141
Match length
                   31
```

```
(AC002311) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   6010
Seq. No.
                   5809 2.R1040
Contig ID
                  uxk7\overline{0}0670728.h1
5'-most EST
                   6011
Seq. No.
                   5809 3.R1040
Contig ID
                   LIB3107-063-Q1-K1-D6
5'-most EST
                   BLASTX
Method
                   g2829897
NCBI GI
                   273
BLAST score
                   8.0e-24
E value
                   91
Match length
                   66
% identity
                   (AC002311) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6012
                   5811 1.R1040
Contig ID
                   jC-qmst02400065e04a2
5'-most EST
                   BLASTX
Method
                   g3288809
NCBI GI
                   259
BLAST score
                   9.0e-22
E value
                   150
Match length
                   43
% identity
                   (AF013169) beta-glucosidase [Pyrococcus furiosus]
NCBI Description
Seq. No.
                   6013
                   5812 1.R1040
Contig ID
                   jC-qmle01810021e01d1
5'-most EST
                   BLASTX
Method
                   g3142294
NCBI GI
                   423
BLAST score
                   2.0e-41
E value
                   93
Match length
                   87
% identity
                   (AC002411) Strong similarity to initiation factor eIF-2,
NCBI Description
                   gb U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and
                   gb_N37529 come from this gene. [Arabidopsis thaliana]
                   6014
Seq. No.
                   5816 1.R1040
Contig. ID
                   jC-qmf102220056b06d1
5'-most EST
                   6015
Seq. No.
                   5818 1.R1040
Contig ID
                   ncj700980756.hl
5'-most EST
                   6016
Seq. No.
                   5819 1.R1040
Contig ID
                   LIB3028-047-Q1-B1-A9
5'-most EST
                   6017
Seq. No.
                   5822 2.R1040
Contig ID
                   LIB3039-052-Q1-E1-H8
5'-most EST
```

BLASTX

Method

NCBI GI

```
NCBI GI
                   q3023637
BLAST score
                   315
                   1.0e-28
E value
Match length
                   132
% identity
                   45
                   PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN
NCBI Description
                   8) >gi 1362899 pir A56236 probable RNA helicase 1 - human
                   >gi 807817 dbj BAA09078 (D50487) RNA helicase (HRH1) [Homo
                   sapiens]
                   6018
Seq. No.
Contig ID
                   5822 3.R1040
5'-most EST
                   LIB3094-062-Q1-K1-F2
                   6019
Seq. No.
                   5827 1.R1040
Contig ID
5'-most EST
                   g4304284
Seq. No.
                   6020
                   5829 1.R1040
Contig ID
                   k11701203595.h2
5'-most EST
Method
                   BLASTN
                   q1553130
NCBI GI
BLAST score
                   153
                   2.0e-80
E value
Match length
                   321
                   87
% identity
                   Gossypium hirsutum ribosomal protein L44 isoform b (RL44),
NCBI Description
                   complete cds
                   6021
Seq. No.
                   5833 1.R1040
Contig ID
                   uxk700673268.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4454032
BLAST score
                   795
                   1.0e-84
E value
                   254
Match length
                   63
% identity
NCBI Description
                   (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                   6022
Contig ID
                   5833 2.R1040
5'-most EST
                   jC-gmst02400036b04d2
                   BLASTX
Method
NCBI GI
                   q4454032
BLAST score
                   272
E value
                   7.0e-24
Match length
                   75
% identity
NCBI Description
                   (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                   6023
Contig ID
                   5833 3.R1040
5'-most EST
                   LIB3170-068-Q1-K1-F2
Method
                   BLASTX
```

g4454032

*3*5.

```
., ;;,,,,
BLAST score
                   209
E value
                   1.0e-16
Match length
                   66
% identity
                   (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6024
Contig ID
                   5845 1.R1040
5'-most EST
                   LIB3028-051-Q1-B1-D6
                   6025
Seq. No.
Contig ID
                   5851 1.R1040
5'-most EST
                   LIB3028-054-Q1-B1-G5
                   BLASTX
Method
NCBI GI
                   q4218120
BLAST score
                   368
E value
                   2.0e-35
Match length
                   83
% identity
                   84
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                   thalianal
Seq. No.
                   6026
Contig ID
                   5851 2.R1040
5'-most EST
                   leu7\overline{0}1155555.h1
                   BLASTX
Method
NCBI GI
                   q4218120
BLAST score
                   188
E value
                   2.0e-14
Match length
                   36
                   97
% identity
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   6027
Seq. No.
Contig ID
                   5859 1.R1040
5'-most EST
                   jC-gmro02910063g01a1
Method
                   BLASTX
NCBI GI
                   g3386621
BLAST score
                   868
E value
                   3.0e-93
Match length
                   224
% identity
                   74
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6028
                   5859 2.R1040
Contig ID
                   kmv700737755.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3386621
                   700
BLAST score
                   6.0e-74
E value
Match length
                   156
% identity
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
```

6029

Seq. No.

Contig ID

```
Contig ID
                   5859 3.R1040
5'-most EST
                   LIB3092-052-Q1-K1-C11
Method
                   BLASTX
NCBI GI
                   g3386621
BLAST score
                   552
                   1.0e-56
E value
                   127
Match length
% identity
                   83
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6030
                   5859 4.R1040
Contig ID
5'-most EST
                   g4290314
                   BLASTX
Method
NCBI GI
                   g3386621
BLAST score
                   536
E value
                   1.0e-54
Match length
                   162
                   67
% identity
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6031
Contig ID
                   5865 1.R1040
                   LIB3029-002-Q1-B1-C5
5'-most EST
                   6032
Seq. No.
                   5865 2.R1040
Contig ID
5'-most EST
                   epx701105279.hl
                   6033
Seq. No.
                   5867 1.R1040
Contig ID
5'-most EST
                   LIB3051-068-Q1-K1-G11
Method
                   BLASTX
NCBI GI
                   g1350707
BLAST score
                   212
                   9.0e-17
E value
                   52
Match length
                   73
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L29 >gi 539923 pir JC2012 ribosomal
                   protein 17K - mouse >gi 404766 (L08651) ribosomal protein
                   [Mus musculus]
                   6034
Seq. No.
                   5867 2.R1040
Contig ID
5'-most EST
                   g4395651
Method
                   BLASTX
NCBI GI
                   g1350707
BLAST score
                   212
                   6.0e-17
E value
Match length
                   52
                   73
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L29 >gi 539923 pir JC2012 ribosomal
                   protein 17K - mouse >gi 40476\overline{6} (L086\overline{5}1) \overline{ribosomal} protein
                   [Mus musculus]
                   6035
Seq. No.
```

5869 1.R1040

```
ssr700557855.hl
5'-most EST
                   6036
Seq. No.
                   5874 1.R1040
Contig ID
                   LIB3087-001-Q1-K1-D3
5'-most EST
                   BLASTX
Method
                   g2435511
NCBI GI
                   337
BLAST score
                   2.0e-31
E value
Match length
                   111
                   57
% identity
                   (AF024504) contains similarity to prolyl 4-hydroxylase
NCBI Description
                   alpha subunit [Arabidopsis thaliana]
Seq. No.
                   6037
Contig ID
                   5877 1.R1040
                   jC-gmle01810087g09a1
5'-most EST
Method
                   BLASTN
                   g2924257
NCBI GI
BLAST score
                   154
                   2.0e-80
E value
Match length
                   541
% identity
                   91
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
                   6038
                   5877 2.R1040
Contig ID
5'-most EST
                   awf700838734.hl
Method
                   BLASTN
                   g2924257
NCBI GI
                   146
BLAST score
                   4.0e-76
E value
                   380
Match length
% identity
                  Tobacco chloroplast genome DNA
NCBI Description
                   6039
Seq. No.
                   5877 3.R1040
Contig ID
5'-most EST
                   fde700872365.hl
Method
                   BLASTN
NCBI GI
                   g1143165
BLAST score
                   196
                   1.0e-106
E value
Match length
                   430
                   86
% identity
                  Nicotiana tabacum ClpP protease (ClpP) mRNA, chloroplast
NCBI Description
                   gene encoding chloroplast protein, complete cds
                   6040
Seq. No.
                   5878 1.R1040
Contig ID
                   epx701107225.h1
5'-most EST
Method
                  BLASTN
                   g18662
NCBI GI
BLAST score
                   359
                   0.0e + 00
E value
                   374
Match length
```

99

% identity

5'-most EST

```
NCBI Description Glycine max hsp 70 gene
Seq. No.
                   6041
                   5893 1.R1040
Contig ID
                  LIB3029-012-Q1-B1-D8
5'-most EST
                   6042
Seq. No.
                   5895 1.R1040
Contig ID
5'-most EST
                   fC-gmst700837068d1
                   6043
Seq. No.
Contig ID
                  5899 1.R1040
                  LIB3029-003-Q1-B1-H1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4432827
BLAST score
                   247
                   9.0e-21
E value
Match length
                   176
% identity
                   36
                   (AC006593) putative ADP-ribose polymerase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   6044
                   5900 1.R1040
Contig ID
                   uC-gmrominsoy065f11b1
5'-most EST
Method
                  BLASTX
                   g1685005
NCBI GI
BLAST score
                   296
E value
                   1.0e-26
Match length
                   121
% identity
                   46
                   (U32644) immediate-early salicylate-induced
NCBI Description
                  glucosyltransferase [Nicotiana tabacum]
                   6045
Seq. No.
                   5906 1.R1040
Contig ID
                   jC-gmst02400029h05a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1707412
BLAST score
                  884
E value
                   5.0e-95
Match length
                   417
                   44
% identity
NCBI Description
                  (X95906) Cleavage and Polyadenylation Specifity Factor
                  protein [Bos taurus]
                   6046
Seq. No.
Contig ID
                   5917 1.R1040
5'-most EST
                   zsg701126164.hl
Seq. No.
                   6047
Contig ID
                   5917 2.R1040
                  LIB3029-011-Q1-B1-H5
5'-most EST
                   6048
Seq. No.
                  5925 1.R1040
Contig ID
```

LIB3029-012-Q1-B1-A6

E value

1.0e-67

```
Seq. No.
                   6049
Contig ID
                   5925 2.R1040
                   awf700836732.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g170005
BLAST score
                   75
E value
                   6.0e - 34
Match length
                   91
% identity
                   96
NCBI Description
                   Soybean lectin (Le1) gene, complete cds
Seq. No.
                   6050
Contig ID
                   5927 1.R1040
5'-most EST
                   uC-gmropic106c06b1
                   BLASTN
Method
NCBI GI
                   g1177602
BLAST score
                   576
E value
                   0.0e + 00
Match length
                   1016
                   89
% identity
                  P.sativum mRNA for pyruvate decarboxylase (PDC1)
NCBI Description
Seq. No.
                   6051
Contig ID
                   5927 2.R1040
5'-most EST
                   uC-gmropic088b10b1
Method
                   BLASTN
NCBI GI
                   q1177602
BLAST score
                   322
E value
                   0.0e + 00
Match length
                   693
% identity
                   P.sativum mRNA for pyruvate decarboxylase (PDC1)
NCBI Description
Seq. No.
                   6052
Contig ID
                   5930 1.R1040
5'-most EST
                   LIB3050-021-Q1-K1-B8
                   BLASTX
Method
NCBI GI
                   q3399767
BLAST score
                   160
E value
                   1.0e-10
Match length
                   112
                   29
% identity
NCBI Description
                   (U76298) uclacyanin I [Arabidopsis thaliana] >gi 3831466
                   (AC005700) uclacyanin I [Arabidopsis thaliana]
                   6053
Seq. No.
                   5930 2.R1040
Contig ID
5'-most EST
                   LIB3109-009-Q1-K1-C1
                   6054
Seq. No.
Contig ID
                   5933 1.R1040
5'-most EST
                   LIB3049-022-Q1-E1-G11
Method
                   BLASTX
NCBI GI
                   g1352681
BLAST score
                   648
```

```
174
Match length
% identity
                  PROTEIN PHOSPHATASE 2C (PP2C) >qi 1076391 pir S55457
NCBI Description
                  phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis
                   thaliana >gi_633028_dbj_BAA07287_ (D38109) protein
                   phosphatase 2C [Arabidopsis thaliana]
Seq. No.
                   5933 2.R1040
Contig ID
5'-most EST
                   LIB3170-059-Q1-J1-B3
Seq. No.
                   6056
Contig ID
                   5933 3.R1040
5'-most EST
                  hrw701059606.hl
Method
                   BLASTX
                   g1352681
NCBI GI
BLAST score
                   783
                   2.0e-83
E value
Match length
                   285
% identity
                  PROTEIN PHOSPHATASE 2C (PP2C) >gi 1076391 pir S55457
NCBI Description
                   phosphoprotein phosphatase (EC 3.\overline{1}.3.16) \overline{2}C - Arabidopsis
                   thaliana >gi 633028 dbj BAA07287 (D38109) protein
                   phosphatase 2C [Arabidopsis thaliana]
                   6057
Seq. No.
                   5933 4.R1040
Contig ID
5'-most EST
                   jC-gmro02910056a01a1
Method
                   BLASTX
NCBI GI
                   q1352681
BLAST score
                   362
                   3.0e-34
E value
Match length
                   165
% identity
NCBI Description
                  PROTEIN PHOSPHATASE 2C (PP2C) >qi 1076391 pir S55457
                   phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis
                  thaliana >gi 633028 dbj BAA07287 (D38109) protein
                  phosphatase 2C [Arabidopsis thaliana]
Seq. No.
                   6058
Contig ID
                   5936 1.R1040
5'-most EST
                   LIB3039-010-01-E1-H9
                   BLASTX
Method
NCBI GI
                   q4097587
BLAST score
                   293
E value
                   3.0e-26
Match length
                  88
% identity
NCBI Description
                   (U64926) NTGP5 [Nicotiana tabacum]
Seq. No.
                  -6059
Contig ID
                   5936 2.R1040
5'-most EST
                   uC-gmropic057f06b1
                   6060
Seq. No.
Contig ID
                   5936 3.R1040
```

jex700905711.h1

5'-most EST

```
Contig ID
                  leu7\overline{0}1144592.h1
5'-most EST
                  BLASTX
Method
                  g3687250
NCBI GI
BLAST score
                  907
                  5.0e-98
E value
                  208
Match length
% identity
                  (AC005169) putative arginine n-methyltransferase
NCBI Description
                  [Arabidopsis thaliana]
                  6062
Seq. No.
Contig ID
                  5938 1.R1040
                  uC-gmflminsoy047g04b1
5'-most EST
Method
                  BLASTX
                  g130720
NCBI GI
                  289
BLAST score
                  8.0e-26
E value
                  112
Match length
% identity
                  PROTEOLIPID PROTEIN PPA1 >gi_101508_pir__A34633 probable
NCBI Description
                  H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein
                  - yeast (Saccharomyces cerevisiae) >gi 172221 (M35294)
                  proteolipid protein of proton ATPase [Saccharomyces
                  cerevisiae] >gi_500700 (U10399) Ppalp: Proteolipid protein
                  of proton ATPase [Saccharomyces cerevisiae]
                  6063
Seq. No.
                  5938 2.R1040
Contig ID
                  q5605673
5'-most EST
Method
                  BLASTX
NCBI GI
                  g130720
                  267
BLAST score
                  4.0e-23
E value
                  108
Match length
% identity
                  PROTEOLIPID PROTEIN PPA1 >gi_101508_pir__A34633 probable
NCBI Description
                  H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein
                  - yeast (Saccharomyces cerevisiae) >gi 172221 (M35294)
                  proteolipid protein of proton ATPase [Saccharomyces
                  cerevisiae] >gi_500700 (U10399) Ppalp: Proteolipid protein
                  of proton ATPase [Saccharomyces cerevisiae]
                  6064
Seq. No.
                  5951 1.R1040
Contig ID
                  sat701008670.hl
5'-most EST
                  BLASTX
Method
                  g1174448
NCBI GI
                  599
BLAST score
                  7.0e-62
E value
                  222
Match length
% identity
                  TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
NCBI Description
                   (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
                   (SSR-ALPHA) >gi 547391 (L32016) alpha-subunit; putative
```

6061

5937 1.R1040

Seq. No.

[Arabidopsis thaliana]

```
6065
Seq. No.
                  5953 1.R1040
Contig ID
                  LIB3049-053-Q1-E1-E7
5'-most EST
                  BLASTX
Method
                  g3334323
NCBI GI
                  958
BLAST score
                  1.0e-104
E value
                  193
Match length
                  92
% identity
                  GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog
NCBI Description
                   [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1_
                   (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis
                  thaliana] >gi_2104550 (AF001535) AGAA.4 [Arabidopsis
                  thaliana]
                  6066
Seq. No.
                  5956 1.R1040
Contig ID
                  txt700733748.hl
5'-most EST
                  BLASTX
Method
                  q4454471
NCBI GI
BLAST score
                  287
                   2.0e-25
E value
                  75
Match length
                  73
% identity
                   (AC006234) putative G protein coupled receptor [Arabidopsis
NCBI Description
                   thaliana]
                   6067
Seq. No.
                   5957 1.R1040
Contig ID
                  LIB3029-011-Q1-B1-B9
5'-most EST
                   6068
Seq. No.
                   5958 1.R1040
Contig ID
                   zhf7\overline{0}0952841.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4115925
BLAST score
                   1023
                   1.0e-111
E value
                   298
Match length
% identity
                   (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                   >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
                   [Arabidopsis thaliana]
                   6069
Seq. No.
Contig ID
                   5958 2.R1040
5'-most EST
                   LIB3049-039-Q1-E1-A8
Method
                   BLASTX
                   g4115925
NCBI GI
BLAST score
                   461
E value
                   7.0e-46
Match length
                   104
                   46
% identity
```

NCBI Description (AF118222) contains similarity to RNA recognition motifs

```
(Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana]
```

```
Seq. No.
                    6070
                    5958 3.R1040
Contig ID
5'-most EST
                    leu701151437.hl
                   BLASTX
Method
NCBI GI
                   q4115925
BLAST score
                    280
E value
                    2.0e-24
                    126
Match length
% identity
                    (AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
NCBI Description
                    >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
                    [Arabidopsis thaliana]
                    6071
Seq. No.
                    5958 4.R1040
Contig ID
5'-most EST
                    vzy700755441.hl
                    6072
Seq. No.
                    5958 5.R1040
Contig ID
5'-most EST
                    gsv701048154.hl
Seq. No.
                    6073
                    5960 1.R1040
Contig ID
                    ncj7\overline{0}0984222.h1
5'-most EST
                    BLASTX
Method
                    g118926
NCBI GI
BLAST score
                    709
                    7.0e-75
E value
                    201
Match length
                    67
% identity
                    DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
NCBI Description
                    >gi 320600 pir E45509 desiccation-related protein (clone
                    PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
                    dessication-related protein [Craterostigma plantagineum]
                    >gi 227781 prf 1710351E abscisic acid responsive protein E
                    [Craterostigma plantagineum]
```

 Seq. No.
 6074

 Contig ID
 5966 1.R1040

 5'-most EST
 smc700750004.h1

 Method
 BLASTX

 NCBI GI
 g542190

 BLAST score
 613

 E value
 2.0e-63

E value 2.0e Match length 287 % identity 45

NCBI Description hypothetical protein 1087 - maize >gi_459269_emb_CAA54960_ (X78029) transcribed sequence 1087 [Zea mays]

Seq. No. 6075

Contig ID 5966_2.R1040 5'-most EST smc700745314.h1

```
BLASTX
Method
                   g542190
NCBI GI
                   373
BLAST score
                   8.0e-36
E value
Match length
                   133
                   44
% identity
                   hypothetical protein 1087 - maize >gi_459269_emb_CAA54960_
NCBI Description
                   (X78029) transcribed sequence 1087 [Zea mays]
                   6076
Seq. No.
                   5967 1.R1040
Contig ID
                   LIB3139-032-P1-N1-E1
5'-most EST
                   BLASTX
Method
                   g4567229
NCBI GI
                   336
BLAST score
                   2.0e-31
E value
                   138
Match length
                   46
% identity
                   (AC007119) putative pectin methylesterase [Arabidopsis
NCBI Description
                   thaliana]
                   6077
Seq. No.
                   5968 1.R1040
Contig ID
                   LIB3106-113-Q1-K1-D12
5'-most EST
                   BLASTX
Method
                   g2935416
NCBI GI
BLAST score
                   1293
                   1.0e-143
E value
                   302
Match length
                   81
% identity
                   (AF047896) isoflavone reductase homolog [Betula pendula]
NCBI Description
                   6078
Seq. No.
                   5970 1.R1040
Contig ID
                   LIB3029-011-Q1-B1-B8
5'-most EST
                   6079
Seq. No.
                   5979 1.R1040
Contig ID
                   jC-gmst02400042e08a1
5'-most EST
                   BLASTX
Method
                   g3914431
NCBI GI
                   1144
BLAST score
                   1.0e-125
E value
                   249
Match length
                   86
% identity
                   PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)
NCBI Description
                   (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)
                   >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha
                   subunit [Spinacia oleracea]
Seq. No.
                   6080
                   5979 2.R1040
Contig ID
                   k117\overline{0}1208578.h1
5'-most EST
                   BLASTX
Method
                   g3914431
NCBI GI
                   631
BLAST score.
```

6.0e-66

E value

% identity

```
151
Match length
                   87
% identity
                   PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)
NCBI Description
                   (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)
                   >gi 2285802 dbj_BAA21651_ (D78173) 26S proteasome alpha
                   subunit [Spinacia oleracea]
                   6081
Seq. No.
                   5983 1.R1040
Contig ID
                   leu701146005.hl
5'-most EST
                   BLASTX
Method
                   g2660676
NCBI GI
                   811
BLAST score
                   1.0e-86
E value
                   206
Match length
% identity
                   73
                   (AC002342) Dreg-2 like protein [Arabidopsis thaliana]
NCBI Description
                   6082
Seq. No.
                   5985 1.R1040
Contig ID
                   awf7\overline{0}0840391.h1
5'-most EST
                   BLASTX
Method
                   g81886
NCBI GI
                   753
BLAST score
                   6.0e-80
E value
                   205
Match length
                   71
% identity
                   tonoplast intrinsic protein alpha - kidney bean
NCBI Description
                   6083
Seq. No.
                   5987 1.R1040
Contig ID
                   zhf700952328.h1
5'-most EST
Seq. No.
                   6084
                   5987_2.R1040
Contig ID
                   jC-gmf102220114f01a1
5'-most EST
                   6085
Seq. No.
                   5994 1.R1040
Contig ID
                   crh7\overline{0}0853990.h1
5'-most EST
Method
                   BLASTX
                   q2245066
NCBI GI
                   1398
BLAST score
                   1.0e-155
E value
                   460
Match length
% identity
                   (Z97342) Beta-Amylase [Arabidopsis thaliana]
NCBI Description
                   6086
Seq. No.
                   5994 2.R1040
Contig ID
                   rca700996317.h1
5'-most EST
                   BLASTX
Method
                   g2245066
NCBI GI
                   259
BLAST score
                   2.0e-22
E value
                   128
Match length
                   45
```

Method

NCBI GI

BLAST score

```
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]
Seq. No.
                   6087
                   5995 1.R1040
Contig ID
5'-most EST
                   kl1701212350.hl
                   6088
Seq. No.
                   5996 1.R1040
Contig ID
                   uaw700662796.hl
5'-most EST
                   6089
Seq. No.
                   5996 2.R1040
Contig ID
                   zzp700833912.h1
5'-most EST
                   BLASTX
Method
                   q2459431
NCBI GI
BLAST score
                   254
                   1.0e-21
E value
Match length
                   158
                   44
% identity
                   (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                   6090
Seq. No.
Contig ID
                   5997 1.R1040
5'-most EST
                  hrw701058407.h1
Method
                  BLASTX
NCBI GI
                   g3395431
BLAST score
                   186
E value
                   1.0e-13
Match length
                   107
% identity
                   (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                   6091
Seq. No.
Contig ID
                   5999 1.R1040
5'-most EST
                   LIB3029-010-Q1-B1-C3
                   6092
Seq. No.
                   5999 4.R1040
Contig ID
5'-most EST
                   asn701135609.hl
                   6093
Seq. No.
                   6000 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910009d06a1
Method
                   BLASTX
NCBI GI
                   q3080451
BLAST score
                   1116
                   1.0e-125
E value
Match length
                   362
                   62
% identity
NCBI Description
                   (AL022605) hypothetical protein [Arabidopsis thaliana]
                   6094
Seq. No.
                   6000 2.R1040
Contig ID
5'-most EST
                   LIB3107-066-Q1-K1-A3
                  BLASTX
```

q3080451 385

```
E value
                  3.0e-37
Match length
                  141
                  54
% identity
                  (AL022605) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  6095
Seq. No.
                  6007 1.R1040
Contig ID
                  LIB3029-010-Q1-B1-B7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2652938
BLAST score
                  902
                  1.0e-97
E value
                  190
Match length
% identity
                  87
                  (Z47554) orf [Zea mays]
NCBI Description
                  6096
Seq. No.
                  6011 1.R1040
Contig ID
                  uaw700661589.hl
5'-most EST
Method
                  BLASTX
                  g126078
NCBI GI
BLAST score
                  510
E value
                  1.0e-51
Match length
                  184
                  62
% identity
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)
NCBI Description
                  >gi_81554_pir__S04046 embryonic abundant protein gD-34 -
                  upland cotton >gi 18501 emb CAA31594 (X13206) D-34 Lea
                  protein [Gossypium hirsutum] >gi_167385 (M19389) storage
                  protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea
                  D-34 gene [Saguinus oedipus]
                  6097
Seq. No.
Contig ID
                  6013 1.R1040
                  LIB3029-010-Q1-B1-A5
5'-most EST
                  6098
Seq. No.
                   6016 1.R1040
Contig ID
5'-most EST
                  LIB3029-010-Q1-B1-A8
Method
                  BLASTX
NCBI GI
                  q4510383
BLAST score
                  559
                  2.0e-57
E value
Match length
                  190
% identity
                   (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   6099
Seq. No.
                   6018 1.R1040
Contig ID
5'-most EST
                  LIB3051-010-Q1-E1-G10
                  BLASTX
Method
                  g3080439
NCBI GI
BLAST score
                  151
                   9.0e-10
E value
                  75
Match length
% identity
                   (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
```

A STATE OF THE STA

```
6100
Seq. No.
                   6018 2.R1040
Contig ID
5'-most EST
                   kl1701207641.h1
                   6101
Seq. No.
                   6022 1.R1040
Contig ID
                   wvk700685854.h1
5'-most EST
                   6102
Seq. No.
                   6025 1.R1040
Contig ID
5'-most EST
                   LIB3106-032-Q1-K1-B12
Method
                   BLASTN
                   g303856
NCBI GI
BLAST score
                   160
E value
                   2.0e-84
Match length
                   384
% identity
                   85
                  Rice mRNA for ubiquitin protein fused to a ribosomal
NCBI Description
                  protein, complete cds
Seq. No.
                   6103
Contig ID
                   6029 1.R1040
                   LIB3107-071-Q1-K1-B8
5'-most EST
Seq. No.
                   6104
                   6029 2.R1040
Contig ID
5'-most EST
                   LIB3051-016-Q1-E1-G10
Method
                   BLASTX
NCBI GI
                   g1435021
BLAST score
                   374
                   1.0e-35
E value
Match length
                   168
% identity
                   53
                   (D26575) DNA-binding protein [Daucus carota]
NCBI Description
                   6105
Seq. No.
                   6030 1.R1040
Contig ID
5'-most EST
                   LIB3051-112-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g3152596
                   629
BLAST score
E value
                   2.0e-65
                   309
Match length
% identity
                   50
                   (AC002986) YUP8H12R.36 [Arabidopsis thaliana]
NCBI Description
                   6106
Seq. No.
Contig ID
                   6030 3.R1040
5'-most EST
                   fC-gmle700682314f1
                   6107
Seq. No.
                   6033 1.R1040
Contig ID
5'-most EST
                  g5126510
Method
                   BLASTX
NCBI GI
                   q3776578
                   332
BLAST score
```

```
1.0e-30
E value
Match length
                  152
                  42
% identity
                  (AC005388) ESTs gb F13915 and gb F13916 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
                  6108
Seq. No.
Contig ID
                  6035 1.R1040
                  crh700855751.h1
5'-most EST
                  BLASTX
Method
                  g3878119
NCBI GI
                  202
BLAST score
E value
                  3.0e-15
                  92
Match length
                  49
% identity
                  (Z49068) similar to GTP-binding protein; cDNA EST
NCBI Description
                  EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709
                  comes from this gene; cDNA EST EMBL: D27708 comes from this
                  gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST
                  yk353
                  6109
Seq. No.
Contig ID
                  6040 1.R1040
5'-most EST
                  LIB3029-009-Q1-B1-C4
Method
                  BLASTN
                  g2347097
NCBI GI
                  67
BLAST score
E value
                  4.0e-29
Match length
                  171
% identity
                  Arabidopsis thaliana ubiquitin-specific protease (AtUBP3)
NCBI Description
                  mRNA, complete cds
Seq. No.
Contig ID
                  6041 1.R1040
                  pxt700943230.h1
5'-most EST
                  6111
Seq. No.
                  6043 1.R1040
Contig ID
5'-most EST
                  zzp700833930.hl
                  BLASTX
Method
NCBI GI
                  q3402711
BLAST score
                  455
                  2.0e-83
E value
                  239
Match length
% identity
                  (AC004261) putative RNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  6112
Seq. No.
Contig ID
                  6043 2.R1040
5'-most EST
                  LIB3051-094-Q1-K1-C7
                  BLASTN
Method
NCBI GI
                  g2347085
BLAST score
                  92
E value
                  6.0e-44
Match length
                  156
```

Contig ID

5'-most EST

```
% identity
                   90
                  Phaseolus vulgaris putative osmoprotector PvLEA-18
NCBI Description
                   (Pvlea-18) mRNA, complete cds
                   6113
Seq. No.
                   6048 1.R1040
Contig ID
                   leu701156292.hl
5'-most EST
Method
                  BLASTX
                   g4337179
NCBI GI
BLAST score
                   314
                   9.0e-29
E value
Match length
                  145
% identity
                   49
                   (AC006416) This gene is continued on the 5' end of BAC
NCBI Description
                  T12M14. [Arabidopsis thaliana]
Seq. No.
                   6114
Contig ID
                   6049 1.R1040
5'-most EST
                   jC-qmf102220108f01a1
Method
                   BLASTX
NCBI GI
                   q2618705
BLAST score
                   876
E value
                   2.0e-94
Match length
                   271
                   68
% identity
                   (AC002510) putative ABC transporter, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   6115
Contig ID
                   6072 1.R1040
5'-most EST
                   qsv701046930.hl
Method
                   BLASTX
NCBI GI
                   q2342727
BLAST score
                   281
E value
                   5.0e-25
Match length
                   68
                   71
% identity
                   (AC002341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6116
Contig ID
                   6075 1.R1040
5'-most EST
                  has700548234.h1
Method
                  BLASTX
NCBI GI
                   g2956717
BLAST score
                   237
                   8.0e-20
E value
                   125
Match length
% identity
                   (Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]
NCBI Description
                   6117
Seq. No.
                   6078 1.R1040
Contig ID
5'-most EST
                   LIB3029-008-Q1-B1-G2
                   6118
Seq. No.
                   6080 1.R1040
```

 $epx7\overline{0}1106595.h1$

```
Method
                  BLASTX
                  g2842757
NCBI GI
                  192
BLAST score
                   3.0e-14
E value
                  109
Match length
                   43
% identity
                  LIGHT-INDUCIBLE PROTEIN CPRF-2 >qi 1806261 emb CAA41453
NCBI Description
                   (X58577) DNA-binding protein; bZIP type [Petroselinum
                   crispum]
                   6119
Seq. No.
Contig ID
                   6080 2.R1040
                   jC-gmf102220102e09a1
5'-most EST
Method
                   BLASTX
                   g2842757
NCBI GI
BLAST score
                   245
                   2.0e-21
E value
Match length
                   156
                   46
% identity
                  LIGHT-INDUCIBLE PROTEIN CPRF-2 >gi 1806261 emb CAA41453
NCBI Description
                   (X58577) DNA-binding protein; bZIP type [Petroselinum
                   crispum]
                   6120
Seq. No.
                   6080 3.R1040
Contig ID
5'-most EST
                   uC-gmropic113g07b1
Method
                   BLASTX
NCBI GI
                   g100163
BLAST score
                   230
                   6.0e-19
E value
Match length.
                   147
% identity
                   40
                  light-induced protein CPRF-2 - parsley
NCBI Description
Seq. No.
                   6121
                   6082 1.R1040
Contig ID
                   pcp700990468.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1914683
BLAST score
                   905
E value
                   1.0e-97
Match length
                   245
                   74
% identity
                   (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
                   6122
Seq. No.
                   6082 2.R1040
Contig ID
                  LIB3093-001-Q1-K1-G12
5'-most EST
                  BLASTX
Method
NCBI GI
                   g1914683
BLAST score
                   413
                   3.0e-40
E value
                   107
Match length
% identity
NCBI Description
                   (Y12013) RAD23, isoform I [Daucus carota]
```

6123

Seq. No.

% identity

```
Contig ID
                   6082 3.R1040
                   crh7\overline{0}0852624.h1
5'-most EST
Method
                   BLASTX
                   q1914683
NCBI GI
BLAST score
                   289
                   7.0e-26
E value
                   74
Match length
                   76
% identity
                   (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
                   6124
Seq. No.
                   6087 1.R1040
Contig ID
                   LIB3029-008-Q1-B1-D3
5'-most EST
                   BLASTX
Method
                   g130718
NCBI GI
BLAST score
                   338
                   1.0e-31
E value
                   100
Match length
                   61
% identity
                   ACID PHOSPHATASE PRECURSOR 1 >gi_170370 (M83211) acid
NCBI Description
                   phosphatase type 1 [Lycopersicon esculentum] >gi_170372
                   (M67474) acid phosphatase type 5 [Lycopersicon esculentum]
                   >gi_445121_prf__1908427A acid phosphatase 1 [Lycopersicon
                   esculentum]
                   6125
Seq. No.
                   6089 1.R1040
Contig ID
5'-most EST
                   LIB3087-008-Q1-K1-A6
                   6126
Seq. No.
                   6089 2.R1040
Contig ID
                   LIB3139-013-P1-N1-G7
5'-most EST
Seq. No.
                   6127
                   6095 1.R1040
Contig ID
                   jC-gmf102220108h05a1
5'-most EST
                   BLASTX
Method
                   q4325342
NCBI GI
BLAST score
                   548
                   5.0e-56
E value
                   240
Match length
                   53
% identity
                   (AF128393) No definition line found [Arabidopsis thaliana]
NCBI Description
                   6128
Seq. No.
                   6102 1.R1040
Contig ID
                   LIB3\overline{1}70-064-Q1-J1-E9
5'-most EST
                   6129
Seq. No.
                   6102 2.R1040
Contig ID
                   jC-gmf102220057h09d1
5'-most EST
                   BLASTX
Method
                   g1171866
NCBI GI
BLAST score
                   273
                   6.0e-24
E value
                   52
Match length
                   94
```

```
NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
NCBI Description
                    (COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild
                    cabbage >gi_562282_emb_CAA57725 (X82274) PSST subunit of
NADH: ubiquinone oxidoreductase [Brassica oleracea]
Seq. No.
                    6130
                    6106 1.R1040
Contig ID
                    pmv700893391.hl
5'-most EST
                    BLASTN
Method
                    g1161251
NCBI GI
BLAST score
                    61
                    2.0e-25
E value
Match length
                    253
                    81
% identity
                    Glycine max nucleosome assembly protein 1 (SNAP-1) mRNA,
NCBI Description
                    complete cds
Seq. No.
                    6131
                    6112 1.R1040
Contig ID
                    qsv7\overline{0}1055056.h1
5'-most EST
                    BLASTX
Method
                    g3261634
NCBI GI
BLAST score
                    187
                    1.0e-13
E value
Match length:
                    190
                    32
% identity
                    (Z79700) hypothetical protein Rv0976c [Mycobacterium
NCBI Description
                    tuberculosis]
                     6132
Seq. No.
                     6114 1.R1040
Contig ID
                    LIB3\overline{0}29-008-Q1-B1-D1
5'-most EST
                    BLASTX
Method
                     g3914002
NCBI GI
BLAST score
                     923
                     1.0e-100
E value
Match length
                     189
                     93
% identity
                    MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279
NCBI Description
                     (AF033862) Lon protease [Arabidopsis thaliana]
Seq. No.
                    6133
                     6115 1.R1040
Contig ID
                     LIB3107-016-Q1-K1-D3
5'-most EST
Method
                     BLASTX
                     g4371285
NCBI GI
BLAST score
                     171
                     4.0e-12
E value
Match length
                     63
                     54
% identity
                     (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                     6134
Seq. No.
```

....

6116 1.R1040

 $epx7\overline{0}1108611.h1$

Contig ID

5'-most EST

```
Seq. No.
                   6135
                   6118 1.R1040
Contig ID
5'-most EST
                  LIB3139-103-P1-N1-A9
Seq. No.
                   6136
                   6118 2.R1040
Contig ID
5'-most EST
                   g5058185
Seq. No.
                   6137
                   6120 1.R1040
Contig ID
5'-most EST
                   LIB3029-007-Q1-B1-H7
Seq. No.
                   6138
Contig ID
                   6121 1.R1040
5'-most EST
                   LIB3029-008-Q1-B1-A11
Seq. No.
                   6139
                   6126 1.R1040
Contig ID
5'-most EST
                   zzp700832478.hl
                   BLASTX
Method
NCBI GI
                   q3482967
BLAST score
                   758
                   1.0e-149
E value
Match length
                   359
                   72
% identity
                   (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                   thaliana] >gi 4559345 gb AAD23006.1 AC006585 1 (AC006585)
                   protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.
Contig ID
                   6127 1.R1040
5'-most EST
                   LIB3167-042-P1-K1-H4
                   BLASTX
Method
NCBI GI
                   q2078350
BLAST score
                   721
E value
                   2.0e-76
Match length
                   199
% identity
NCBI Description
                   (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                   6141
                   6127 2.R1040
Contig ID
5'-most EST
                   leu701152348.h1
                   BLASTX
Method
NCBI GI
                   q2078350
BLAST score
                   529
E value
                   6.0e-54
Match length
                   136
% identity
                   71
NCBI Description
                   (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                   6142
Contig ID
                   6129 1.R1040
                   LIB3029-008-Q1-B1-B2
5'-most EST
Seq. No.
                   6143
```

6133 1.R1040

Contig ID

```
5'-most EST
                  sat701006002.h2
Method
                  BLASTX
                   g2244939
NCBI GI
BLAST score
                   346
E value
                   6.0e-32
                   304
Match length
                   31
% identity
NCBI Description
                   (Z97339) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   6133 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810044h11d1
Seq. No.
                   6133 3.R1040
Contig ID
5'-most EST
                   vzy700756777.h1
                   6146
Seq. No.
Contig ID
                   6136 1.R1040
5'-most EST
                   asn701133071.h1
                  BLASTN
Method
                   g18729
NCBI GI
                   64
BLAST score
E value
                   2.0e-27
                   68
Match length
% identity
                  Soybean (Glycine max) 18S ribosomal RNA
NCBI Description
Seq. No.
                   6147
Contig ID
                   6136 2.R1040
                   sat701008527.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   a18729
BLAST score
                   269
E value
                   1.0e-149
Match length
                   458
                   90
% identity
                  Soybean (Glycine max) 18S ribosomal RNA
NCBI Description
Seq. No.
Contig ID
                   6144 1.R1040
5'-most EST
                   leu701157711.h1
                   BLASTX
Method
NCBI GI
                   q2623297
BLAST score
                   143
                   1.0e-08
E value
Match length
                   49
                   55
% identity
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3790583 (AF079180) RING-H2 finger protein RHCla
                   [Arabidopsis thaliana]
Seq. No.
                   6149
                   6144 2.R1040
Contig ID
                   jC-gmf102220063c05a1
5'-most EST
```

6150

Seq. No.

```
6145 1.R1040
Contig ID
                   LIB3167-027-P1-K1-A6
5'-most EST
                   BLASTX
Method
                   g2462834
NCBI GI
                   364
BLAST score
                   2.0e-34
E value
                   182
Match length
                   43
% identity
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   6151
Seq. No.
                   6145 3.R1040
Contig ID
                   wvk700684271.h1
5'-most EST
                   BLASTX
Method
                   g3337357
NCBI GI
                   165
BLAST score
                   5.0e-13
E value
                   68
Match length
                   62
% identity
                   (AC004481) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   6152
Seq. No.
                   6145 4.R1040
Contig ID
                   jex700906373.h1
5'-most EST
                   BLASTX
Method
                   g3337357
NCBI GI
                   278
BLAST score
E value
                   5.0e-25
Match length
                   86
% identity
                   (AC004481) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   6153
Seq. No.
                   6150 1.R1040
Contig ID
                   zsg7\overline{0}1121114.h1
5'-most EST
                   6154
Seq. No.
                   6158 1.R1040
Contig ID
                   LIB3029-007-Q1-B1-E9
5'-most EST
                   6155
Seq. No.
                   6159 1.R1040
Contig ID
                   LIB3029-007-Q1-B1-D3
5'-most EST
                   BLASTX
Method
                   g2204234
NCBI GI
BLAST score
                   485
                   4.0e-49
E value
                   118
Match length
                   81
% identity
                   (Y13862) enoyl-ACP reductase [Nicotiana tabacum]
NCBI Description
                   6156
Seq. No.
                   6160 1.R1040
Contig ID
5'-most EST
                   uaw700661722.h1
                   BLASTX
Method
                   g3264830
NCBI GI
```

212

BLAST score

E value 7.0e-17 Match length 149 44 % identity NCBI Description (AF072405) cotton fiber expressed protein 2 [Gossypium hirsutum] 6157 Seq. No. 6169 1.R1040 Contig ID 5'-most EST LIB3029-007-Q1-B1-C7 Method BLASTX NCBI GI g2497540 BLAST score 412 E value 2.0e-51 Match length 161 66 % identity NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G 6158 Seq. No. 6171 1.R1040 Contig ID 5'-most EST LIB3109-015-Q1-K1-F1 Seq. No. 6159 6171 2.R1040 Contig ID 5'-most EST LIB3\overline{1}06-023-Q1-K1-C3 Method BLASTX NCBI GI g3769673 BLAST score 224 3.0e-18 E value Match length 120 48 % identity (AF095285) Tic20 [Pisum sativum] NCBI Description 6160 Seq. No. 6171_4.R1040 Contig ID 5'-most EST $jsh7\overline{0}1069881.h1$ 6161 Seq. No. 6172 1.R1040 Contig ID 5'-most EST LIB3029-007-Q1-B1-D1 6162 Seq. No. 6182 1.R1040 Contig ID 5'-most EST LIB3029-007-Q1-B1-A1 BLASTX Method NCBI GI g2982283 BLAST score 369 E value 3.0e-35 Match length 126 57 % identity (AF051226) PREG-like protein [Picea mariana] NCBI Description

Seq. No. 6163

Contig ID 6195_1.R1040

5'-most EST LIB3040-023-Q1-E1-E6

Method BLASTX
NCBI GI g4160280
BLAST score 1414

BLAST score

277

```
E value
                     1.0e-157
 Match length
                     302
                     82
 % identity
 NCBI Description
                     (AJ006224) purple acid phosphatase [Ipomoea batatas]
 Seq. No.
                     6164
                     6196 1.R1040
 Contig ID
 5'-most EST
                     vzy700754476.h1
 Method
                    BLASTX
 NCBI GI
                     g2407613
 BLAST score
                    705
 E value
                     8.0e-74
 Match length
                     442
                     40
 % identity
                     (AF017995) 3-phosphoinositide dependent protein kinase-1
 NCBI Description
                     [Homo sapiens] >gi_2505936_emb_CAA75341_ (Y15056) PkB kinase [Homo sapiens] >gi_4505695_ref_NP_002604.1_pPDPK1_
                     3-phosphoinositide dependent protein kinase-1
                     6165
 Seq. No.
 Contig ID
                     6201 1.R1040
 5'-most EST
                    rlr700899564.h1
 Method
                    BLASTN
 NCBI GI
                    g4519414
BLAST score
                    182
 E value
                    1.0e-97
 Match length
                     470
 % identity
                    85
                    Citrus unshiu (CitVATP c-2) mRNA for vacuolar H+-ATPase c
 NCBI Description
                    subunit, complete cds
                     6166
 Seq. No.
                     6203 1.R1040
 Contig ID
 5'-most EST
                    LIB3029-006-Q1-B1-H1
 Method
                    BLASTX
 NCBI GI
                    g2829918
 BLAST score
                    194
 E value
                    8.0e-15
 Match length
                    71
 % identity
                     (AC002291) similar to "tub" protein gp U82468 2072162
 NCBI Description
                     [Arabidopsis thaliana]
                     6167
 Seq. No.
 Contig ID
                     6208 1.R1040
                    k11701203850.h1
 5'-most EST
 Seq. No.
                    6168
 Contig ID
                    6217 1.R1040
                    LIB3029-006-Q1-B1-E9
 5'-most EST
                    6169
 Seq. No.
 Contig ID
                    6221 1.R1040
                    hyd700726494.hl
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g3212116
```

NCBI GI

```
E value
                  4.0e-24
Match length
                  127
                  44
% identity
                  (Y17393) prefoldin subunit 2 [Mus musculus]
NCBI Description
                  6170
Seq. No.
Contig ID
                  6221 2.R1040
5'-most EST
                  LIB3051-096-Q1-K1-A8
                  BLASTX
Method
NCBI GI
                  g3212116
                  260
BLAST score
                  2.0e-22
E value
                  102
Match length
                  47
% identity
                  (Y17393) prefoldin subunit 2 [Mus musculus]
NCBI Description
                  6171
Seq. No.
                  6221 6.R1040
Contig ID
5'-most EST
                  LIB3049-038-Q1-E1-E10
                  6172
Seq. No.
                  6222 1.R1040
Contig ID
                  LIB3029-006-Q1-B1-B9
5'-most EST
                  BLASTX
Method
NCBI GI
                  g19463.00
BLAST score
                  164
E value
                  2.0e-11
Match length
                  36
% identity
NCBI Description
                  (Y12529) hypothetical protein [Silene latifolia]
Seq. No.
                  6225 1.R1040
Contig ID
5'-most EST
                  LIB3029-006-Q1-B1-C12
Seq. No.
                  6229 1.R1040
Contig ID
5'-most EST
                  LIB3049-024-Q1-E1-A4
Seq. No.
Contig ID
                  6230 1.R1040
5'-most EST
                  jC-gmro02800033g12a1
Method
                  BLASTX
NCBI GI
                  g3334349
BLAST score
                  510
E value
                  1.0e-51
Match length
                  176
% identity
                  GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)
NCBI Description
                  >gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase
                  [Arabidopsis thaliana]
                  6176
Seq. No.
                  6230 2.R1040
Contig ID
5'-most EST
                  LIB3039-012-Q1-E1-A2
Method
                  BLASTX
```

g3334349

5'-most EST

```
BLAST score
                   1181
                   1.0e-130
E value
Match length
                   343
% identity
                   68
NCBI Description
                   GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)
                   >gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase
                   [Arabidopsis thaliana]
Seq. No.
                   6177
                   6230 4.R1040
Contig ID
5'-most EST
                   k117\overline{0}1214567.h1
Method
                   BLASTX
NCBI GI
                   q3334349
BLAST score
                   609
E value
                   6.0e-69
Match length
                   175
                   78
% identity
NCBI Description
                   GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)
                   >gi 2564215 emb CAA05162 (AJ002062) glycyl-tRNA synthetase
                   [Arabidopsis thaliana]
                   6178
Seq. No.
Contig ID
                   6230 5.R1040
                   pmv700890116.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3334349
BLAST score
                   449
E value
                   6.0e-45
Match length
                   101
                   86
% identity
NCBI Description
                   GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)
                   >gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase
                   [Arabidopsis thaliana]
                   6179
Seq. No.
Contig ID
                   6231 1.R1040
5'-most EST
                   LIB3029-006-Q1-B1-D11
                   6180
Seq. No.
                   6238 1.R1040
Contig ID
5'-most EST
                   uC-qmronoir018a07b1
Method
                   BLASTN
NCBI GI
                   q3241920
BLAST score
                   38
E value
                   2.0e-11
Match length
                   338
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   6181
Contig ID
                   6238 2.R1040
5'-most EST
                   LIB3051-084-Q1-K1-C8
                   6182
Seq. No.
                   6244 1.R1040
Contig ID
```

Se.

gsv701046253.hl

NCBI GI

```
Method
                    BLASTN
NCBI GI
                    q436031
BLAST score
                    112
E value
                    9.0e-56
Match length
                    328
% identity
                    84
NCBI Description
                    Nicotiana tabacum (TSC40-4) 60S ribosomal protein L34 mRNA,
                    complete cds
                    6183
Seq. No.
Contig ID
                    6244 2.R1040
5'-most EST
                    LIB3039-035-01-E1-G6
                    BLASTX
Method
NCBI GI
                    a730558
BLAST score
                    471
                    5.0e-47
E value
Match length
                    95
                    95
% identity
                    60S RIBOSOMAL PROTEIN L34 >gi 1076636 pir__S48027 ribosomal
NCBI Description
                    protein L34 - common tobacco >gi 2129964 pir S48028
                    ribosomal protein L34.e, cytosolic - common tobacco
                    >gi_436030 (L27089) 60S ribosomal protein L34 [Nicotiana
                    tabacum] >gi_436032 (L27107) 60S ribosomal protein L34
                    [Nicotiana tabacum]
Seq. No.
                    6184
                    6244 3.R1040
Contig ID
5'-most EST
                    leu701149904.h1
                    BLASTX
Method
NCBI GI
                    q730557
BLAST score
                    379
                    2.0e-36
E value
Match length
                    75
% identity
NCBI Description
                    60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal
                    protein L34 - garden pea >gi 498908 (U10047) ribosomal
                   protein L34 homolog [Pisum sativum]
Seq. No.
                    6185
                    6247 1.R1040
Contig ID
5'-most EST
                    jC-qmle01810005c06a1
Method
                    BLASTX
NCBI GI
                    g3183454
BLAST score
                    648
E value
                    2.0e-67
Match length
                    278
% identity
                    47
NCBI Description
                    HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION
                   >gi_2632217_emb_CAA10859_ (AJ222587) YkwC protein [Bacillus
subtilis] >gi_2633767_emb_CAB13269_ (Z99111) similar to
3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]
                    6186
Seq. No.
                    6247 2.R1040
Contig ID
                   ncj700986168.hl
5'-most EST
Method
                   BLASTX
```

g3183454

NCBI Description

```
BLAST score
                    211
E value
                    1.0e-16
Match length
                    87
                    49
% identity
                    HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION
NCBI Description
                    \label{eq:capacity} $$ \sim 2632217\_emb\_CAA10859\_ (AJ222587) $$ YkwC protein [Bacillus subtilis] $$ \sim 2633767\_emb\_CAB13269\_ (Z99111) similar to
                    3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]
Seq. No.
                    6187
                    6251 1.R1040
Contig ID
5'-most EST
                    uC-gmropic114f01b1
Seq. No.
                    6188
                    6258 1.R1040
Contig ID
                    txt700732131.hl
5'-most EST
Method
                    BLASTX
NCBI GI
                    q3176098
BLAST score
                    1128
E value
                    1.0e-123
Match length
                    312
% identity
                    71
                   (Y15036) annexin [Medicago truncatula]
NCBI Description
Seq. No.
                    6189
                    6261 1.R1040
Contig ID
5'-most EST
                    LIB3107-010-Q1-K1-F3
Method
                    BLASTX
                    q4376815
NCBI GI
BLAST score
                    400
E value
                    1.0e-38
Match length
                    178
% identity
NCBI Description
                    (AE001637) GutQ/KpsF Family Sugar-P Isomerase [Chlamydia
                    pneumoniae]
Seq. No.
                    6190
                    6266 1.R1040
Contig ID
                    zhf700962155.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g2911068
BLAST score
                    744
E value
                    6.0e-79
Match length
                    145
% identity
                    88
NCBI Description
                    (AL021960) G10 - like protein [Arabidopsis thaliana]
Seq. No.
                    6191
Contig ID
                    6284 1.R1040
                    ncj700978444.hl
5'-most EST
Method
                    BLASTX
NCBI GI
                    g4240305
BLAST score
                    275
E value
                    8.0e-24
Match length
                    215
% identity
```

(AB020715) KIAA0908 protein [Homo sapiens]

Seq. No.

6197

```
6192
Seq. No.
                  6285 1.R1040
Contig ID
                  LIB3029-005-Q1-B1-D10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2244816
BLAST score
                  201
E value
                   1.0e-15
Match length
                  60
                   75
% identity
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   6193
Seq. No.
                   6290 1.R1040
Contig ID
5'-most EST
                  LIB3094-059-01-K1-C1
                  BLASTX
Method
                  q729775
NCBI GI
BLAST score
                   482
                   1.0e-48
E value
Match length
                   116
                   78
% identity
                  HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION
NCBI Description
                   FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR)
                   >gi_100264_pir__S25481 heat shock transcription factor 8 -
                   Peruvian tomato >gi 19492 emb_CAA47869_ (X67600) heat shock
                   transcription factor 8 [Lycopersicon peruvianum]
                   6194
Seq. No.
                   6291 1.R1040
Contig ID
5'-most EST
                  LIB3049-023-Q1-E1-H9
                   6195
Seq. No.
                   6293 1.R1040
Contig ID
5'-most EST
                   k117\overline{0}1205910.h1
Method
                   BLASTX
NCBI GI
                   q3915020
BLAST score
                   2619
                   0.0e + 00
E value
Match length
                   639
% identity
                  SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE
NCBI Description
                   GLUCOSYLTRANSFERASE) >gi_1022365_emb_CAA91217_ (Z56278)
                   sucrose phosphate synthase [Vicia faba]
Seq. No.
                   6196
                   6295 1.R1040
Contig ID
5'-most EST
                   q4287190
Method
                   BLASTX
NCBI GI
                   q3434971
BLAST score
                   278
E value
                   2.0e-24
Match length
                   73
% identity
                   (AB008105) ethylene responsive element binding factor 3
NCBI Description
                   [Arabidopsis thaliana]
```

```
6295 2.R1040
Contig ID
5'-most EST
                   uxk7\overline{0}0672508.h1
                   BLASTX
Method
NCBI GI
                   g1208496
BLAST score
                   243
                   1.0e-20
E value
                   56
Match length
                   82
% identity
                   (D38124) EREBP-3 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   6198
                   6301 1.R1040
Contig ID
                   LIB3051-116-Q1-K1-G3
5'-most EST
                   BLASTX
Method
                   g3935184
NCBI GI
BLAST score
                   578
E value
                   2.0e-59
                   197
Match length
                   56
% identity
                   (AC004557) F17L21.27 [Arabidopsis thaliana]
NCBI Description
                   6199
Seq. No.
                   6307 1.R1040
Contig ID
5'-most EST
                   6HA - \overline{0}2 - Q1 - B1 - F1
                   BLASTX
Method
NCBI GI
                   g558606
BLAST score
                   382
                   6.0e-37
E value
                   109
Match length
                   62
% identity
                   (X70688) Nthsp18p [Nicotiana tabacum]
NCBI Description
                   6200
Seq. No.
                   6313_1.R1040
Contig ID
                   pmv700892451.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2997590
BLAST score
                   523
E value
                   0.0e + 00
Match length
                   1032
                   88
% identity
                   Pisum sativum glucose-6-phosphate/phosphate-translocator
NCBI Description
                   precursor (GPT) mRNA, nuclear gene encoding plastid
                  protein, complete cds
                   6201
Seq. No.
Contig ID
                   6313 2.R1040
                   jex700908125.hl
5'-most EST
Method
                   BLASTN
                   g2997590
NCBI GI
BLAST score
                   156
                   2.0e-82
E value
Match length
                   329
% identity
                   Pisum sativum glucose-6-phosphate/phosphate-translocator
NCBI Description
                   precursor (GPT) mRNA, nuclear gene encoding plastid
```

protein, complete cds

% identity

39

```
6202
Seq. No.
                   6313 3.R1040
Contig ID
5'-most EST
                   wvk700683529.h1
                   6203
Seq. No.
                   6315 1.R1040
Contig ID
5'-most EST
                   LIB3049-012-Q1-E1-F2
Method
                   BLASTX
                   q3913633
NCBI GI
BLAST score
                   540
E value
                   5.0e-55
                   162
Match length
% identity
                   64
NCBI Description
                   HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown
                   protein [Arabidopsis thaliana]
                   6204
Seq. No.
Contig ID
                   6316 1.R1040
5'-most EST
                   hyd700725490.h1
Method
                   BLASTX
                   g4006859
NCBI GI
BLAST score
                   319
E value
                   3.0e-29
                   180
Match length
% identity
                   46 -
                   (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
                   6205
Seq. No.
                   6319 1.R1040
Contig ID
5'-most EST
                   LIB3049-006-Q1-E1-A2
                   6206
Seq. No.
                   6322 1.R1040
Contig ID
5'-most EST
                   LIB3029-005-Q1-B1-A2
Method
                   BLASTX
NCBI GI
                   g1620898
BLAST score
                   994
E value
                   1.0e-108
Match length
                   265
% identity
                   73
NCBI Description
                   (D87957) protein involved in sexual development [Homo
                   sapiens]
                   6207
Seq. No.
Contig ID
                   6323 1.R1040
5'-most EST
                   vzy7\overline{0}0752174.h1
                   6208
Seq. No.
                   6324 1.R1040
Contig ID
                   LIB3029-004-Q1-B1-G7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2407068
BLAST score
                   224
E value
                   9.0e-18
Match length
                   122
```

BLAST score

E value

396

0.0e + 00

```
NCBI Description (AF014955) TFAR19 [Homo sapiens]
                   6209
Seq. No.
Contig ID
                   6326 1.R1040
                   LIB3029-004-Q1-B1-F11
5'-most EST
                   6210
Seq. No.
Contig ID
                   6331_1.R1040
5'-most EST
                   LIB3072-060-Q1-K1-D7
Method
                   BLASTN
                   g18653
NCBI GI
BLAST score
                   508
E value
                   0.0e + 00
Match length
                   548
                   98
% identity
NCBI Description
                   Soybean gene for heat shock protein Gmhsp18.5-C (class I)
                   6211
Seq. No.
                   6331 2.R1040
Contig ID
5'-most EST
                   g560<del>6</del>297
Method
                   BLASTN
                   g18653
NCBI GI
BLAST score
                   290
                   1.0e-162
E value
Match length
                   579
                   89
% identity
NCBI Description Soybean gene for heat shock protein Gmhsp18.5-C (class I)
                   6212
Seq. No.
                   6331 3.R1040
Contig ID
5'-most EST
                   LIB3170-041-Q1-J1-A9
Method
                   BLASTN
                   g18655
NCBI GI
BLAST score
                   631
E value
                   0.0e+00
Match length
                   813
% identity
                   95
NCBI Description
                   Soybean heat-shock gene hs6871 sequence
                   6213
Seq. No.
Contig ID
                   6331 4.R1040
5'-most EST
                   epx7\overline{0}1105644.h1
Method
                   BLASTN
NCBI GI
                   g18655
BLAST score
                   251
                   1.0e-139
E value
Match length
                   387
% identity
NCBI Description
                   Soybean heat-shock gene hs6871 sequence
                   6214
Seq. No.
Contig ID
                   6331 5.R1040
5'-most EST
                   epx701107217.hl
Method
                   BLASTN
NCBI GI
                   g18655
```

BLAST score

63

```
396
Match length
% identity
                   100
NCBI Description
                   Soybean heat-shock gene hs6871 sequence
Seq. No.
                   6215
Contig ID
                   6331 6.R1040
5'-most EST
                   LIB3072-019-Q1-E1-H5
Method
                   BLASTN
NCBI GI
                   g18653
BLAST score
                   205
E value
                   1.0e-111
Match length
                   313
% identity
                   91
NCBI Description
                   Soybean gene for heat shock protein Gmhsp18.5-C (class I)
                   6216
Seq. No.
                   6331 7.R1040
Contig ID
5'-most EST
                   hrw701060690.h1
Method
                   BLASTN
                   g169984
NCBI GI
BLAST score
                   351
E value
                   0.0e+00
Match length
                   359
                   99
% identity
NCBI Description
                   Soybean (Glycine max) low MW heat shock protein gene
                   (Gmhsp17.6-L)
                   6217
Seq. No.
Contig ID
                   6331 8.R1040
5'-most EST
                   epx7\overline{0}1104850.h1
Method
                   BLASTN
                   g1431738
NCBI GI
BLAST score
                   147
E value
                   4.0e-77
Match length
                   235
% identity
NCBI Description
                   Soybean (Glycine max) low MW heat shock protein gene
                   (Gmhsp17.5-M)
                   6218
Seq. No.
                   6331 10.R1040
Contig ID
5'-most EST
                   hrw7\overline{0}1061389.h1
Method
                   BLASTN
NCBI GI
                   g1431738
BLAST score
                   182
E value
                   6.0e-98 .
Match length
                   266
% identity
                   Soybean (Glycine max) low MW heat shock protein gene
NCBI Description
                   (Gmhsp17.5-M)
                   6219
Seq. No.
Contig ID
                   6331 12.R1040
5'-most EST
                   uC-gmrominsoy134f10b1
Method
                   BLASTN
NCBI GI
                   g18653
```

NCBI Description

```
5.0e-27
E value
Match length
                   191
                   91
% identity
NCBI Description
                   Soybean gene for heat shock protein Gmhsp18.5-C (class I)
                   6220
Seq. No.
                   6331 13.R1040
Contig ID
5'-most EST
                   hrw701062361.h1
Method
                   BLASTN
                   g18653
NCBI GI
BLAST score
                   214
E value
                   1.0e-117
                   262
Match length
% identity
                   96
NCBI Description
                   Soybean gene for heat shock protein Gmhsp18.5-C (class I)
                   6221
Seq. No.
Contig ID
                   6331 14.R1040
5'-most EST
                   zsg7\overline{0}1128782.h1
Method
                   BLASTN
                   g169986
NCBI GI
BLAST score
                   87
E value
                   2.0e-41
Match length
                   154
% identity
                   90
NCBI Description
                   Soybean (Glycine max) heat shock protein (Gmhsp17.5-E)
                   gene, complete cds
Seq. No.
                   6222
                   6340 1.R1040
Contig ID
5'-most EST
                   gsv701050470.hl
                   6223
Seq. No.
                   6340 3.R1040
Contig ID
5'-most EST
                   uC-gmropic111b05b1
Seq. No.
                   6224
Contig ID
                   6346 1.R1040
                   LIB3049-010-Q1-E1-C11
5'-most EST
Method
                   BLASTX
                   q4539303
NCBI GI
BLAST score
                   469
                   9.0e-47
E value
Match length
                   164
% identity
                   56
NCBI Description
                   (AL049480) putative protein [Arabidopsis thaliana]
Seq. No.
                   6225
Contig ID
                   6346 2.R1040
5'-most EST
                   dpv7\overline{0}1100045.h2
Method
                   BLASTX
NCBI GI
                   g4539303
BLAST score
                   245
E value
                   9.0e-21
Match length
                   101
% identity
```

(AL049480) putative protein [Arabidopsis thaliana]

```
Seq. No.
                   6226
Contig ID
                   6348 1.R1040
5'-most EST
                   LIB3029-004-Q1-B1-E5
Method
                   BLASTX
NCBI GI
                   g2213590
BLAST score
                   216
E value
                   3.0e-17
Match length
                   128
                   38
% identity
NCBI Description
                   (AC000348) T7N9.10 [Arabidopsis thaliana]
                   6227
Seq. No.
                   6350 1.R1040
Contig ID
5'-most EST
                   LIB3072-024-Q1-E1-G1
                   BLASTN
Method
                   g460802
NCBI GI
BLAST score
                   54
                   3.0e-21
E value
Match length
                   238
                   81
% identity
                   P.amygdalus, Batsch (Texas) ole1 mRNA
NCBI Description
                   6228
Seq. No.
                   6350 2.R1040
Contig ID
5'-most EST
                   LIB3072-056-Q1-K1-D10
                   BLASTX
Method
                   q3914199
NCBI GI
                   222
BLAST score
                   5.0e-18
E value
Match length
                   141
% identity
                   40
                   OLEOSIN 1 >gi_460803_emb_CAA55008_ (X78118) oleosin [Prunus
NCBI Description
                   dulcis]
                   6229
Seq. No.
Contig ID
                   6354 1.R1040
5'-most EST
                   q560<del>6</del>027
Method
                   BLASTX
                   q3688188
NCBI GI
BLAST score
                   2538
E value
                   0.0e + 00
Match length
                   608
% identity
                   (AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   6230
Contig ID
                   6354 3.R1040
5'-most EST
                   txt700734851.h1
Method
                   BLASTN
NCBI GI
                   q1177604
BLAST score
                   165
E value
                   1.0e-87
Match length
                   429
% identity
                  P.sativum mRNA for pyruvate decarboxylase (PDC2)
NCBI Description
```

BLAST score

318

```
6231
Seq. No.
Contig ID
                   6354 4.R1040
5'-most EST
                   bnu700967544.h1
Method
                   BLASTX
                   g3688188
NCBI GI
BLAST score
                   306
E value
                   6.0e-28
Match length
                   94
% identity
                   66
NCBI Description
                   (AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis
                   thaliana]
                   6232
Seq. No.
                   6359 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy055c05b1
Method
                   BLASTX
NCBI GI
                   g4006829
BLAST score
                   707
                   2.0e-74
E value
Match length
                   207
% identity
                   67
                   (AC005970) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   6233
Seq. No.
                   6359 2.R1040
Contig ID
5'-most EST
                   k117\overline{0}1211035.h1
Method
                   BLASTX
                   g3805765
NCBI GI
BLAST score
                   161
                   8.0e-11
E value
Match length
                   48
% identity
                   67
NCBI Description
                   (AC005693) putative protein kinase [Arabidopsis thaliana]
                   6234
Seq. No.
Contig ID
                   6359 3.R1040
5'-most EST
                   ssr700553651.hl
Seq. No.
                   6235
                   6361 1.R1040
Contig ID
5'-most EST
                   uaw7\overline{0}0663807.h1
Method
                   BLASTX
                   g452519
NCBI GI
BLAST score
                   181
E value
                   1.0e-12
Match length
                   131
% identity
NCBI Description
                   (D26362) similar to Human homolog of Drosophila female
                   sterile homeotic mRNA ( HUMFSHG) [Homo sapiens]
                   6236
Seq. No.
Contig ID
                   6362 1.R1040
5'-most EST
                   txt700731402.h1
Method
                   BLASTN
                   g18638
NCBI GI
```

```
1.0e-179
E value
Match length
                   384
                   98
% identity
NCBI Description
                   Soybean Gy3 gene for glycinin subunit G3
Seq. No.
                   6364 1.R1040
Contig ID
5'-most EST
                   zzp700832050.h1
Method
                   BLASTX
NCBI GI
                   g1723440
BLAST score
                   495
                   2.0e-49
E value
                   246
Match length
                   43
% identity
NCBI Description
                   HYPOTHETICAL 35.9 KD PROTEIN C56F8.08 IN CHROMOSOME I
                   >gi_1204230_emb CAA93579 (Z69728) unknown
                   [Schizosaccharomyces pombe]
                   6238
Seq. No.
Contig ID
                   6364 2.R1040
                   LIB3051-053-Q1-K2-C4
5'-most EST
                   6239
Seq. No.
Contig ID
                   6368 1.R1040
5'-most EST
                   uC-gmrominsoy188h04b1
Method
                   BLASTX
                   q2827552
NCBI GI
BLAST score
                   331
                   1.0e-30
E value
Match length
                   96
% identity
                   61
NCBI Description
                   (AL021635) predicted protein [Arabidopsis thaliana]
                   6240
Seq. No.
                   6373 1.R1040
Contig ID
5'-most EST
                   jex700906521.h1
Method
                   BLASTN
                   q18731
NCBI GI
BLAST score
                   1060
E value
                   0.0e + 00
Match length
                   1621
% identity
                   97
NCBI Description
                   Soybean RPB1-B1 gene for the largest subunit of RNA
                   polymerase II (EC 2.7.7.6)
Seq. No.
                   6241
Contig ID
                   6385 1.R1040
5'-most EST
                   q5509589
Method
                   BLASTX
NCBI GI
                   q1063276
BLAST score
                   787
E value
                   5.0e-84
Match length
                   220
% identity
                   69
NCBI Description
                   (X92893) geranylgeranyl pyrophosphate synthase
```

[Catharanthus roseus]

Match length

317

```
6242
Seq. No.
Contig ID
                  6386 1.R1040
5'-most EST
                  zpv700758409.h1
Method
                  BLASTX
                  g633890
NCBI GI
BLAST score
                  973
E value
                  1.0e-105
Match length
                  280
                  69
% identity
NCBI Description
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
                  vulgare]
Seq. No.
                  6243
                  6386 4.R1040
Contig ID
5'-most EST
                  uxk700668322.h1
Method
                  BLASTX
                  g633890
NCBI GI
BLAST score
                  170
E value
                  5.0e-12
Match length
                  44
% identity
                  73
                  (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                  vulgare]
Seq. No.
                  6244
                  6390 1.R1040
Contig ID
5'-most EST
                  LIB3039-010-Q1-E1-C8
Method
                  BLASTX
                  g3617770
NCBI GI
BLAST score
                  552
E value
                  1.0e-56
Match length
                  138
                  73
% identity
NCBI Description
                  (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
                  6245
Seq. No.
Contig ID
                  6390_2.R1040
5'-most EST
                  LIB3029-003-Q1-B1-G10
Method
                  BLASTX
NCBI GI
                  g2501064
BLAST score
                  302
E value
                  2.0e-27
Match length
                  113
% identity
                  58
                  PROBABLE THREONYL-TRNA SYNTHETASE, CYTOPLASMIC
NCBI Description
                  (THREONINE--TRNA LIGASE) (THRRS) >gi_2191162 (AF007270)
                  Similar to threonyl-tRNA synthetase; coded for by A.
                  thaliana cDNA R65376 [Arabidopsis thaliana]
Seq. No.
                  6246
                  6397 1.R1040
Contig ID
5'-most EST
                  LIB3072-011-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                  g1141781
BLAST score
                  233
E value
                  1.0e-128
```

```
93
% identity
NCBI Description
                   Vigna radiata EM protein mRNA, complete cds
Seq. No.
                   6247
                   6399 1.R1040
Contig ID
                   txt700734368.h1
5'-most EST
                   6248
Seq. No.
Contig ID
                   6399 2.R1040
5'-most EST
                   crh7\overline{0}0853112.h1
Seq. No.
                   6249
Contig ID
                   6400 1.R1040
5'-most EST
                   LIB3029-003-Q1-B1-E11
                   BLASTX
Method
                   g3738230
NCBI GI
BLAST score
                   286
E value
                   1.0e-25
Match length
                   85
                   60
% identity
NCBI Description
                   (AB007790) DREB2A [Arabidopsis thaliana]
                   >gi_4126706_dbj_BAA36705_ (AB016570) DREB2A [Arabidopsis
                   thaliana]
                   6250
Seq. No.
Contig ID
                   6401 1.R1040
5'-most EST
                   uC-qmrominsoy047c11b1
Method
                   BLASTX
                   q1001449
NCBI GI
BLAST score
                   154
E value
                   6.0e-10
Match length
                   91
% identity
                   41
                   (D63999) hypothetical protein [Synechocystis sp.]
NCBI Description
                   6251
Seq. No.
Contig ID
                   6404 1.R1040
5'-most EST
                   LIB3139-022-P1-N1-H3
Method
                   BLASTX
NCBI GI
                   q3551958
BLAST score
                   714
E value
                   2.0e-75
Match length
                   197
% identity
NCBI Description
                   (AF082032) senescence-associated protein 12 [Hemerocallis
                   hybrid cultivar]
Seq. No.
                   6252
Contig ID
                   6404_2.R1040
5'-most EST
                   uC-gmrominsoy207h01b1
Method
                   BLASTX
NCBI GI
                   q2708750
BLAST score
                   501
E value
                   2.0e-50
Match length
                   253
% identity
NCBI Description
                   (AC003952) putative physical impedence protein [Arabidopsis
```

thaliana]

Seq. No. 6253

Contig ID 6405 1.R1040

5'-most EST LIB3094-061-Q1-K1-B3

Seq. No. 6254

Contig ID 6405_2.R1040

5'-most EST LIB3049-009-Q1-E1-A11

Method BLASTX
NCBI GI g4325372
BLAST score 665
E value 3.0e-69
Match length 282
% identity 54

NCBI Description (AF128396) contains similarity to protein disulfide

isomerases [Arabidopsis thaliana]

Seq. No. 6255

Contig ID 6405_3.R1040 5'-most EST uxk700669734.h1

Seq. No. 6256

Contig ID 6405 4.R1040

5'-most EST uC-gmronoir058g07b1

Seq. No. 6257

Contig ID 6405_5.R1040 5'-most EST awf700836446.h1

Seq. No. 6258

Contig ID 6405 6.R1040

5'-most EST LIB3\overline{1}06-035-Q1-K1-D1

Seq. No. 6259

Contig ID 6405_8.R1040

5'-most EST jC-gmf102220139g01a1

Seq. No. 6260

Contig ID 6406_1.R1040

5'-most EST LIB3050-006-Q1-E1-G2

Seq. No. 6261

Contig ID 6408_1.R1040

5'-most EST LIB3049-012-Q1-E1-H8

Seq. No. 6262

Contig ID 6408_2.R1040

5'-most EST LIB3107-039-Q1-K1-D10

Seq. No. 6263

Contig ID 6411_1.R1040

5'-most EST LIB3170-057-Q1-K1-D6

Method BLASTX
NCBI GI g2129944
BLAST score 410
E value 1.0e-39

193 Match length 47 % identity RNA-binding protein RZ-1 - wood tobacco
>gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1
[Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_ (D28861)
RNA binding protein, RZ-1 [Nicotiana sylvestris] NCBI Description 6264 Seq. No. Contig ID 6416 1.R1040 5'-most EST LIB3029-003-Q1-B1-C4 Seq. No. 6265 6428 1.R1040 Contig ID uC-gmflminsoy056c09b1 5'-most EST BLASTX Method q4049341 NCBI GI 166 BLAST score 3.0e-11 E value 146 Match length 35 % identity (AL034567) putative protein [Arabidopsis thaliana] NCBI Description 6266 Seq. No. 6433 1.R1040 Contig ID 5'-most EST ncj700987169.hl BLASTX Method g169363 NCBI GI BLAST score 377 E value 9.0e-36 Match length 151 54 % identity (M75856) PVPR3 [Phaseolus vulgaris] NCBI Description 6267 Seq. No. 6433 2.R1040 Contig ID 5'-most EST LIB3087-001-Q1-K1-D6 Seq. No. 6268 6434 1.R1040 Contig ID LIB3107-021-Q1-K1-E3 5'-most EST 6269 Seq. No. 6434 2.R1040 Contig ID

5'-most EST LIB3051-002-Q1-E1-H11

Seq. No. 6270

Contig ID 6435_1.R1040 5'-most EST gsv701054428.h1

Seq. No. 6271

Contig ID 6440_1.R1040

5'-most EST LIB3074-035-Q1-K1-C9

Method BLASTX
NCBI GI g3377820
BLAST score 436
E value 5.0e-43
Match length 123

```
% identity
                   70
NCBI Description
                   (AF076275) contains similarity to coatomer zeta chains
                   [Arabidopsis thaliana]
                   6272
Seq. No.
                   6440 2.R1040
Contig ID
                   LIB3040-023-Q1-E1-D9
5'-most EST
                   BLASTX
Method
                   g3377820
NCBI GI
BLAST score
                   280
                   5.0e-25
E value
                   64
Match length
                   80
% identity
NCBI Description
                   (AF076275) contains similarity to coatomer zeta chains
                   [Arabidopsis thaliana]
Seq. No.
                   6273
                   6441 1.R1040
Contig ID
5'-most EST
                   q4292967
Method
                   BLASTN
                   g438898
NCBI GI
BLAST score
                   136
                   3.0e-70
E value
                   407
Match length
                   85
% identity
NCBI Description
                   Soybean glutamine phosphoribosylpyrophosphate
                   amidotransferase mRNA, complete cds
                   6274
Seq. No.
                   6442 1.R1040
Contig ID
                   trc700561456.hl
5'-most EST
                   6275
Seq. No.
                   6442 2.R1040
Contig ID
                   LIB3072-015-Q1-E1-D10
5'-most EST
                   6276
Seq. No.
Contig ID
                   6445 1.R1040°
                   gsv7\overline{0}1046109.h1
5'-most EST
                   6277
Seq. No.
                   6445 2.R1040
Contig ID
5'-most EST
                   uC-gmropic038e03b1
                   6278
Seq. No.
                   6452 1.R1040
Contig ID
                   uaw7\overline{0}0666570.h1
5'-most EST
Method
                   BLASTN
                   g534940
NCBI GI
                   57
BLAST score
E value
                   4.0e-23
                   78
Match length
                   93
% identity
                   S.tuberosum mitochondrial DNA for ribosomal protein S10
NCBI Description
                   6279
Seq. No.
```

6453_1.R1040

Contig ID

```
nci700981278.hl
5'-most EST
Method
                    BLASTN
NCBI GI
                    g169930
BLAST score
                    392
                    0.0e + 00
E value
Match length
                    897
                    87
% identity
                    Glycine max calcium dependent protein kinase mRNA
NCBI Description
Seq. No.
                    6453 2.R1040
Contig ID
                    fC-qmse700674513a2
5'-most EST
Method
                    BLASTX
NCBI GI
                    g116054
BLAST score
                    309
E value
                    1.0e-28
                    76
Match length
                    74
% identity
                    CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK)
NCBI Description
                    >gi_280393_pir__A43713 calcium-dependent protein kinase (EC
                    2.7.1.-) - soybean >gi 169931 (M64987) Glycine max calcium
                    dependent protein kinase mRNA. [Glycine max]
Seq. No.
                    6281
                    6456 1.R1040
Contig ID
5'-most EST
                    leu701153778.hl
                    BLASTX
Method
                    q115515
NCBI GI
BLAST score
                    402
                    8.0e-39
E value
Match length
                    149
                    37
% identity
                    CALMODULIN >gi_71683_pir__MCAA calmodulin - alfalfa
NCBI Description
                    >gi_19579_emb_CAA36644_ (X52398) calmodulin (AA 1-149) [Medicago_sativa] >gi_170070 (L01430) calmodulin [Glycine
                    max] >gi_170074 (L014\overline{3}2) calmodulin [Glycine max]
                    >gi_506852 (L20507) calmodulin [Vigna radiata] >gi_4103957
                    (AF030032) calmodulin [Phaseolus vulgaris]
                    >gi 1583767_prf _ 2121384A calmodulin [Glycine max]
>gi 1583769_prf _ 2121384C calmodulin [Glycine max]
Seq. No.
                    6456 3.R1040
Contig ID
5'-most EST
                    LIB3029-002-Q1-B1-E4
                    6283
Seq. No.
Contig ID
                    6456 4.R1040
5'-most EST
                    jsh701069327.h1
Method
                    BLASTX
NCBI GI
                    q4379369
BLAST score
                    331
                    7.0e-31
E value
Match length
                    122
                    33
% identity
                    (X90560) Calmodulin [Cloning vector pBluescript]
NCBI Description
```

6284

Seq. No.

NCBI GI

```
6456 5.R1040
Contig ID
                   LIB3106-007-Q1-K1-A9
5'-most EST
Seq. No.
                   6285
                   6457 1.R1040
Contig ID
                   sat7\overline{0}1009851.h1
5'-most EST
                   6286
Seq. No.
                   6457 2.R1040
Contig ID
5'-most EST
                   fC-gmse700675662f2
Method
                   BLASTX
                   g2760839
NCBI GI
                   177
BLAST score
                   2.0e-12
E value
                   62
Match length
                   29
% identity
                   (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                   6287
Seq. No.
                   6457 3.R1040
Contig ID
                   crh700850651.hl
5'-most EST
                   6288
Seq. No.
                   6461 1.R1040
Contig ID
5'-most EST
                   uC-gmropic066d11b1
                   6289
Seq. No.
Contig ID
                   6464 1.R1040
                   LIB3029-002-Q1-B1-F5
5'-most EST
                   6290
Seq. No.
                   6465 1.R1040
Contig ID
5'-most EST
                   g4396524
Method
                   BLASTX
                   g4091806
NCBI GI
BLAST score
                   824
                   4.0e-88
E value
Match length
                   309
% identity
                   60
                   (AF052585) CONSTANS-like protein 2 [Malus domestica]
NCBI Description
Seq. No.
                   6291
                   6467 1.R1040
Contig ID
5'-most EST
                   LIB3\overline{0}29-002-Q1-B1-G1
Method
                   BLASTX
NCBI GI
                   g3036807
                   513
BLAST score
E value
                   6.0e-52
                   167
Match length
% identity
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                   6292
Seq. No.
Contig ID
                   6478 1.R1040
5'-most EST
                   1eu7\overline{0}1145927.h1
Method
                   BLASTX
```

g1084415

```
398
BLAST score
                  1.0e-38
E value
Match length
                  123
                  65
% identity
                  RNA-binding protein - Wood tobacco >gi 624925 dbj BAA05170
NCBI Description
                   (D26182) RNA-binding glycine rich protein (RGP-2)
                   [Nicotiana sylvestris]
                  6293
Seq. No.
                  6478 2.R1040
Contig ID
5'-most EST
                  jC-gmst02400028g05a1
Method
                  BLASTX
                  g2493318
NCBI GI
BLAST score
                  453
                  6.0e-45
E value
                  102
Match length
                  83
% identity
                  BLUE COPPER PROTEIN PRECURSOR >qi 562779 emb CAA80963
NCBI Description
                  (Z25471) blue copper protein [Pisum sativum]
                  >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]
Seq. No.
                  6294
Contig ID
                  6478 3.R1040
5'-most EST
                  uC-gmrominsoy316g06b1
Method
                  BLASTX
NCBI GI
                  g1084415
BLAST score
                  344
E value
                  2.0e-32
                  110
Match length
% identity
                  RNA-binding protein - Wood tobacco >gi 624925 dbj BAA05170
NCBI Description
                   (D26182) RNA-binding glycine rich protein (RGP-2)
                  [Nicotiana sylvestris]
                  6295
Seq. No.
                  6478_4.R1040
Contig ID
5'-most EST
                  LIB3094-002-Q1-K1-G1
                  BLASTX
Method
NCBI GI
                  g1084415
BLAST score
                  307
E value
                  4.0e-28
Match length
                  107
% identity
                  59
NCBI Description
                  RNA-binding protein - Wood tobacco >gi 624925 dbj BAA05170
                  (D26182) RNA-binding glycine rich protein (RGP-2)
                  [Nicotiana sylvestris]
Seq. No.
                  6296
Contig ID
                  6488 1.R1040
5'-most EST
                  kmv700740304.hl
Method
                  BLASTX
NCBI GI
                  q2500426
BLAST score
                  343
E value
                  9.0e-32
Match length
                  124
% identity
NCBI Description
                  30S RIBOSOMAL PROTEIN S9 >gi 1652399 dbj BAA17321 (D90905)
```

6297 Seq. No. Contig ID 6489 1.R1040 rca700997926.hl 5'-most EST BLASTX Method g1931652 NCBI GI 209 BLAST score E value 2.0e-16 101 Match length 50 % identity (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog NCBI Description [Arabidopsis thaliana] Seq. No. 6298 6498 1.R1040 Contig ID LIB3029-001-Q1-B1-H10 5'-most EST 6299 Seq. No. 6500 1.R1040 Contig ID uC-gmronoir008d08b1 5'-most EST BLASTX Method NCBI GI g3738320 BLAST score 459 E value 3.0e-45Match length 303 % identity 36 (AC005170) putative cinnamoyl CoA reductase [Arabidopsis NCBI Description thaliana] 6300 Seq. No. 6500 2.R1040 Contig ID LIB3051-010-Q1-E1-D4 5'-most EST BLASTX Method q3738320 NCBI GI BLAST score 280 E value 7.0e-25 Match length 129 % identity (AC005170) putative cinnamoyl CoA reductase [Arabidopsis NCBI Description thaliana] 6301 Seq. No. Contig ID 6520 1.R1040 $hyd7\overline{0}0728002.h1$ 5'-most EST BLASTX Method NCBI GI q2880051 BLAST score 227 E value 4.0e-18 Match length 101 47 % identity (AC002340) putative protein kinase [Arabidopsis thaliana] NCBI Description Seq. No. 6302 6522 1.R1040 Contig ID

30S ribosomal protein S9 [Synechocystis sp.]

 $dpv7\overline{0}1097360.h1$

BLASTX

5'-most EST Method

```
q4165018
NCBI GI
BLAST score
                   1037
                   1.0e-156
E value
Match length
                   615
                   48
% identity
                   (D89053) Acyl-CoA synthetase 3 [Homo sapiens]
NCBI Description
                   6303
Seq. No.
Contig ID
                   6522 2.R1040
                   LIB3029-001-Q1-B1-D4
5'-most EST
                   BLASTX
Method
                   g1468969
NCBI GI
                   172
BLAST score
                   6.0e-12
E value
Match length
                   56
                   55
% identity
                  (D30666) brain acyl-CoA synthtase II [Rattus norvegicus]
NCBI Description
                   6304
Seq. No.
Contig ID
                   6522 3.R1040
                   uaw7\overline{0}0662748.h1
5'-most EST
                   BLASTX
Method
                   g1468969
NCBI GI
BLAST score
                   380
                   1.0e-36
E value
                   134
Match length
% identity
                   57
                  (D30666) brain acyl-CoA synthtase II [Rattus norvegicus]
NCBI Description
                   6305
Seq. No.
                   6526 1.R1040
Contig ID
                   kl1701206060.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3482913
BLAST score
                   646
                   2.0e-67
E value
Match length
                   253
% identity
                   52
                   (AC003970) Similar to MtN21, gi 2598575, Megicago
NCBI Description
                   truncatula nodulation induced gene [Arabidopsis thaliana]
                   6306
Seq. No.
Contig ID
                   6532 1.R1040
                   LIB3040-015-Q1-E1-C6
5'-most EST
                   6307
Seq. No.
                   6532 2.R1040
Contig ID
5'-most EST
                   LIB3040-053-Q1-E1-F12
                   6308
Seq. No.
                   6533 1.R1040
Contig ID
                   crh700851849.h1
5'-most EST
Method
                   BLASTX
                   q265975
NCBI GI
                   173
BLAST score
                   8.0e-12
E value
```

134

Match length

```
% identity
                   37
NCBI Description
                  RD29B=responsive-to-dessication protein [Arabidopsis
                   thaliana, Columbia ecotype, Peptide, 604 aa]
                   >gi_445066_prf__1908381B rd29B gene [Arabidopsis thaliana]
Seq. No.
                   6309
                   6533 2.R1040
Contig ID
                   awf700837810.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2654206
BLAST score
                   183
                   5.0e-13
E value
                   295
Match length
                   19
% identity
                   (AF035535) cold acclimation protein [Spinacia oleracea]
NCBI Description
                   >gi 2661094 (AF035536) cold acclimation protein [Spinacia
                   oleracea]
                   6310
Seq. No.
                   6535 1.R1040
Contig ID
                   LIB3029-001-Q1-B1-E9
5'-most EST
Seq. No.
                   6311
                   6536 1.R1040
Contig ID
                   LIB3139-053-P1-N1-F11
5'-most EST
                   6312
Seq. No.
Contig ID
                   6538 1.R1040
5'-most EST
                   uC-gmrominsoy172b01b1
                   BLASTX
Method
                   g2244852
NCBI GI
BLAST score
                   615
                   9.0e-64
E value
                   195
Match length
                   63
% identity
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   6313
Seq. No.
Contig ID
                   6538 3.R1040
                   zhf700957864.h1
5'-most EST
                   6314
Seq. No.
                   6543 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy272d12b1
Method
                   BLASTX
NCBI GI
                   g1871185
BLAST score
                   163
                   5.0e-11
E value
Match length
                   44
% identity
```

Seq. No. 6315

NCBI Description

Contig ID 6544_1.R1040

5'-most EST LIB3029-001-Q1-B1-D1

Method BLASTX NCBI GI g4539423

(U90439) seven in absentia isolog [Arabidopsis thaliana]

NCBI GI

Δ :___

```
341
BLAST score
E value
                   4.0e-32
Match length
                   120
% identity
                   58
                   (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                   [Arabidopsis thaliana]
                   6316
Seq. No.
                   6545 1.R1040
Contig ID
5'-most EST
                   gsv701051793.hl
Method
                   BLASTX
NCBI GI
                   g132659
                   732
BLAST score
                   2.0e-77
E value
                  241
Match length
                   60
% identity
NCBI Description
                  50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13)
                   >gi_81483_pir__A32033 ribosomal protein L13 precursor,
                   chloroplast - spinach > gi 170133 (J04461) ribosomal protein
                  L13 [Spinacia oleracea]
                   6317
Seq. No.
Contig ID
                   6551_1.R1040
                   uC-gmronoir007f09b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2911058
BLAST score
                   275
E value
                   2.0e-38
Match length
                   112
% identity
                   (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6318
                   6551 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400002c05a1
                   6319
Seq. No.
Contig ID
                   6560 1.R1040
5'-most EST
                   fC-gmse7000763420f1
Method
                  BLASTX
NCBI GI
                  g3413699
BLAST score
                   473
E value
                   3.0e-47
Match length
                  115
                   73
% identity
                   (AC004747) putative heat shock protein [Arabidopsis
NCBI Description
                   thaliana]
                   6320
Seq. No.
                   6596 1.R1040
Contig ID
5'-most EST
                  LIB3029-009-Q1-B1-F4
                   6321
Seq. No.
Contig ID
                   6598 1.R1040
5'-most EST
                  LIB3170-086-Q1-J1-C3
Method
                  BLASTN
```

g2924257

Method

BLASTX

```
BLAST score
                   246
E value
                   1.0e-135
Match length
                   880
% identity
                   76
NCBI Description
                   Tobacco chloroplast genome DNA
                   6322
Seq. No.
                   6602 1.R1040
Contig ID
5'-most EST
                   bth700847367.hl
                   BLASTN
Method
NCBI GI
                   g466530
BLAST score
                   266
                   1.0e-147
E value
Match length
                   878
% identity
                   83
                   Citrullus vulgaris mRNA for cysteine synthase, complete cds
NCBI Description
                   6323
Seq. No.
Contig ID
                   6606_1.R1040
5'-most EST
                   LIB3139-118-P1-N1-F10
Method
                   BLASTN
                   g4097879
NCBI GI
BLAST score
                   251
E value
                   1.0e-138
Match length
                   815
% identity
                   86
                   Bean pod mottle virus complete segment RNA1 polyprotein -
NCBI Description
                   gene, complete cds
                   6324
Seq. No.
Contig ID
                   6608 1.R1040
                   LIB3\overline{0}94-071-Q1-K1-E1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1762945
BLAST score
                   415
E value
                   3.0e-40
Match length
                   155
% identity
                                  able to induce HR-like lesions [Nicotiana
NCBI Description
                   (U66269) ORF;
                   tabacum]
Seq. No.
                   6325
                   6608 2.R1040
Contig ID
5'-most EST
                   LIB3170-014-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g1762945
BLAST score
                   258
E value
                   2.0e-44
Match length
                   136
% identity
NCBI Description
                   (U66269) ORF; able to induce HR-like lesions [Nicotiana
                   tabacum]
Seq. No.
                   6326
Contig ID
                   6609 1.R1040
5'-most EST
                   LIB3109-002-Q1-K1-A10
```

NCBI Description

```
NCBI GI
                   q4056420
BLAST score
                   454
E value
                   8.0e-45
Match length
                   164
% identity
                   53
NCBI Description
                   (AC005322) ESTs gb T144077 and gb T43352 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   6327
Contig ID
                   6609 2.R1040
5'-most EST
                   LIB3039-047-Q1-E1-B9
                   BLASTX
Method
NCBI GI
                   q3298546
BLAST score
                   175
E value
                   1.0e-12
Match length
                   61
                   54
% identity
NCBI Description
                   (AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.
                   6328
                   6612 1.R1040
Contig ID
                   LIB3109-037-Q1-K1-G5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2191149
BLAST score
                   351
E value
                   2.0e-39
Match length
                   188
% identity
                   (AF007269) Similar to protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6329
                   6625 1.R1040
Contig ID
5'-most EST
                   LIB3029-011-Q1-B1-G12
                   6330
Seq. No.
Contig ID
                   6629 1.R1040
5'-most EST
                   uaw700664958.hl
Method
                   BLASTX
NCBI GI
                   q3763916
BLAST score
                   274
E value
                   4.0e-24
Match length
                   164
                   37
% identity
NCBI Description
                   (AC004450) unknown protein [Arabidopsis thaliana]
                   >gi 4531439 gb AAD22124.1 AC006224_6 (AC006224) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   6331
                   6632 1.R1040
Contig ID
                   q551\overline{0}323
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4049518
BLAST score
                   463
                   9.0e-46
E value
                   230
Match length
% identity
                   42
```

```
[Schizosaccharomyces pombe]
                   6332
Seq. No.
Contig ID
                   6637 1.R1040
5'-most EST
                   hyd7\overline{0}0725528.h1
                   6333
Seq. No.
                   6638 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810021b02a1
Method
                   BLASTX
                   g3080407
NCBI GI
BLAST score
                   424
E value
                   1.0e-84
Match length
                   221
                   73
% identity
NCBI Description
                   (AL022604) hypothetical protein [Arabidopsis thaliana]
                   6334
Seq. No.
                   6638 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy089f09b1
Method
                   BLASTX
NCBI GI
                   g3080407
BLAST score
                   435
                   5.0e-43
E value
Match length
                   138
                   79
% identity
NCBI Description
                   (AL022604) hypothetical protein [Arabidopsis thaliana]
                   6335
Seq. No.
                   6639 1.R1040
Contig ID
5'-most EST
                   qsv7\overline{0}1049521.h1
Method
                   BLASTX
                   g461736
NCBI GI
BLAST score
                   1763
E value
                   0.0e + 00
Match length
                   385
% identity
                   91
NCBI Description
                   MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR
                   >gi 478786 pir S29316 chaperonin 60 - cucurbit
                   >gi 12546 emb CAA50218 (X70868) chaperonin 60 [Cucurbita
                   sp.]
Seq. No.
                   6336
Contig ID
                   6643 1.R1040
5'-most EST
                   LIB3107-013-Q1-K1-E2
                   BLASTX
Method
                   g3738327
NCBI GI
BLAST score
                   374
E value
                   1.0e-35
Match length
                   148
% identity
                   49
                   (AC005170) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                   thaliana]
                   6337
Seq. No.
```

6643 2.R1040

jC-gmst02400029a10a1

Contig ID 5'-most EST

```
Method
                   BLASTX
                   q3738327
NCBI GI
BLAST score
                   365
                   7.0e-35
E value
                   119
Match length
                   57
% identity
                   (AC005170) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                   thaliana]
                   6338
Seq. No.
                   6644 1.R1040
Contig ID
                   hyd7\overline{0}0730480.h1
5'-most EST
                   BLASTX
Method
                   g3935152
NCBI GI
BLAST score
                   1752
                   0.0e + 00
E value
                   413
Match length
% identity
                   (AC005106) T25N20.16 [Arabidopsis thaliana]
NCBI Description
                   6339
Seq. No.
                   6652 1.R1040
Contig ID
                   LIB3170-074-Q1-K1-E10
5'-most EST
                   6340
Seq. No.
                   6652 2.R1040
Contig ID
                   jC-gmle01810088e06a1
5'-most EST
Seq. No.
                   6341
Contig ID
                   6654 1.R1040
                   LIB3030-012-Q1-B1-D11
5'-most EST
                   BLASTX
Method
                   g3582343
NCBI GI
BLAST score
                   167
                   9.0e-12
E value
                   100
Match length
                   34
% identity
                   (AC005496) putative flavonol 3-o-glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   6342
Seq. No.
                   6655 1.R1040
Contig ID
                   pcp700994725.h1
5'-most EST
                   BLASTX
Method
                   g2961384
NCBI GI
                   618
BLAST score
                   5.0e-70
E value
Match length
                   254
                   52
% identity
                   (AL022141) aldehyde dehydrogenase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   6343
Seq. No.
                   6656 1.R1040
Contig ID
 5'-most EST
                   g4397369
                   BLASTX
Method
```

g4539007

NCBI GI

NCBI Description

```
BLAST score
                   561
E value
                   1.0e-57
Match length
                   112
% identity
                   91
                   (AL049481) cytochrome c [Arabidopsis thaliana]
NCBI Description
                   6344
Seq. No.
                   6656 2.R1040
Contig ID
5'-most EST
                   LIB3039-029-Q1-E1-F11
Method
                   BLASTX
NCBI GI
                   q118013
BLAST score
                   579
E value
                   7.0e-60
Match length
                   111
% identity
                   96
                  CYTOCHROME C >gi 65497 pir CCMB cytochrome c - mung bean
NCBI Description
                   6345
Seq. No.
Contig ID
                   6661 1.R1040
5'-most EST
                   LIB3093-003-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   g4204912
BLAST score
                   1215
E value
                   1.0e-134
Match length
                   396
                   61
% identity
                  (U58918) MEK kinase [Arabidopsis thaliana]
NCBI Description
                   6346
Seq. No.
                   6661 2.R1040
Contig ID
5'-most EST
                   LIB3139-095-P1-N1-H3
Method
                   BLASTX
NCBI GI
                   g4204912
BLAST score
                   225
E value ·
                   5.0e-18
Match length
                   129
% identity
                   44
                   (U58918) MEK kinase [Arabidopsis thaliana]
NCBI Description
                   6347
Seq. No.
                   6661 3.R1040
Contig ID
5'-most EST
                   jC-gmle01810063e05d1
Seq. No.
                   6661 7.R1040
Contig ID
5'-most EST
                   LIB3170-024-Q1-J1-A4
Seq. No.
                   6349
Contig ID
                   6670 1.R1040
5'-most EST
                   LIB3030-012-Q1-B1-A8
Method
                   BLASTX
NCBI GI
                   q996020
BLAST score
                   387
E value
                   2.0e-66
Match length
                   237
                   53
% identity
```

(X91638) BRM protein [Gallus gallus]

```
6350
 Seq. No.
                    6672 1.R1040
 Contig ID
                   LIB3030-012-Q1-B1-B10
 5'-most EST
 Seq. No.
                    6673 1.R1040
 Contig ID
 5'-most EST
                   uC-gmflminsoy024d02b1
 Seq. No.
                   6678 1.R1040
 Contig ID
                   sat701014952.hl
 5'-most EST
 Seq. No.
 Contig ID
                    6683 1.R1040
 5'-most EST
                   rlr700900487.h1
 Method
                   BLASTX
 NCBI GI
                   q2708532
 BLAST score
                   970
 E value
                    1.0e-105
 Match length
                    301
 % identity
 NCBI Description
                   (AF029351) putative RNA binding protein [Nicotiana tabacum]
                    6354
Seq. No.
 Contig ID
                    6687 1.R1040
 5'-most EST
                    jC-qmle01810000g09a1
                    6355
 Seq. No.
                    6687 2.R1040
 Contig ID
 5'-most EST
                    zpv700760473.h1
 Seq. No.
                    6356
 Contig ID
                    6694 1.R1040
 5'-most EST
                    LIB3030-011-Q1-B1-H10
 Method
                    BLASTX
 NCBI GI
                    q1504020
 BLAST score
                    122
 E value
                    6.0e-10
 Match length
                    55
                    67
 % identity
                    (D86973) similar to Yeast translation activator GCN1
 NCBI Description
                    (P1:A48126) [Homo sapiens]
 Seq. No.
                    6357
 Contig ID
                    6699 1.R1040
 5'-most EST
                   LIB3051-103-Q1-K1-G7
 Method
                   BLASTX
 NCBI GI
                    q461812
 BLAST score
                    414
 E value
                    2.0e-40
 Match length
                   193
 % identity
                    44
                   CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
 NCBI Description
                    GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                    Cytochrome P-450 protein [Catharanthus roseus]
```

>gi 445604 prf 1909351A cytochrome P450 [Catharanthus

NCBI Description

```
Seq. No.
                   6358
Contig ID
                   6699 2.R1040
5'-most EST
                   uC-gmronoir043h10b1
Seq. No.
                   6359
                   6699 5.R1040
Contig ID
5'-most EST
                   zhf700952542.h1
                   6360
Seq. No.
Contig ID
                   6699 6.R1040
5'-most EST
                   zhf700961126.hl
                   6361
Seq. No.
Contig ID
                   6703 1.R1040
5'-most EST
                   LIB3030-012-Q1-B1-A12
Method
                   BLASTX
                   g4467124
NCBI GI
BLAST score
                   172
E value
                   3.0e-12
Match length
                   107
                   43
% identity
NCBI Description
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   6362
Contig ID
                   6703 2.R1040
5'-most EST
                   jC-gmf102220102h03a1
Method
                   BLASTX
NCBI GI
                   q4467124
BLAST score
                   159
E value
                   1.0e-10
Match length
                   43
                   70
% identity
NCBI Description
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
                   6363
Seq. No.
Contig ID
                   6704_1.R1040
5'-most EST
                   LIB3030-011-Q1-B1-B11
                   BLASTX
Method
                   g4006915
NCBI GI
BLAST score
                   215
E value
                   3.0e-17
Match length
                   111
% identity
                   44
NCBI Description
                   (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   6364
Contig ID
                   6706 1.R1040
                   zhf700965022.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4415908
BLAST score
                   431
E value
                   3.0e-42
Match length
                   152
% identity
                   49
```

roseus]

(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.

6371

```
6365
Seq. No.
                   6713_1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy119a09b1
Method
                   BLASTX
NCBI GI
                   g3080437
BLAST score
                   859
                   3.0e-92
E value
                   379
Match length
                   54
% identity
                   (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                   6366
Seq. No.
                   6715 1.R1040
Contig ID
5'-most EST
                   xpa700797631.h1
                   6367
Seq. No.
                   6715 2.R1040
Contig ID
5'-most EST
                   LIB3040-043-Q1-E1-G1
                   6368
Seq. No.
Contig ID
                   6716 1.R1040
                   LIB3\overline{0}51-079-Q1-K1-C3
5'-most EST
                   BLASTN
Method
NCBI GI
                   g488576
BLAST score
                   204
E value
                   1.0e-111
                   416
Match length
                   87
% identity
                   Medicago sativa Regen S clone pH3c131 histone H3.2 mRNA,
NCBI Description
                   complete cds
                   6369
Seq. No.
                   6716_2.R1040
Contig ID
                   LIB3049-029-Q1-E1-D2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g488576
                   193
BLAST score
E value
                   1.0e-104
Match length
                   413
                   87
% identity
NCBI Description
                   Medicago sativa Regen S clone pH3c131 histone H3.2 mRNA,
                   complete cds
Seq. No.
                   6370
                   6716 3.R1040
Contig ID
5'-most EST
                   LIB3049-019-Q1-E1-H7
Method
                   BLASTN
NCBI GI
                   g1208641
BLAST score
                   81
E value
                   1.0e-37
Match length
                   197
% identity
                   Amphicarpa bracteata histone H3 gene, partial cds, clone
NCBI Description
                   H3-B2AMC
```

```
Contig ID
                  6716 4.R1040
5'-most EST
                  LIB3T70-062-Q1-J1-G11
Method
                  BLASTN
NCBI GI
                  g488576
BLAST score
                  65
E value
                  8.0e-28
Match length
                  139
                  91
% identity
                  Medicago sativa Regen S clone pH3c131 histone H3.2 mRNA,
NCBI Description
                  complete cds
Seq. No.
                  6372
                  6720 1.R1040
Contig ID
5'-most EST
                  LIB3030-011-Q1-B1-E12
                  BLASTX
Method
NCBI GI
                  g2618691
BLAST score
                  449
E value
                  6.0e-60
Match length
                  185
% identity
                  64
NCBI Description
                   (AC002510) putative chloroplast envelope Ca2+-ATPase
                  [Arabidopsis thaliana]
Seq. No.
                  6373
                  6722 1.R1040
Contig ID
                  pmv700895035.h1
5'-most EST
Method
                  BLASTX
                  g3643594
NCBI GI
BLAST score
                  557
E value
                  1.0e-56
Match length
                  249
                  77
% identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                  6374
                  6722 2.R1040
Contig ID
5'-most EST
                  LIB3050-023-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g3643594
BLAST score
                  539
E value
                  2.0e-98
Match length
                  246
                  76
% identity
NCBI Description
                  (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                  6375
                  6722 3.R1040
Contig ID
                  LIB3030-010-Q1-B1-G6
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3643594
BLAST score
                  271
E value
                  1.0e-23
Match length
                  63
% identity
NCBI Description
                  (AC005395) unknown protein [Arabidopsis thaliana]
```

6376

Seq. No.

```
6726 1.R1040
Contig ID
5'-most EST
                   pmv700892405.h1
                  BLASTX
Method
NCBI GI
                  q4455369
BLAST score
                   323
                   1.0e-29
E value
                  174
Match length
% identity
                   41
NCBI Description
                   (AL035524) hypothetical protein [Arabidopsis thaliana]
                   6377
Seq. No.
Contig ID
                   6732 1.R1040
5'-most EST
                   uC-gmflminsoy115g08b1
                   6378
Seq. No.
Contig ID
                   6734 1.R1040
5'-most EST
                   jC-gmf102220106h03a1
                   BLASTX
Method
                   g2911059
NCBI GI
BLAST score
                   909
E value
                   3.0e-98
                  197
Match length
                   84
% identity
                   (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6379
Contig ID
                   6736 1.R1040
                   pxt700943944.h1
5'-most EST
                   BLASTX
Method
                   g1076668
NCBI GI
BLAST score
                   1095
E value
                   1.0e-129
                   243
Match length
                   93
% identity
                  NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                   >gi 639834 emb CAA58823 (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
                   6380
Seq. No.
                   6737 1.R1040
Contig ID
5'-most EST
                   LIB3030-010-Q1-B1-E9
Seq. No.
                   6381
                   6738 1.R1040
Contig ID
5'-most EST
                   uC-gmropic036c09b1
                   BLASTN
Method
NCBI GI
                   g2337888
BLAST score
                   35
E value
                   6.0e-10
Match length
                   139
                   81
% identity
                   Genomic sequence for Arabidopsis thaliana BAC F14J16,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   6382
Seq. No.
```

6741 1.R1040

kl1701213610.h1

Contig ID

5'-most EST

```
Method
                  BLASTX
NCBI GI
                   g3876874
BLAST score
                   344
E value
                   9.0e-32
                   408
Match length
                   28
% identity
NCBI Description
                   (Z81535) Similarity to Human signal recognition particle
                  receptor alpha subunit (SW:P08240) [Caenorhabditis elegans]
                                                    3.
Seq. No.
                   6742 1.R1040
Contig ID
                  LIB3030-010-Q1-B1-F7
5'-most EST
                  BLASTX
Method
NCBI GI
                   q3395584
                   291
BLAST score
                   5.0e-34
E value
                   147
Match length
% identity
NCBI Description
                   (AL031179) importin beta subunit [Schizosaccharomyces
Seq. No.
                   6384
Contig ID
                   6744 1.R1040
5'-most EST
                   LIB3030-010-Q1-B1-G1
Method
                   BLASTX
NCBI GI
                   q2055273
BLAST score
                   1716
E value
                   0.0e + 00
Match length
                   386
% identity
NCBI Description
                   (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
Seq. No.
                   6385
                   6745 1.R1040
Contig ID
5'-most EST
                   q4290785
Seq. No.
                   6386
                   6745 2.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy002h05b1
                   6387
Seq. No.
Contig ID
                   6746 1.R1040
5'-most EST
                   1eu7\overline{0}1156386.h1
Method
                   BLASTX
NCBI GI
                   q4056467
BLAST score
                   335
E value
                   4.0e-31
Match length
                   126
% identity
                   52
                   (AC005990) Strong similarity to gb AB006693 spermidine
NCBI Description
                   synthase from Arabidopsis thaliana. ESTs gb AA389822,
                   gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256
                   come from this gene. [Arabidopsis thaliana]
Seq. No.
                   6388
```

6746 3.R1040

LIB3040-035-Q1-E1-B3

Contig ID 5'-most EST

77,

NCBI Description

```
6389
Seq. No.
                   6753 1.R1040
Contig ID
5'-most EST
                   k11701206385.h1
                   BLASTX
Method
NCBI GI
                   g3819099
BLAST score
                   152
                   1.0e-09
E value
Match length
                   84
% identity
                   42
                   (AJ009825) copper amine oxidase [Cicer arietinum]
NCBI Description
                   6390
Seq. No.
Contig ID
                   6756 1.R1040
                   LIB3170-003-Q1-K1-B4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2769642
BLAST score
                   760
                   1.0e-80
E value
Match length
                   224
% identity
                   64
NCBI Description
                   (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon
                   esculentum]
                   6391
Seq. No.
                   6757 1.R1040
Contig ID
5'-most EST
                   LIB3\overline{1}07-079-Q1-K1-B11
                   6392
Seq. No.
                   6757 2.R1040
Contig ID
                   jex700906928.h1
5'-most EST
Seq. No.
                   6393
                   6758 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810085e04a1
                   6394
Seq. No.
Contig .ID
                   6762 1.R1040
5'-most EST
                   jC-gmst02400014g11a1
                   BLASTX
Method
NCBI GI
                   g3337366
BLAST score
                   413
E value
                   3.0e-40
                   199
Match length
                   21
% identity
                   (AC004481) unknown protein [Arabidopsis thaliana]
NCBI Description
                   6395
Seq. No.
                   6763 1.R1040
Contig ID
5'-most EST
                   ncj700982144.hl
Method
                   BLASTX
NCBI GI
                   g231610
BLAST score
                   1445
E value
                   1.0e-161
Match length
                   374
                   78
% identity
```

ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

NCBI Description

```
6396
Seq. No.
                   6765_1.R1040
Contig ID
                   jsh7\overline{0}1066574.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4337175
BLAST score
                   510
E value
                   2.0e-51
Match length
                   137
                   69
% identity
NCBI Description
                   (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                   gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                   gb_AA720210 come from this gene. [Arabidopsis thaliana]
                   6397
Seq. No.
Contig ID
                   6766_1.R1040
                   g5058357
5'-most EST
Method
                   BLASTN
                   g3873174
NCBI GI
BLAST score
                   35
E value
                   9.0e-10
Match length
                   179
% identity
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC F14N23,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   6398
Contig ID
                   6766 2.R1040
                   LIB3\overline{0}93-011-Q1-K1-D4
5'-most EST
                   6399
Seq. No.
Contig ID
                   6766_3.R1040
                   jC-gmro02910047f09a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4191616
                   588
BLAST score
E value
                   7.0e-61
Match length
                   157
% identity
                   (AF120334) GTP-binding protein NGB [Homo sapiens]
NCBI Description
Seq. No.
                   6400
Contig ID
                   6766 4.R1040
5'-most EST
                   uC-qmrominsoy229a04b1
Method
                   BLASTX
                   q4191616
NCBI GI
BLAST score
                   377
E value
                   2.0e-36
Match length
                   93
% identity
                   69
```

>gi_67880_pir__ PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

(AF120334) GTP-binding protein NGB [Homo sapiens]

BLAST score

344

```
Seq. No.
                   6401
                   6766 5.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1149247.h1
Method
                   BLASTX
NCBI GI
                   g4191616
BLAST score
                   268
E value
                   2.0e-23
Match length
                   70
% identity
                   67
NCBI Description
                   (AF120334) GTP-binding protein NGB [Homo sapiens]
Seq. No.
                   6766 8.R1040
Contig ID
5'-most EST
                   smc700744313.h1
Seq. No.
                   6403
Contig ID
                   6766 10.R1040
5'-most EST
                   gsv7\overline{0}1044187.h1
Method
                   BLASTX
NCBI GI
                   q4191616
BLAST score
                   154
E value
                   2.0e-10
Match length
                   42
% identity
                   67
                   (AF120334) GTP-binding protein NGB [Homo sapiens]
NCBI Description
                                 * *
                   6404
Seq. No.
Contig ID
                   6768 1.R1040
5'-most EST
                   LIB3092-044-Q1-K1-D7
Method
                   BLASTX
NCBI GI
                   q3023271
BLAST score
                   1511
E value
                   0.0e + 00
Match length
                   381
                   86
% identity
NCBI Description
                   GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
                   (FALDH) (GSH-FDH) >gi 1675394 (U77637) class III ADH enzyme
                   [Oryza sativa]
Seq. No.
                   6405
Contig ID
                   6768 2.R1040
5'-most EST
                   LIB3109-028-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g1841502
BLAST score
                   453
E value
                   2.0e-47
Match length
                   105
% identity
                   90
NCBI Description
                   (Y11029) glutothione-dependent formaldehyde dehydrogenase
                   [Zea mays]
Seq. No.
                   6406
                   6769 1.R1040
Contig ID
5'-most EST
                   LIB3030-010-Q1-B1-C8
Method
                   BLASTX
NCBI GI
                   g3925363
```

```
2.0e-32
E value
Match length
                   96
                   79
% identity
NCBI Description
                   (AF067961) homeodomain protein [Malus domestica]
                   6407
Seq. No.
                   6774 1.R1040
Contig ID
5'-most EST
                   gsv701056309.hl
Seq. No.
                   6408
Contig ID
                   6774 2.R1040
5'-most EST
                   hrw7\overline{0}1060177.h1
                   6409
Seq. No.
                   6775 1.R1040
Contig ID
                   fde7\overline{0}0876739.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4522012
BLAST score
                   899
E value
                   7.0e-97
Match length
                   310
% identity
                   57
NCBI Description
                   (AC007069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   6410
                   6778_1.R1040
Contig ID
                   pxt700946334.h1
5'-most EST
Method
                   BLASTX
                   g3063470
NCBI GI
BLAST score
                   396
E value
                   2.0e-38
Match length
                   70
                   97
% identity
                   (AC003981) F22013.32 [Arabidopsis thaliana]
NCBI Description
                   6411
Seq. No.
Contig ID
                   6782 1.R1040
5'-most EST
                   uC-gmrominsoy243g03b1
Seq. No.
                   6412
Contig ID
                   6782 2.R1040
5'-most EST
                   awf700840314.h1
                   6413
Seq. No.
Contig ID
                   6782_3.R1040
5'-most EST
                   uC-gmflminsoy078f04b1
Seq. No.
                   6414
Contig ID
                   6783 1.R1040
5'-most EST
                   uC-gmrominsoy142c04b1
Method
                   BLASTX
NCBI GI
                   q3540219
BLAST score
                   891
E value
                   5.0e-96
                   390
Match length
% identity
                   (D87686) KIAA0017 protein [Homo sapiens]
NCBI Description
```

```
6415
Seq. No.
Contig ID
                   6784 1.R1040
5'-most EST
                   uaw700661165.h1
Method
                   BLASTX
                   g322787
NCBI GI
BLAST score
                   755
E value
                   7.0e-80
Match length
                   348
% identity .
                   46
                   pyruvate kinase (EC 2.7.1.40), cytosolic - potato
NCBI Description
                   6416
Seq. No.
                   6784 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400072a04a1
                   6417
Seq. No.
                   6785_1.R1040
Contig ID
5'-most EST
                   LIB3030-010-Q1-B1-B3
                   6418
Seq. No.
Contig ID
                   6787 1.R1040
                   LIB3\overline{0}30-009-Q1-B1-G5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3292830
BLAST score
                   346
                   4.0e-32
E value
Match length
                   263
                   37
% identity
                   (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                   6419
Seq. No.
Contig ID
                   6791 1.R1040
5'-most EST
                   uC-gmflminsoy018e10b1
Method
                   BLASTX
NCBI GI
                   g2828151
BLAST score
                   302
E value
                   2.0e-27
                   100
Match length
                   59
% identity
                   (AF042386) cyclophilin-33B [Homo sapiens]
NCBI Description
                   >gi_4406229_gb_AAD19907_ (AF104013) peptidyl-prolyl
                   cis-trans isomerase E [Homo sapiens]
                   6420
Seq. No.
                   6796_1.R1040
Contig ID
5'-most EST
                   LIB3030-009-Q1-B1-H7
                   BLASTX
Method
NCBI GI
                   g4263704
BLAST score
                   526
E value
                   3.0e-53
Match length
                   239
                   43
% identity
NCBI Description
                   (AC006223) putative sugar starvation-induced protein
                   [Arabidopsis thaliana]
```

1201

6421

Seq. No.

```
6796 3.R1040
Contig ID
5'-most EST
                   zhf700958381.h1
Method
                   BLASTX
NCBI GI
                   q4263704
BLAST score
                   163
E value
                   4.0e-11
                   64
Match length
                   42
% identity
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
                   6422
Seq. No.
                   6797 1.R1040
Contig ID
5'-most EST
                  LIB3109-048-Q1-K1-B1
                  BLASTX
Method
NCBI GI
                   g4105782
                   986
BLAST score
                   1.0e-107
E value
                   215
Match length
                   85
% identity
                   (AF049922) PGP169-12 [Petunia x hybrida]
NCBI Description
                   6423
Seq. No.
                   6799 1.R1040
Contig ID
5'-most EST
                   g4291450
Method
                  BLASTN
NCBI GI
                  g3241924
BLAST score
                   37
                   1.0e-10
E value
                  128
Match length
                   88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNC6, complete sequence [Arabidopsis thaliana]
                   6424
Seq. No.
                   6800 1.R1040
Contig ID
5'-most EST
                  LIB3030-009-Q1-B1-F2
Method
                  BLASTX
                  g626009
NCBI GI
BLAST score
                  800
E value
                   1.0e-85
Match length
                  200
% identity
                   71
                  capsanthin-capsorubin synthase (EC 1.-.-.) - pepper
NCBI Description
                   >gi_468748_emb_CAA54495_ (X77289) capsanthin/capsorubin
                   synthase [Capsicum annuum] >gi_522120_emb_CAA53759_
                   (X76165) capsanthin/capsorubin sythase [Capsicum annuum]
Seq. No.
                   6425
Contig ID
                   6804_2.R1040
5'-most EST
                  wrg700789208.h2
Method
                  BLASTX
NCBI GI
                  g1922242
BLAST score
                   235
                   1.0e-19
E value
Match length
                   60
                  85
% identity
```

```
NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   6426
                   6804 3.R1040
Contig ID
5'-most EST
                   zpv700763346.h1
Method
                   BLASTX
NCBI GI
                   g1922242
BLAST score
                   210
E value
                   1.0e-16
Match length
                   53
% identity
                   (Y10084) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   6805 1.R1040
5'-most EST
                   LIB3030-009-Q1-B1-G1
Method
                   BLASTX
NCBI GI
                   q2462828
BLAST score
                   298
E value
                   5.0e-27
Match length
                   118
% identity
                   46
NCBI Description
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
                   6428
Seq. No.
Contig ID
                   6805 2.R1040
5'-most EST
                   zsq7\overline{0}1124373.h1
Method
                   BLASTX
NCBI GI
                   q2462828
BLAST score
                   167
E value
                   6.0e-12
Match length
                   59
% identity
                   47
NCBI Description
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   6429
Contig ID
                   6806 1.R1040
5'-most EST
                   jC-qmro02910014f01a1
Method
                   BLASTX
NCBI GI
                   q4508083
BLAST score
                   500
E value
                   3.0e-50
Match length
                   307
% identity
NCBI Description
                   (AC005882) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   6430
Contig ID
                   6807 1.R1040
5'-most EST
                   LIB3170-007-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   q3687251
BLAST score
                   542
E value
                   3.0e-55
Match length
                   142
                   73
% identity
```

NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

```
6431
Seq. No.
Contig ID
                   6810 1.R1040
5'-most EST
                   LIB3049-001-Q1-E1-G8
Method
                   BLASTX
NCBI GI
                   g2213625
BLAST score
                   478
                   1.0e-47
E value
Match length
                   169
% identity
                   54
NCBI Description
                   (AC000103) F21J9.17 [Arabidopsis thaliana]
                   6432
Seq. No.
Contig ID
                   6810 2.R1040
                   LIB3030-009-Q1-B1-D9
5'-most EST
                   6433
Seq. No.
                   6810 4.R1040
Contig ID
5'-most EST
                   pxt700941967.h1
                   6434
Seq. No.
Contig ID
                   6811_1.R1040
5'-most EST
                   uC-gmflminsoy008h02b1
Method
                   BLASTX
NCBI GI
                   g232024
BLAST score
                   234
E value
                   6.0e-19
Match length
                   253
% identity
                   34
                  PROTEIN E6 >gi 421806 pir A46130 fiber protein - upland
NCBI Description
                   cotton >gi_2129498_pir__S65061 fiber protein E6 (clone
                   CKE6-1A) - upland cotton >gi 167323 (M92051) 5' start site
                   is putative; putative [Gossypium hirsutum] >gi 1000084
                   (U30505) E6 [Gossypium hirsutum]
Seq. No.
                   6435
Contig ID
                   6811_2.R1040
5'-most EST
                   g4295094
Method
                   BLASTX
                   g167324
NCBI GI
BLAST score
                   170
                   1.0e-11
E value
Match length
                   191
% identity
                   (M92051) 5' start site is putative; putative [Gossypium
NCBI Description
                   hirsutum]
Seq. No.
                   6436
Contig ID
                   6812 1.R1040
5'-most EST
                   LIB3065-008-Q1-N1-F6
                   BLASTX
Method
NCBI GI
                   q2245080
BLAST score
                   151
E value
                  9.0e-10
Match length
                  80
% identity
                   45
```

NCBI Description (Z97343) myosin heavy chain homolog [Arabidopsis thaliana]

Seq. No.

6444

```
6437
Seq. No.
                    6815 1.R1040
Contig ID
                    leu7\overline{0}1152947.h1
5'-most EST
                   BLASTX
Method
                    g3273202
NCBI GI
                    345
BLAST score
                    3.0e-32
E value
Match length
                    121
% identity
                    60
                    (AB010918) responce reactor4 [Arabidopsis thaliana]
NCBI Description
                    6438
Seq. No.
                    6819 1.R1040
Contig ID
                    leu7\overline{0}1150644.h1
5'-most EST
Seq. No.
                    6439
                    6819 2.R1040
Contig ID
5'-most EST
                    trc7\overline{0}0561862.h1
                    6440
Seq. No.
                    6819 3.R1040
Contig ID
5'-most EST
                   LIB3055-007-Q1-N1-F11
Seq. No.
                    6441
                    6820_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy034b03b1
Method
                   BLASTX
NCBI GI
                   g3935157
BLAST score
                   1255
                   1.0e-139
E value
Match length
                   274
% identity
                   86
                    (AC005106) T25N20.21 [Arabidopsis thaliana]
NCBI Description
                    6442
Seq. No.
                    6821 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy201e01b1
Method
                   BLASTX
                   g2982293
NCBI GI
BLAST score
                   152
E value
                   1.0e-19
Match length
                   81
% identity
                   59
NCBI Description
                    (AF051231) ISP42-like protein [Picea mariana]
                    6443
Seq. No.
Contig ID
                    6822_1.R1040
5'-most EST
                   ncj700988638.h1
Method
                   BLASTX
NCBI GI
                   g2098705
BLAST score
                   494
                    9.0e-50
E value
Match length
                   137
% identity
NCBI Description
                    (U82973) pectinesterase [Citrus sinensis]
```

6830 1.R1040 Contig ID pxt700945726.hl 5'-most EST BLASTN Method g1223921 NCBI GI BLAST score 127 5.0e-65 E value 331 Match length % identity NCBI Description

Vigna radiata vicilin peptidohydrolase, cysteinyl endopeptidase mRNA, complete cds

Seq. No. 6445

Contig ID 6832 1.R1040

5'-most EST jC-gmle01810024f07a1

Seq. No. 6446

6832 2.R1040 Contig ID

5'-most EST LIB3030-009-Q1-B1-B7

6447 Seq. No.

Contig ID 6832 3.R1040

LIB3138-120-Q1-N1-E4 5'-most EST

6448 Seq. No.

Contig ID 6835 1.R1040.

5'-most EST LIB3030-009-Q1-B1-A6

Method BLASTX g632149 NCBI GI BLAST score 366 E value 2.0e-34 Match length 256

% identity 38

NCBI Description narbonin - Vicia pannonica >gi 396829 emb CAA80981

(Z25534) narbonin [Vicia pannonica]

6449 Seq. No.

Contig ID 6836 1.R1040 zhf700965238.h1 5'-most EST

Method BLASTX NCBI GI g1362162 BLAST score 184 E value 7.0e-39 173 Match length % identity

beta-glucosidase BGQ60 precursor - barley >gi 804656 NCBI Description

(L41869) beta-glucosidase [Hordeum vulgare]

Seq. No. 6450

Contig ID 6841 2.R1040

5'-most EST LIB3139-068-P1-N1-H10

6451 Seq. No.

Contig ID 6844 1.R1040

5'-most EST LIB3170-053-Q1-K1-A5

Method BLASTX NCBI GI q1330401 BLAST score 206

```
E value
                   5.0e-16
Match length
                   118
% identity
                   36
NCBI Description
                   (U58762) T27F7.1 gene product [Caenorhabditis elegans]
                   6452
Seq. No.
                   6844 3.R1040
Contig ID
                   LIB3030-008-Q1-B1-H9
5'-most EST
                   6453
Seq. No.
                   6845 1.R1040
Contig ID
                   LIB3092-010-Q1-K1-E11
5'-most EST
                   6454
Seq. No.
                   6846 1.R1040
Contig ID
5'-most EST
                   LIB3107-014-Q1-K1-G8
Method
                   BLASTX
                  g2132930
NCBI GI
               395
BLAST score
                   4.0e-38
E value
Match length
                   155
% identity
                   49
NCBI Description
                  probable membrane protein YOR262w - yeast (Saccharomyces
                   cerevisiae) >gi 1420591 emb CAA99484 (Z75170) ORF YOR262w
                   [Saccharomyces cerevisiae]
                   6455
Seq. No.
Contig ID
                   6847 1.R1040
5'-most EST
                   LIB3030-008-Q1-B1-H10
Method
                   BLASTX
                   g2244792
NCBI GI
BLAST score
                   172
                   8.0e-12
E value
Match length
                   151
                   34
% identity
                   (Z97336) ankyrin homolog [Arabidopsis thaliana]
NCBI Description
                   6456
                                                                ٠.ق.
Seq. No.
Contig ID
                   6848 1.R1040
                   LIB3030-008-Q1-B1-F4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1483218
                   369
BLAST score
                   3.0e-35
E value
                   164
Match length
                   50
% identity
                   (X99793) induced upon wounding stress [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   6457
                   6850 1.R1040
Contig ID
5'-most EST
                   kl1701203944.h2
Method
                   BLASTX
NCBI GI
                   q3193301
BLAST score
                   677
E value
                   6.0e-71
```

247

Match length

5'-most EST

```
% identity
NCBI Description
                   (AF069298) Arabidopsis putative chloroplast outer envelope
                   86-like protein T10P11.19 (GB: AC002330) [Arabidopsis
                   thalianal
                   6458
Seq. No.
Contig ID
                   6851 1.R1040
5'-most EST
                   ssr700554846.hl
Seq. No.
                   6459
Contig ID
                   6856 1.R1040
5'-most EST
                   leu7\overline{0}1156170.h1
Method
                   BLASTX
NCBI GI
                   q1107526
BLAST score
                   1116
E value
                   1.0e-122
Match length
                   351
% identity
                   63
NCBI Description
                   (X87931) SIEP1L protein [Beta vulgaris]
Seq. No.
                   6460
Contig ID
                   6856_2.R1040
5'-most EST
                   g5753379
                   BLASTX
Method
NCBI GI
                   g2983289
BLAST score
                   154
E value
                   5.0e-10
Match length
                   73
                   42
% identity
NCBI Description
                   (AE000703) chaperone DnaJ [Aquifex aeolicus]
Seq. No.
                   6461
Contig ID
                   6858 1.R1040
                   epx7\overline{0}1104218.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3702339
BLAST score
                   1046
                   1.0e-114
E value
Match length
                   340
% identity
NCBI Description
                   (AC005397) unknown protein [Arabidopsis thaliana]
                   6462
Seq. No. ..
Contig ID
                   6861 1.R1040
5'-most EST
                   LIB3\overline{0}51-049-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   q4164473
BLAST score
                   367
E value
                   1.0e-34
Match length
                   105
                   69
% identity
NCBI Description
                   (AF061157) negatively light-regulated protein [Vernicia
                   fordii]
Seq. No.
                   6463
                   6861 2.R1040
Contig ID
```

 $sat7\overline{0}1002758.h2$

Method

BLASTX

```
6464
Seq. No.
                  6861 3.R1040
Contig ID
5'-most EST
                  gsv7\overline{0}1049989.h1
Seq. No.
                  6465
Contig ID
                  6862 1.R1040
5'-most EST
                  epx701105792.h1
                  BLASTX
Method
NCBI GI
                  g1709358
BLAST score
                  1224
                  1.0e-135
E value
                  411
Match length
                  57
% identity
                  NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE
NCBI Description
                  PHOSPHOHYDROLASE) (NTPASE) >gi 629638 pir S48859
                  nucleoside triphosphatase - garden pea
                  >gi 2129890 pir S65147 nucleoside triphosphatase
                  precursor, chromatin-associated - garden pea
                  >qi 563612 emb CAA83655 (Z32743) nucleoside triphosphatase
                   [Pisum sativum] >gi 4519173 dbj BAA75506.1 (AB022319)
                  nucleoside triphosphatase (NTPase) [Pisum sativum]
                  6466
Seq. No.
                  6862.2.R1040
Contig ID
5'-most EST
                   zsq701126616.hl
Method
                  BLASTX
NCBI GI
                  g1709358
BLAST score
                  750
                  2.0e-79
E value
                  287
Match length
                  50
% identity
NCBI Description
                  NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE
                  PHOSPHOHYDROLASE) (NTPASE) >gi 629638 pir S48859
                  nucleoside triphosphatase - garden pea
                  >gi_2129890_pir__S65147 nucleoside triphosphatase
                  precursor, chromatin-associated - garden pea
                  >gi 563612 emb CAA83655 (Z32743) nucleoside triphosphatase
                   [Pisum sativum] >gi 4519173 dbj BAA75506.1_ (AB022319)
                  nucleoside triphosphatase (NTPase) [Pisum sativum]
                  6467
Seq. No.
Contig. ID
                  6864 1.R1040
5'-most EST
                  pcp7\overline{0}0989872.h1
Method
                  BLASTX
NCBI GI
                  g3702314
BLAST score
                  224
E value
                  9.0e-25
                  191
Match length
% identity
                   (AC002535) similar to SWI/SNF complex subunit BAF170
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  6468
Contig ID
                  6864 2.R1040
5'-most EST
                  uC-gmropic011f04b1
```

Match length

288

```
NCBI GI
                   g3702314
BLAST score
                   426
E value
                   6.0e-42
Match length
                   135
                   60
% identity
NCBI Description
                   (AC002535) similar to SWI/SNF complex subunit BAF170
                   [Arabidopsis thaliana]
Seq. No.
                   6469
Contig ID
                   6866 1.R1040
5'-most EST
                   LIB3030-008-Q1-B1-E11
Method
                   BLASTX
NCBI GI
                   q3047116
BLAST score
                   163
E value
                   3.0e-11
Match length
                   38
                   89
% identity
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6868 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy126d11b1
                   6471
Seq. No.
                   6869 1.R1040
Contig ID
5'-most EST
                   vwf700676052.h1
Method
                   BLASTX
NCBI GI
                   g4191616
BLAST score
                   635
                   3.0e-66
E value
Match length
                   234
% identity
                   53
                   (AF120334) GTP-binding protein NGB [Homo sapiens]
NCBI Description
                   6472
Seq. No.
Contig ID
                   6871 1.R1040
5'-most EST
                   jC-gmf102220132ab02d1
             \mathcal{X}_{\mathcal{U}}
                   6473
Seq. No.
Contig ID
                   6872 1.R1040
5'-most EST
                   fde700876618.hl
Method
                   BLASTX
NCBI GI
                   g2213584
BLAST score
                   827
E value
                   3.0e-88
Match length
                   295
% identity
                   55
NCBI Description
                   (AC000348) T7N9.4 [Arabidopsis thaliana]
                   6474
Seq. No.
Contig ID
                   6874 1.R1040
5'-most EST
                   kl1701208032.h1
Method
                   BLASTX
NCBI GI
                   g2330647
BLAST score
                   688
E value
                   4.0e-72
```

45.5°

E value

7.0e-51

```
% identity
                   52
NCBI Description
                   (Y14557) ribonucleoprotein [Pisum sativum]
                   6475
Seq. No.
Contig ID
                   6874 2.R1040
5'-most EST
                   LIB3167-023-P4-K4-B11
Method
                   BLASTX
NCBI GI
                   g2330647
BLAST score
                   230
E value
                   7.0e-19
Match length
                   160
                   30
% identity
NCBI Description
                   (Y14557) ribonucleoprotein [Pisum sativum]
                   6476
Seq. No.
                   6876 1.R1040
Contig ID
5'-most EST
                   LIB3030-008-Q1-B1-F12
                   6477
Seq. No.
                   6877 1.R1040
Contig ID
5'-most EST
                   LIB3049-025-Q1-E1-E1
                   6478
Seq. No.
                   6877 2.R1040
Contig ID
5'-most EST
                   LIB3030-008-Q1-B1-F2
Method
                   BLASTX
                   g1749546
NCBI GI
BLAST score
                   245
                   9.0e-21
E value
                   89
Match length
                   61
% identity
NCBI Description
                   (D89169) similar to Saccharomyces cerevisiae SCD6 protein,
                   SWISS-PROT Accession Number P45978 [Schizosaccharomyces
                   pombe]
                   6479
Seq. No.
Contig ID
                   6877 3.R1040
5'-most EST
                   uC-gmrominsoy116b10b1
Method
                   BLASTX
                   g3080366
NCBI GI
BLAST score
                   172
E value
                   3.0e-12
Match length
                   60
% identity
                   (AL022580) putative protein [Arabidopsis thaliana]
NCBI Description
                   6480
Seq. No.
Contig ID
                   6877 4.R1040
                   LIB3\overline{1}07-014-Q1-K1-C9
5'-most EST
                   6481
Seq. No.
Contig ID
                   6878 1.R1040
5'-most EST
                   LIB3107-009-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   g1619602
BLAST score
                   503
```

```
147
Match length
% identity
                    65
NCBI Description
                    (Y08726) MtN3 [Medicago truncatula]
                    6482
Seq. No.
                    6878 3.R1040
Contig ID
                    k117\overline{0}1206730.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g1619602
BLAST score
                    272
E value
                    2.0e-24
Match length
                    63
% identity
                    81
NCBI Description
                    (Y08726) MtN3 [Medicago truncatula]
                    6483
Seq. No.
                    6880 1.R1040
Contig ID
5'-most EST
                    LIB3051-022-Q1-K1-D4
Method
                    BLASTX
NCBI GI
                    g1708975
BLAST score
                    448
E value
                    7.0e-44
Match length
                    396
                    35
% identity
NCBI Description
                    METHIONINE GAMMA-LYASE (L-METHIONINASE)
                    >gi_1084040_pir__JC4174 methionine gamma-lyase (EC
                    4.4.1.11) - Pseudomonas putida >gi_902932_dbj_BAA13642_
                    (D88554) L-methionine gamma-lyase [Pseudomonas putida]
                    >gi_2217945_dbj_BAA20553_ (D89015) L-methionine gamma-lyase
[Pseudomonas putida] >gi_1096717_prf__2112270A Met
                    gamma-lyase [Pseudomonas putida]
Seq. No.
                    6484
Contig ID
                    6880_2.R1040
5'-most EST
                    g560<del>6</del>623
                    BLASTX
Method
NCBI GI
                    g1709007
BLAST score
                    172
E value
                    4.0e-12
Match length
                    102
                    38
% identity
                    O-SUCCINYLHOMOSERINE SULFHYDRYLASE (OSH SULFHYDRYLASE)
NCBI Description
                    >gi_607830 (U10904) O-succinylhomoserine sulfhydrylase
                    [Pseudomonas aeruginosa]
Seq. No.
                    6485
Contig ID
                    6880 3.R1040
5'-most EST
                    LIB3065-005-Q1-N1-A2
Seq. No.
                    6486
                    6881 1.R1040
Contig ID
5'-most EST
                    LIB3056-004-Q1-N1-D10
Method
                    BLASTX
NCBI GI
                    q481815
BLAST score
                    195
                    1.0e-14
E value
Match length
                    188
```

13.

Method

```
% identity
NCBI Description
                   vegetative storage protein - western balsam poplar x
                   cottonwood >gi_309839 (L20233) vegetative storage protein
                   [Populus trichocarpa x Populus deltoides]
                   6487
Seq. No.
                   6884 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy103a04b1
Method
                   BLASTX
NCBI GI
                   g4415937
BLAST score
                   160
E value
                   8.0e-11
Match length
                   133
% identity
                   28
NCBI Description
                   (AC006418) hypothetical protein [Arabidopsis thaliana]
                   6488
Seq. No.
Contig ID
                   6886 1.R1040
5'-most EST
                   LIB3030-008-Q1-B1-D10
Method
                   BLASTN
NCBI GI
                   g402752
BLAST score
                   219
E value
                   1.0e-120
Match length
                   419
% identity
                   96
NCBI Description
                  G.max gene fusA
                   6489
Seq. No.
Contig ID
                   6887 1.R1040
                   q5688103
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3549669
BLAST score
                   640
E value
                   8.0e-67
Match length
                   216
% identity
NCBI Description
                  (AL031394) putative protein [Arabidopsis thaliana]
                   6490
Seq. No.
Contig ID
                   6888 1.R1040
5'-most EST
                  hyd700731116.h1
                  BLASTX
Method
NCBI GI
                  g3152666
BLAST score
                   221
E value
                   9.0e-18
Match length
                  111
% identity
                   38
NCBI Description
                   (AF064606) KB07 protein [Homo sapiens]
Seq. No.
                   6491
                   6889 1.R1040
Contig ID
5'-most EST
                  LIB3030-008-Q1-B1-D3
                   6492
Seq. No.
Contig ID
                  6891 1.R1040
```

LIB3051-013-Q1-E1-E11

BLASTX

Method

BLASTN

```
NCBI GI
                   g2052508
BLAST score
                   917
E value
                   1.0e-120
Match length
                   360
                   61
% identity
NCBI Description
                   (U95759) lysine-ketoglutarate reductase/saccharopine
                   dehydrogenase bifunctional enzyme [Arabidopsis thaliana]
Seq. No.
                   6493
                   6891 2.R1040
Contig ID
5'-most EST
                   zhf700963155.h1
Method
                   BLASTX
NCBI GI
                   a2052510
BLAST score
                   858
E value
                   2.0e-92
Match length
                   232
                   72
% identity
NCBI Description
                   (U95758) lysine-ketoglutarate reductase/saccharopine
                   dehydrogenase bifunctional enzyme [Arabidopsis thaliana]
                   6494
Seq. No.
                   6894 1.R1040
Contig ID
5'-most EST
                   vwf700674245.h1
                   6495
Seq. No.
Contig ID
                   6894 2.R1040
5'-most EST
                   fde700873040.hl
                   6496
Seq. No.
Contig ID
                   6897 1.R1040
                   jex700905170.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2979553
BLAST score
                   586
E value
                   3.0e-60
Match length
                   291
% identity
                   40
NCBI Description
                   (AC003680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   6497
Contig ID
                   6899 1.R1040
5'-most EST
                   uC-qmflminsoy008e10b1
Method.
                   BLASTX
NCBI GI
                   g416758
BLAST score
                   338
E value
                   3.0e-35
Match length
                   124
% identity
NCBI Description
                   SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130)
                   carboxypeptidase Y-like protein [Arabidopsis thaliana]
                   >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis
                   thaliana]
                   6498
Seq. No.
                   6901 1.R1040
Contig ID
5'-most EST
                   zhf700952535.h1
```

```
g169127
NCBI GI
BLAST score
                  209
                  1.0e-113
E value
                  561
Match length
                  84
% identity
NCBI Description
                  Pisum sativum (clone pCLp) nuclear encoded precursor to
                  chloroplast protein mRNA, complete cds
                  6499
Seq. No.
                  6901 2.R1040
Contig ID
                  awf700839723.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g461753
                  307
BLAST score
                  6.0e-28
E value
                  127
Match length
% identity
                  45
                  ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
NCBI Description
                  PRECURSOR >gi 419773 pir S31164 ATP-dependent ClpB
                  proteinase regulatory chain homolog precursor, chloroplast
                  - garden pea >gi_169128 (L09547) nuclear encoded precursor
                  to chloroplast protein [Pisum sativum]
                  6500
Seq. No.
                  6907 1.R1040
Contig ID
5'-most EST
                  LIB3030-008-Q1-B1-C10
                  BLASTX
Method
NCBI GI
                  g1731141
BLAST score
                  165
                  3.0e-11
E value
                  153
Match length
                  38
% identity
                  HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II
NCBI Description
                  >gi_3878112_emb_CAA87788_ (Z47811) similar to
                  glycerophosphoryl diester phosphodiesterase domain; cDNA
                  EST EMBL: D27842 comes from this gene; cDNA EST EMBL: D27841
                  comes from this gene; cDNA EST EMBL: D32990 comes from this
                  gene; cDNA EST EMBL: D35712 comes...
                  >gi_3879502_emb_CAA87796_ (Z47812) similar to
                  glycerophosphoryl diester phosphodiesterase domain; cDNA
                  EST EMBL: D27842 comes from this gene; cDNA EST EMBL: D27841
                  comes from this gene; cDNA EST EMBL: D32990 comes from this
                  gene; cDNA EST EMBL: D35712 comes
Seq. No.
                  6501
                  6916_1.R1040
Contig ID
5'-most EST
                  g4293044
Method
                  BLASTX
NCBI GI
                  g3287681
BLAST score
                  468
E value
                  3.0e-96
                  304
Match length
                  66
% identity
                  (AC003979) ESTs gb_Z34075, gb_Z34835 and gb_AA404888 come
```

6502 Seq. No.

NCBI Description

from this gene. [Arabidopsis thaliana]

Contig ID

```
Contig ID
                   6920 1.R1040
5'-most EST
                   ssr700555158.hl
Seq. No.
                   6503
                   6922 1.R1040
Contig ID
5'-most EST
                   LIB3030-008-Q1-B1-A3
Method
                   BLASTX
NCBI GI
                   g3135254
BLAST score
                   415
E value
                   9.0e-41
Match length
                   127
% identity
                   62
                   (AC003058) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   6504
Seq. No.
Contig ID
                   6923 1.R1040
5'-most EST
                   zsq701122147.hl
                   6505
Seq. No.
                   6923 2.R1040
Contig ID
5'-most EST
                   LIB3109-046-Q1-K1-F8
                   6506
Seq. No.
                   6925_1.R1040
Contig ID
                   jC-g\overline{m}st02400061e07a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2982266
BLAST score
                   437
E value
                   3.0e-43
Match length
                   101
                   83
% identity
NCBI Description
                   (AF051216) probable fibrillarin [Picea mariana]
                   6507
Seq. No.
                   6925_2.R1040
Contig ID
5'-most EST
                   gsv7\overline{0}1045236.h1
Method
                   BLASTX
NCBI GI
                   g2982266
                   1044
BLAST score
                   1.0e-114
E value
                   244
Match length
% identity
                   (AF051216) probable fibrillarin [Picea mariana]
NCBI Description
                   6508
Seq. No.
                   6925 3.R1040
Contig ID
5'-most EST
                   ssr7\overline{0}0557074.h1
Method
                   BLASTN
                   g21002
NCBI GI
BLAST score
                   80
E value
                   1.0e-36
Match length
                   226
% identity
                   11
NCBI Description
                   Bean DNA for glycine-rich cell wall protein GRP 1.8
Seq. No.
```

6925_4.R1040

```
LIB3051-067-Q1-K1-A11
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2982266
BLAST score
                   452
                   5.0e-45
E value
                   104
Match length
% identity
                   82
                   (AF051216) probable fibrillarin [Picea mariana]
NCBI Description
                   6510
Seq. No.
                   6925 5.R1040
Contig ID
                   vzy700754605.hl
5'-most EST
Method
                   BLASTX
                   g2982266
NCBI GI
BLAST score
                   433
E value
                   1.0e-42
                   97
Match length
% identity
                   82
                   (AF051216) probable fibrillarin [Picea mariana]
NCBI Description
                   6511
Seq. No.
                   6925 6.R1040
Contig ID
5'-most EST
                   jC-gmst02400009b07a1
                   6512
Seq. No.
                   6925 7.R1040
Contig ID
                   jsh701067142.hl
5'-most EST
Method
                   BLASTN
                   g21002
NCBI GI
                   84
BLAST score
                   1.0e-39
E value
                   206
Match length
                   9
% identity
                  Bean DNA for glycine-rich cell wall protein GRP 1.8
NCBI Description
                   6513
Seq. No.
Contig ID
                   6926 1.R1040
5'-most EST
                   rlr700897678.h1
                   6514
Seq. No.
                   6933 1.R1040
Contig ID
5'-most EST
                   g4305391
                   BLASTX
Method
                   g2576411
NCBI GI
                   745
BLAST score
                   5.0e-85
E value
                   226
Match length
% identity
                   (AF012833) similar to dynamin-like protein encoded by
NCBI Description
                   GenBank Accession Number X99669 [Arabidopsis thaliana]
                   6515
Seq. No.
                   6933 2.R1040
Contig ID
                   leu701152583.h1
5'-most EST
                   BLASTX
Method
                   g2576411
NCBI GI
```

221

BLAST score

Seq. No.

```
E value
                   6.0e-18
Match length
                   71
                   63
% identity
NCBI Description
                    (AF012833) similar to dynamin-like protein encoded by
                   GenBank Accession Number X99669 [Arabidopsis thaliana]
                   6516
Seq. No.
                   6933 3.R1040
Contig ID
5'-most EST
                   zhf7\overline{0}0955208.h1
Method
                   BLASTX
NCBI GI
                   g2576411
BLAST score
                   329
E value
                   1.0e-30
                   101
Match length
                   67
% identity
NCBI Description
                    (AF012833) similar to dynamin-like protein encoded by
                   GenBank Accession Number X99669 [Arabidopsis thaliana]
                   6517
Seq. No.
                   6934 1.R1040
Contig ID
                   LIB3030-007-Q1-B1-G6
5'-most EST
                   BLASTX
Method
                   g1707015
NCBI GI
BLAST score
                   171
E value
                   5.0e-12
Match length
                   131
% identity
                   32
NCBI Description
                   (U78721) protein phosphatase 2C isolog [Arabidopsis
                   thaliana]
Seq. No.
                   6518
                   6935 1.R1040
Contig ID
                   zhf700963017.h1
5'-most EST
                   BLASTX
Method
                   q4468812
NCBI GI
BLAST score
                   808
E value
                   2.0e-86
Match length
                   221
% identity
NCBI Description
                    (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                   6519
Contig ID
                   6937 1.R1040
                   LIB3109-031-Q1-K1-D10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1351651
BLAST score
                   215
E value
                   6.0e-17
Match length
                   163
% identity
                   HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I
NCBI Description
                   >gi_2130353_pir__S62553 hypothetical protein SPAC24B11.08c
- fission yeast (Schizosaccharomyces pombe)
                   >gi 1061296 emb CAA91773 (Z67757) unknown
                   [Schizosaccharomyces pombe]
```

Match length

```
6938 1.R1040
Contig ID
5'-most EST
                   zhf700963141.hl
Method
                   BLASTN
NCBI GI
                   g1853969
BLAST score
                   78
E value
                   7.0e-36
Match length
                   283
% identity
                   82
NCBI Description
                   Vigna unguiculata mRNA for CPRD46 protein, complete cds
Seq. No.
                   6521
Contig ID
                   6945 1.R1040
5'-most EST
                   uC-gmropic055e06b1
Seq. No.
                   6522
                   6947 1.R1040
Contig ID
5'-most EST
                   zhf700957949.h1
                   6523
Seq. No.
Contig ID
                   6948 1.R1040
5'-most EST
                   k117\overline{0}1206149.h1
Method
                   BLASTX
                   g2281627
NCBI GI
BLAST score
                   329
                   8.0e-36
E value
Match length
                   138
% identity
                   60
                   (AF003094) AP2 domain containing protein RAP2.1
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   6524
                   6948 2.R1040
Contig ID
5'-most EST
                   trc700565376.h1
                   6525
Seq. No.
Contig ID
                   6949 1.R1040
5'-most EST
                   txt700733044.h1
Method
                   BLASTX
                   g3393062
NCBI GI
                   620
BLAST score
                   3.0e-64
E value
Match length
                   208
% identity
                   55
                   (Y17386) putative In2.1 protein [Triticum aestivum]
NCBI Description
                   6526
Seq. No.
Contig ID
                   6949 2.R1040
5'-most EST
                   uC-gmronoir045f04b1
Seq. No.
                   6527
                   6951_1.R1040
Contig ID
5'-most EST
                   vzy7\overline{0}0751782.h1
Method
                   BLASTX
NCBI GI
                   q2351380
BLAST score
                   526
                   3.0e-53
E value
```

Seq. No.

```
% identity
                   41
NCBI Description
                   (U54559) translation initiation factor eIF3 p40 subunit
                   [Homo sapiens] >gi_4503515_ref_NP_003747.1_pEIF3S3_ UNKNOWN
Seq. No.
                   6528
                   6951 2.R1040
Contig ID
5'-most EST
                   kmv700738117.h1
                   BLASTX
Method
NCBI GI
                   g2351380
BLAST score
                   133
                   7.0e-13
E value
Match length
                   149
% identity
                   36
                   (U54559) translation initiation factor eIF3 p40 subunit
NCBI Description
                   [Homo sapiens] >gi_4503515_ref_NP_003747.1_pEIF3S3_ UNKNOWN
                   6529
Seq. No.
                   6952 1.R1040
Contig ID
                   LIB3030-006-Q1-B1-E12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1762584
BLAST score
                   269
E value
                   2.0e-23
                   99
Match length
                   49
% identity
NCBI Description
                   (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
                   [Arabidopsis thaliana]
                   6530
Seq. No.
                   6952 2.R1040
Contig ID
5'-most EST
                   uC-gmropic049h03b1
Method
                   BLASTX
NCBI GI
                   g1762584
BLAST score
                   187
E value
                   6.0e-14
Match length
                   59
% identity
                   59
NCBI Description
                   (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
                   [Arabidopsis thaliana]
                   6531
Seq. No.
Contig ID
                   6956 1.R1040
5'-most EST
                   LIB3170-021-Q1-K1-A12
Seq. No.
                   6532
Contig ID
                   6960_1.R1040
5'-most EST
                   uC-gmrominsoy066e08b1
Method
                   BLASTX
NCBI GI
                   g3182915
BLAST score
                   630
E value
                   2.0e-65
Match length
                   180
% identity
                   62
                  ADP-RIBOSYLATION FACTOR >gi 1842150 dbj BAA19225
NCBI Description
                   (AB001051) ADP-ribosylation factor [Dugesia japonica]
```

```
6960 2.R1040
Contig ID
5'-most EST
                   asn701134890.h2
Method
                   BLASTX
NCBI GI
                   q461532
BLAST score
                   432
E value
                   1.0e-42
Match length
                   113
% identity
NCBI Description
                   ADP-RIBOSYLATION FACTOR >gi_1362500_pir__D49993
                   ADP-ribosylation factor - Ajellomyces capsulata >gi_407693
                   (L25117) ADP-ribosylation factor [Histoplasma capsulatum]
                   6534
Seq. No.
                   6963 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910051g04a1
Method
                   BLASTX
                   q2829918
NCBI GI
BLAST score
                   1073
                   1.0e-117
E value
Match length
                   309
% identity
                   72
NCBI Description
                   (AC002291) similar to "tub" protein gp_U82468_2072162
                   [Arabidopsis thaliana]
Seq. No.
                   6535
                   6963 2.R1040
Contig ID
                   LIB3052-013-Q1-N1-C6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2829918
BLAST score
                   472
E value
                   5.0e-47
Match length
                   176
                   67
% identity
                   (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   6536
                   6963 3.R1040
Contig ID
                   dpv7\overline{0}1103595.h1
5'-most EST
Method
                   BLASTX
                   q2829918
NCBI GI
BLAST score
                   335
                   2.0e-31
E value
                   95
Match length
                   71
% identity
                   (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   6537
                   6963 5.R1040
Contig ID
                   LIB3170-032-Q1-K1-G11
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2829918
BLAST score
                   191
E value
                   2.0e-14
Match length
                   69
```

64

% identity

```
NCBI Description
                   (AC002291) similar to "tub" protein gp U82468 2072162
                   [Arabidopsis thaliana]
Seq. No.
                  6538
Contig ID
                  6963 6.R1040
5'-most EST
                  zzp700831683.h1
Method
                  BLASTX
NCBI GI
                  g2829918
BLAST score
                  226
E value
                  2.0e-18
                  70.
Match length
                  73
% identity
                   (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                   [Arabidopsis thaliana]
                  6539
Seq. No.
                  6963 7.R1040
Contig ID
5'-most EST
                  awf700841234.h1
Method
                  BLASTX
NCBI GI
                  g2829918
BLAST score
                  219
                  7.0e-24
E value
                  80
Match length
% identity
                   (AC002291) similar to "tub" protein gp U82468 2072162
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  6540
                  6965 1.R1040
Contig ID
5'-most EST
                  LIB3049-055-Q1-E1-G12
Method
                  BLASTX
NCBI GI
                  g3335347
BLAST score
                  481
                  5.0e-48
E value
Match length
                  163
% identity
NCBI Description
                  (AC004512) Contains similarity to ARI, RING finger protein
                  gb X98309 from Drosophila melanogaster. ESTs gb T44383,
                  gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and
                  gb AA042359 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  6541
                  6965 2.R1040
Contig ID
5'-most EST
                  sat701007023.h1
                  BLASTX
Method
NCBI GI
                  g3335347
BLAST score
                  1324
E value
                  1.0e-147
Match length
                  272
% identity
NCBI Description
                  (AC004512) Contains similarity to ARI, RING finger protein
                  gb_X98309 from Drosophila melanogaster. ESTs gb T44383,
                  gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and
                  gb AA042359 come from this gene. [Arabidopsis thaliana]
                  6542
Seq. No.
```

6965_3.R1040

Contig ID

```
5'-most EST
                  LIB3051-106-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3335347
BLAST score
                  819
E value
                  1.0e-87
Match length
                  250
% identity
                  61
                  (AC004512) Contains similarity to ARI, RING finger protein
NCBI Description
                  gb_X98309 from Drosophila melanogaster. ESTs gb_T44383,
                  gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and
                  gb AA042359 come from this gene. [Arabidopsis thaliana]
                  6543
Seq. No.
                  6965 4.R1040
Contig ID
                  fde700877103.hl
5'-most EST
Method
                  BLASTX
                  q3335347
NCBI GI
BLAST score
                  180
                  4.0e-13
E value
                  92
Match length
% identity
                  (AC004512) Contains similarity to ARI, RING finger protein
NCBI Description
                  gb_X98309 from Drosophila melanogaster. ESTs gb_T44383,
                  gb W43120, gb N65868, gb H36013, gb AA042241, gb_T76869 and
                  gb AA042359 come from this gene. [Arabidopsis thaliana]
                  6544
Seq. No.
Contig ID
                  6966 1.R1040
5'-most EST
                  jC-gmf102220089g12a1
                  6545
Seq. No.
                  6968 1.R1040
Contig ID
                  LIB3040-043-Q1-E1-A10
5'-most EST
Method
                  BLASTX
                  g2129726
NCBI GI
BLAST score
                  953
                  1.0e-103
E value
Match length
                  226
% identity
                  81
NCBI Description
                  RNA polymerase II third largest chain RPB35.5A -
                  Arabidopsis thaliana >gi_514318 (L34770) RNA polymerase II
                  third largest subunit [Arabidopsis thaliana]
                  >gi 4544370 gb_AAD22281.1_AC006920_5 (AC006920) RNA
                  polymerase II, third largest subunit [Arabidopsis thaliana]
                  6546
Seq. No.
Contig ID
                  6972 1.R1040
5'-most EST
                  leu701151137.hl
Method
                  BLASTX
NCBI GI
                  q2281086
BLAST score
                  361
                  4.0e-34
E value
Match length
                  195
% identity
NCBI Description
                  (AC002333) indole-3-acetate beta-glucosyltransferase isolog
```

[Arabidopsis thaliana]

NCBI Description

```
6547
Seq. No.
Contig ID
                   6974_1.R1040
5'-most EST
                   jC-qmst02400009f05a1
Method
                   BLASTX
                   g3600054
NCBI GI
BLAST score
                   221
E value
                   6.0e-18
Match length
                   129
                   38
% identity
NCBI Description
                   (AF080120) No definition line found [Arabidopsis thaliana]
                   6548
Seq. No.
Contig ID
                   6976 1.R1040
5'-most EST
                  bth700844626.h1
                   BLASTX
Method
                   q4115931
NCBI GI
BLAST score
                   472
E value
                   3.0e-47
Match length
                   182
                   58
% identity
NCBI Description
                   (AF118223) contains similarity to Guillardia theta ABC
                   transporter (GB:AF041468) [Arabidopsis thaliana]
                   6549
Seq. No.
Contig ID
                   6976 2.R1040
5'-most EST
                  LIB3051-059-Q1-K2-G7
                  BLASTX
Method
                   g4115931
NCBI GI
BLAST score
                   371
E value
                   2.0e-35
Match length
                  149
% identity
                   59
NCBI Description
                   (AF118223) contains similarity to Guillardia theta ABC
                  transporter (GB:AF041468) [Arabidopsis thaliana]
                   6550
Seq. No.
Contig ID
                   6977 1.R1040
5'-most EST
                   zzp700832937.hl
Method
                  BLASTX
                  g2980770
NCBI GI
BLAST score
                  1214
E value
                  1.0e-134
Match length
                  323
% identity
                   72
NCBI Description
                   (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   6551
Contig ID
                   6977_2.R1040
5'-most EST
                  uC-gmrominsoy080d04b1
Method
                  BLASTX
NCBI GI
                  q2980770
BLAST score
                  398
E value
                   1.0e-38
Match length
                  120
% identity
                   64
```

(AL022198) putative protein kinase [Arabidopsis thaliana]

```
6552
Seq. No.
                   6982 1.R1040
Contig ID
5'-most EST
                   LIB3049-044-Q1-E1-G2
                   6553
Seq. No.
                   6983 1.R1040
Contig ID
5'-most EST
                   gsv701053487.hl
                   BLASTX
Method
NCBI GI
                   g2275210
BLAST score
                   454
                   5.0e-45
E value
Match length
                   175
                   51
% identity
                   (AC002337) peptidyl-prolyl cis-trans isomerase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   6554
Seq. No.
                   6983 2.R1040
Contig ID
                   fua701043243.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2275210
BLAST score
                   194
                   8.0e-33
E value
                   174
Match length
                   50
% identity
NCBI Description
                   (ACO02337) peptidyl-prolyl cis-trans isomerase isolog
                   [Arabidopsis thaliana]
                   6555
Seq. No.
                   6985 1.R1040
Contig ID
                   uaw7\overline{0}0665809.h1
5'-most EST
                   6556
Seq. No.
                   6987 1.R1040
Contig ID
5'-most EST
                   g4395747
Method
                   BLASTN
NCBI GI
                   g19655
BLAST score
                   466
E value
                   0.0e + 00
Match length
                   510
                   98
% identity
                   M.sativa 26S rRNA
NCBI Description
                   6557
Seq. No.
                   6987 2.R1040
Contig ID
5'-most EST
                   zpv700760254.hl
Method
                   BLASTN
NCBI GI
                   g311302
BLAST score
                   42
E value
                   1.0e-13
                   102
Match length
                   85
% identity
NCBI Description
                   N.sylvestris mRNA
                   6558
Seq. No.
                   6987 3.R1040
Contig ID
```

 $asn7\overline{0}1140057.h1$

```
BLASTN
Method
                  g311302
NCBI GI
BLAST score
                   33
                   6.0e-09
E value
                  89
Match length
                   84
% identity
NCBI Description N.sylvestris mRNA
                   6559
Seq. No.
                   6987_4.R1040
Contig ID
                   LIB3107-029-Q1-K1-B2
5'-most EST
Method
                   BLASTN
                   g22553
NCBI GI
                   76
BLAST score
E value
                   1.0e-34
Match length
                   80
                   99
% identity
NCBI Description
                  Tomato 25S ribosomal RNA gene
                   6560
Seq. No.
                   6989 1.R1040
Contig ID
                   rlr700896221.hl
5'-most EST
                   6561
Seq. No.
                   6991 1.R1040
Contig ID
                   jC-gmst02400049e03d1
5'-most EST
Seq. No.
                   6562
Contig ID
                   6994 1.R1040
5'-most EST
                   LIB3030-007-Q1-B1-A1
Method
                   BLASTN
                   g3290208
NCBI GI
BLAST score
                   51
E value
                   1.0e-19
Match length
                   71
                   93
% identity
                  Malus domestica MADS-box protein 1 mRNA, complete cds
NCBI Description
                   6563
Seq. No.
                   6999 1.R1040
Contig ID
                   LIB3051-025-Q1-K1-F2
5'-most EST
                   6564
Seq. No.
Contig ID
                   6999 2.R1040
5'-most EST
                   LIB3107-015-Q1-K1-A2
                   6565
Seq. No.
                   7001 1.R1040
Contig ID
                   uC-gmropic043c05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3482933
BLAST score
                   1260
                   1.0e-139
E value
Match length
                   552
% identity
                   49
                   (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
```

thaliana]

NCBI Description

```
6566
Seq. No.
Contig ID
                   7001 2.R1040
5'-most EST
                   fC-gmle700873234y1
Method
                   BLASTX
NCBI GI
                   g3482933
BLAST score
                   691
                   2.0e-72
E value
Match length
                   395
% identity
                   42
NCBI Description
                   (AC003970) Similar to cdc2 protein kinases [Arabidopsis
                   thaliana]
                   6567
Seq. No.
Contig ID
                   7001 5.R1040
5'-most EST
                   rca700999051.hl
                   6568
Seq. No.
Contig ID
                   7001 6.R1040
5'-most EST
                   fC-gmro700870190d1
                   6569
Seq. No.
                   7010 1.R1040
Contig ID
5'-most EST
                   LIB3030-006-Q1-B1-G3
Method
                   BLASTX
NCBI GI
                   g2191161
BLAST score
                   760
E value
                   7.0e-81
Match length
                   218
% identity
NCBI Description
                   (AF007270) contains similarity to B. subtilus flagellar
                   biosynthesis protein FLHA (SW:P35620) [Arabidopsis
                   thaliana]
                   6570
Seq. No.
Contig ID
                   7011 1.R1040
5'-most EST
                   LIB3109-001-Q1-K2-A9
Method
                   BLASTX
                   g4206122
NCBI GI
BLAST score
                   1068
E value
                   1.0e-128
Match length
                   283
% identity
                   80
NCBI Description
                   (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
                   crystallinum]
Seq. No.
                   6571
Contig ID
                   7012 1.R1040
5'-most EST
                   fua701040701.hl
Method
                   BLASTX
NCBI GI
                   g1621268
BLAST score
                   1243
E value
                   1.0e-146
Match length
                   364
                   70
% identity
```

(Z81012) unknown [Ricinus communis]

```
6572
Seq. No.
Contig ID
                   7016 1.R1040
                   epx7\overline{0}1109085.h1
5'-most EST
Method
                   BLASTX
                   g2827655
NCBI GI
                   270
BLAST score
E value
                   1.0e-23
                   109
Match length
                   51
% identity
NCBI Description
                   (AL021637) hypothetical protein [Arabidopsis thaliana]
                   6573
Seq. No.
Contig ID
                   7017 1.R1040
                   pmv7\overline{0}0890924.h1
5'-most EST
                   6574
Seq. No.
                   7017 2.R1040
Contig ID
5'-most EST
                   jsh7\overline{0}1070327.h1
                   6575
Seq. No.
Contig ID
                   7017 3.R1040
5'-most EST
                   wvk7\overline{0}0685462.h1
                   6576
Seq. No.
Contig ID
                   7020 1.R1040
5'-most EST
                   LIB3106-034-Q1-K1-D2
Method
                   BLASTX
                   q2506211
NCBI GI
BLAST score
                   1679
                   0.0e + 00
E value
                   333
Match length
                   97
% identity
                   VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                   SUBUNIT) (VAA3-1) >gi_849136 (U26709) vacuolar H+-ATPase
                   subunit A [Vigna radiata]
Seq. No.
                   6577
Contig ID
                   7020 2.R1040
5'-most EST
                   LIB3139-035-P1-N1-B8
                   BLASTX
Method
NCBI GI
                   q3169287
BLAST score
                   1893
E value
                   0.0e + 00
Match length
                   387
                   95
% identity
                   (AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium
NCBI Description
                   hirsutum]
                   6578
Seq. No.
                   7020 4.R1040
Contig ID
                   LIB3170-084-Q1-K1-A5
5'-most EST
Method
                   BLASTN
NCBI GI
                   q849135
                   83
BLAST score
                   9.0e-39
E value
                   134
Match length
```

96

% identity

```
NCBI Description Vigna radiata vacuolar H+-ATPase subunit A mRNA, complete
                   6579
Seq. No.
                   7020 6.R1040
Contig ID
                   jex7\overline{0}0905426.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g849135
BLAST score
                   140
                   5.0e-73
E value
                   180
Match length
% identity
                   94
                   Vigna radiata vacuolar H+-ATPase subunit A mRNA, complete
NCBI Description
                   6580
Seq. No.
                   7022 1.R1040
Contig ID
5'-most EST
                   LIB3092-021-Q1-K1-D2
Method
                   BLASTX
                   q4079809
NCBI GI
BLAST score
                   253
                   3.0e-21
E value
Match length
                   198
% identity
                   (AF071172) HERC2 [Homo sapiens]
NCBI Description
                   6581
Seq. No.
Contig ID
                   7023 1.R1040
                   jex7\overline{0}0904926.h1
5'-most EST
Method
                   BLASTX
                   g3080389
NCBI GI
BLAST score
                   375
                   3.0e-72
E value
Match length
                   187
                   74
% identity
                   (AL022603) putative membrane associated protein
NCBI Description
                   [Arabidopsis thaliana]
                   6582
Seq. No.
                   7024 1.R1040
Contig ID
                   pmv700894358.h1
5'-most EST
                   6583
Seq. No.
                   7025_1.R1040\(
Contig ID
                   leu7\overline{0}1145072.h1
5'-most EST
                   BLASTX
Method
                   g4455313
NCBI GI
BLAST score
                   469
                   6.0e-47
E value
Match length
                   155
                   54
% identity
                   (AL035528) fatty acid elongase-like protein (cer2-like)
NCBI Description
                   [Arabidopsis thaliana]
                   6584
Seq. No.
                   7025 2.R1040
Contig ID
```

LIB3055-005-Q1-N1-C10

E value

6.0e-39

```
Method
                   BLASTX
NCBI GI
                   q4455313
BLAST score
                   418
E value
                   5.0e-41
Match length
                   153
% identity
                   50
NCBI Description
                   (AL035528) fatty acid elongase-like protein (cer2-like)
                   [Arabidopsis thaliana]
Seq. No.
                   7029 1.R1040
Contig ID
5'-most EST
                   LIB3051-026-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   q4510385
BLAST score
                   186
E value
                   1.0e-13
Match length
                   48
                   75
% identity
NCBI Description
                   (AC007017) unknown protein [Arabidopsis thaliana]
                   6586
Seq. No.
Contig ID
                   7029 2.R1040
5'-most EST
                   hyd700726122.h1
                   6587
Seq. No.
Contig ID
                   7029 3.R1040
5'-most EST
                   k117\overline{0}1212057.h1
                   6588
Seq. No.
                   7029 4.R1040
Contig ID
5'-most EST
                   zzp700835108.h1
                   6589
Seq. No.
Contig ID
                   7031 1.R1040
5'-most EST
                   LIB3030-006-Q1-B1-F1
Method
                   BLASTX
NCBI GI
                   q3834314
BLAST score
                   588
E value
                   6.0e-61
Match length
                   159
% identity
                   75
NCBI Description
                   (AC005679) Similar to gene pi010 glycosyltransferase
                   gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs
                   gb_T46079 and gb_AA394466 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   6590
Contig ID
                   7033 1.R1040
5'-most EST
                   LIB3107-038-Q1-K1-H5
Seq. No.
                   6591
                   7037 1.R1040
Contig ID
                   vzy7\overline{0}0750957.h1
5'-most EST
Method
                   BLASTX
                   g3080416
NCBI GI
BLAST score
                   237
```

```
Match length
                   102
% identity
                   86
NCBI Description
                   (AL022604) UDP-galactose transporter - like protein
                   [Arabidopsis thaliana]
                   6592
Seq. No.
Contig ID
                   7039 1.R1040
5'-most EST
                   zsg701129960.h1
Method
                   BLASTX
NCBI GI
                   g3213227
BLAST score
                   167
                   2.0e-11
E value
Match length
                   90
% identity
                   34
NCBI Description
                   (AF035209) putative v-SNARE Vtila [Mus musculus]
                   >gi 3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]
                   6593
Seq. No.
                   7041 1.R1040
Contig ID
5'-most EST
                   LIB3\overline{0}49-026-Q1-E1-F1
Seq. No.
                   6594
Contig ID
                   7046_1.R1040
5'-most EST
                   jC-gmst02400030d06a1
Method
                   BLASTX
NCBI GI
                   g2811122
BLAST score
                   267
E value
                   4.0e-23
Match length
                   152
                   40
% identity
NCBI Description
                   (U87318) NaDC-2 [Xenopus laevis]
                   6595
Seq. No.
Contig ID
                   7047 1.R1040
5'-most EST
                   jex7\overline{0}0909603.h1
Seq. No.
                   6596
Contig ID
                   7056_1.R1040
5'-most EST
                   uC-gmropic023e04b1
Method
                   BLASTX
NCBI GI
                   g4455210
BLAST score
                   138
E value
                   6.0e-09
Match length
                   112
% identity
                   46
                   (AL035440) putative aspartate-tRNA ligase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   6597
                   7058 1.R1040
Contig ID
5'-most EST
                   g4290079
Seq. No.
                   6598
                   7058 2.R1040
Contig ID
5'-most EST
                   jC-gmf102220076c05a1
```

Z. ~

6599

Seq. No.

```
Contig ID
                   7060 1.R1040
5'-most EST
                   LIB3139-118-P1-N1-E3
Method
                   BLASTX
NCBI GI
                   g1737222
BLAST score
                   2812
E value
                   0.0e+00
Match length
                   583
% identity
                   86
NCBI Description
                   (U79958) BP-80 vacuolar sorting receptor [Pisum sativum]
Seq. No.
                   6600
                   7060 2.R1040
Contig ID
5'-most EST
                   zhf700953252.h1
                   BLASTX
Method
NCBI GI
                   q1737222
BLAST score
                   461
E value
                   9.0e-46
Match length
                   105
% identity
                   84
NCBI Description
                   (U79958) BP-80 vacuolar sorting receptor [Pisum sativum]
                   6601
Seq. No.
Contig ID
                   7060 3.R1040
5'-most EST
                   LIB3040-016-Q1-E1-C12
Method
                   BLASTX
NCBI GI
                   g2911587
BLAST score
                   436
E value
                   5.0e-43
Match length
                   160
% identity
                   54
NCBI Description
                   (AJ224442) methyltransferase [Homo sapiens]
                   6602
Seq. No.
                   7060 4.R1040
Contig ID
5'-most EST
                   djj7\overline{0}0605996.h2
Method
                   BLASTN
                   g414831
NCBI GI
BLAST score
                   67
E value
                   5.0e-29
                   71
Match length
% identity
                   99
NCBI Description
                   Glycine max (Rablp) mRNA, complete cds
Seq. No.
Contig ID
                   7060 5.R1040
5'-most EST
                   LIB3109-032-Q1-K1-C2
Seq. No.
                   7061 1.R1040
Contig ID
                   LIB3030-006-Q1-B1-B11
5'-most EST
Seq. No.
                   6605
                   7062 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy060c08b1
Seq. No.
                   7062 2.R1040
Contig ID
```

```
5'-most EST
                  LIB3030-006-Q1-B1-B12
Method
                  BLASTX
                  q2500583
NCBI GI
BLAST score
                  148
E value
                  5.0e-09
Match length
                  101
                  36
% identity
                  RNA-BINDING PROTEIN EWS >gi_1083465_pir__A55726 RNA-binding
NCBI Description
                  protein Ews - mouse >gi_488513_emb_CAA55815_ (X79233) EWS
                   [Mus musculus]
                   6607
Seq. No.
                  7064 1.R1040
Contig ID
                  LIB3139-107-P1-N1-B4
5'-most EST
                  BLASTX
Method
                  g3785990
NCBI GI
                  510
BLAST score
                  2.0e-51
E value
Match length
                  172
                   60
% identity
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4220487 (AC006069) hypothetical protein [Arabidopsis
                  thaliana]
                   6608
Seq. No.
                  7068 1.R1040
Contig ID
5'-most EST
                  g4397127
Method
                  BLASTX
                  g2352492
NCBI GI
BLAST score
                  571
                  1.0e-58
E value
Match length
                  237
                   49
% identity
                   (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                  thaliana] >gi_2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
Seq. No.
                   6609
                  7070 1.R1040
Contig ID
5'-most EST
                  kmv700741748.h1
                  BLASTX
Method
NCBI GI
                  g399940
BLAST score
                  1968
E value
                  0.0e + 00
Match length
                  451
% identity
NCBI Description
                  MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR
                  >gi_100004_pir__S25005 heat shock protein, 70K - kidney
                  bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock
                  protein [Phaseolus vulgaris]
                  6610
Seq. No.
Contig ID
                  7070 2.R1040
                  hrw701060186.h1
5'-most EST
                  BLASTN
Method
                  q20834
NCBI GI
```

204

BLAST score

```
1.0e-111
E value
Match length
                   400
                   88
% identity
NCBI Description
                  P.sativum PHSP1 mRNA for HSP70
                   6611
Seq. No.
Contig ID
                   7072 1.R1040
                   LIB3170-034-Q1-K1-F4
5'-most EST
Method
                   BLASTX
                   g2462744
NCBI GI
BLAST score
                   291
E value
                   4.0e-26
Match length
                   86
                   65
% identity
                   (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   6612
Seq. No.
                   7073 1.R1040
Contig ID
5'-most EST
                   pcp700994935.h1
Method
                   BLASTX
NCBI GI
                   g1304599
BLAST score
                   307
E value
                   1.0e-27
                   222
Match length
% identity
                   26
                   (U41315) ZNF127-Xp [Homo sapiens]
NCBI Description
Seq. No.
                   6613
                   7073 2.R1040
Contig ID
                   fde7\overline{0}0872991.h1
5'-most EST
Seq. No.
                   6614
Contig ID
                   7079_1.R1040
                   LIB3<u>1</u>70-032-Q1-K1-F3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3021336
BLAST score
                   261
E value
                   2.0e-22
Match length
                   122
                   50
% identity
                   (AJ224957) RGA-like [Arabidopsis thaliana]
NCBI Description
                   6615
Seq. No.
                   7079 2.R1040
Contig ID
                   LIB3039-051-Q1-E1-F6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3785986
BLAST score
                   265
E value
                   6.0e-23
Match length
                   111
                   50
% identity
NCBI Description
                   (AC005560) RGA1 protein [Arabidopsis thaliana]
                   6616
Seq. No.
Contig ID
                   7080 1.R1040
```

LIB3030-005-Q1-B1-H8

E value

1.0e-25

```
Seq. No.
                   6617
Contig ID
                   7086 1.R1040
                   jsh701069332.hl
5'-most EST
                   6618
Seq. No.
                   7091 1.R1040
Contig ID
                  LIB3107-032-Q1-K1-C5
5'-most EST
                  BLASTN
Method
                   g4415928
NCBI GI
                   51
BLAST score
                   2.0e-19
E value
                   103
Match length
                   87
% identity
                  Arabidopsis thaliana chromosome II BAC F13A10 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   6619
                   7091 2.R1040
Contig ID
                   uC-gmropic098e09b1
5'-most EST
Method
                   BLASTX
                   g4415936
NCBI GI
                   255
BLAST score
                   8.0e-22
E value
Match length
                   184
                   36
% identity
                   (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6620
                   7099 1.R1040
Contig ID
                   LIB3039-009-Q1-E1-G3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3281861
BLAST score
                   194
                   1.0e-14
E value
                   122
Match length
% identity
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   6621
Seq. No.
                   7100 1.R1040
Contig ID
                   jC-gmle01810056d04a1
5'-most EST
Method
                   BLASTX
                   g4115379
NCBI GI
                   309
BLAST score
E value
                   3.0e-28
Match length
                   101
% identity
                   59
NCBI Description
                   (AC005967) putative carbonyl reductase [Arabidopsis
                   thaliana]
                   6622
Seq. No.
                   7100 2.R1040
Contig ID
5'-most EST
                   zsq701119727.h1
Method
                   BLASTX
NCBI GI
                   g4115379
BLAST score
                   287
```

BLAST score

```
Match length
                   101
% identity
                   58
NCBI Description
                   (AC005967) putative carbonyl reductase [Arabidopsis
                   thaliana]
Seq. No.
                   6623
                   7100 3.R1040
Contig ID
5'-most EST
                   LIB3030-005-Q1-B1-G6
Method
                   BLASTX
NCBI GI
                   q4115379
BLAST score
                   239
E value
                   4.0e-20
Match length
                   84
% identity
NCBI Description
                   (AC005967) putative carbonyl reductase [Arabidopsis
                   thaliana]
                   6624
Seq. No.
                   7100 5.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1145195.h1
                   BLASTX
Method
NCBI GI
                   g4115379
BLAST score
                   174
E value
                   1.0e-12
Match length
                   51
% identity
                   (AC005967) putative carbonyl reductase [Arabidopsis
NCBI Description
                   thaliana]
                   6625
Seq. No.
Contig ID
                   7103 1.R1040
                   jC-gmf102220073c07a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1421730
BLAST score
                   281
E value
                   7.0e-25
Match length
                   92
                   58
% identity
NCBI Description
                   (U43082) RF2 [Zea mays]
Seq. No.
                   6626
Contig ID
                   7103 2.R1040
5'-most EST
                   uC-gmropic062f11b1
Method
                   BLASTX
NCBI GI
                   g1421730
BLAST score
                   167
E value
                   2.0e-11
                   75
Match length
% identity
NCBI Description
                   (U43082) RF2 [Zea mays]
Seq. No.
                   7107 1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1155568.h1
Method
                   BLASTX
                   g3559807
NCBI GI
```

```
4.0e-61
E value
Match length
                   124
% identity
                   60
NCBI Description
                   (Y15628) HCF136 protein [Arabidopsis thaliana]
Seq. No.
                   6628
                   7108 1.R1040
Contig ID
5'-most EST
                   vzy700752446.hl
Seq. No.
                   6629
Contig ID
                   7108 2.R1040
5'-most EST
                   jC-gmle01810026a04a1
                   6630
Seq. No.
                   7112 1.R1040
Contig ID
5'-most EST
                  LIB3030-005-Q1-B1-E7
                   6631
Seq. No.
                   7114 1.R1040
Contig ID
5'-most EST
                   fua701039921.h1
Method
                   BLASTN
NCBI GI
                   g438130
BLAST score
                   237
E value
                   1.0e-130
Match length
                   673
% identity
NCBI Description
                  S.tuberosum mitochondrial gene for the 59kDa subunit of the
                   NAD+-dependent malic enzyme
                   6632
Seq. No.
Contig ID
                   7114 2.R1040
5'-most EST
                   LIB3030-005-Q1-B1-E9
Method
                   BLASTX
                   g585452
NCBI GI
BLAST score
                   715
E value
                   1.0e-75
Match length
                   168
% identity
                   80
                  MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM
NCBI Description
                   PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)
                   (NAD-ME) >gi_1076666_pir__A53318 malate dehydrogenase
                   (decarboxylating) (EC 1.1.1.39) 59K chain precursor,
                   mitochondrial - potato >gi_438131_emb_CAA80547_ (Z23002)
                   precursor of the 59kDa subunit of the mitochondrial
                   NAD+-dependent malic enzyme [Solanum tuberosum]
Seq. No.
                   6633
Contig ID
                   7117 1.R1040
5'-most EST
                   LIB3030-005-Q1-B1-F2
                   6634
Seq. No.
                   7121 1.R1040
Contig ID
5'-most EST
                   jex7\overline{0}0907344.h1
                   6635
Seq. No.
                   7123 1.R1040
Contig ID
```

fua701042593.h1

```
Method
                   BLASTX
NCBI GI
                   q1703036
BLAST score
                   189
E value
                   5.0e-14
Match length
                   79
                   47
% identity
NCBI Description
                   5'-AMP-ACTIVATED PROTEIN KINASE, BETA-1 SUBUNIT (AMPK
                   BETA-1 CHAIN) (40 KD SUBUNIT) >gi_1335858 (U42411)
                   5'-AMP-activated protein kinase, beta subunit [Rattus
                   norvegicus]
                   6636
Seq. No.
                   7123 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy026h11b1
Seq. No.
                   6637
                   7124 1.R1040
Contig ID
5'-most EST
                   1eu7\overline{0}1150036.h1
Method
                   BLASTN
NCBI GI
                   g18569
BLAST score
                   425
                   0.0e+00
E value
Match length
                   476
                   100
% identity
NCBI Description
                  G.max coxII gene for cytochrome oxidase subunit
                   6638
Seq. No.
Contig ID
                   7125 1.R1040
                   LIB3030-005-Q1-B1-C9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4263777
BLAST score
                   1389
                   1.0e-154
E value
Match length
                   348
                   70
% identity
NCBI Description
                   (AC006068) putative serine carboxypeptidase II [Arabidopsis
                   thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative
                   serine carboxypeptidase II [Arabidopsis thaliana]
                   6639
Seq. No.
Contig ID
                   7127 1.R1040
5'-most EST
                   uC-qmropic037q05b1
Method
                   BLASTX
NCBI GI
                   q2344887
BLAST score
                   740
E value
                   2.0e-78
Match length
                   223
% identity
NCBI Description
                   (AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.
                   6640
Contig ID
                   7127 2.R1040
5'-most EST
                   LIB3030-005-Q1-B1-D10
Seq. No.
                   6641
                   7129 1.R1040
Contig ID
```

 $uaw7\overline{0}0665131.h1$

```
6642
 Seq. No.
                    7129 2.R1040
 Contig ID
 5'-most EST
                    zhf700962637.h1
 Seq. No.
                    6643
 Contig ID
                    7132 1.R1040
 5'-most EST
                    LIB3051-106-Q1-K1-H12
                    BLASTN
 Method
                    g975703
 NCBI GI
 BLAST score
                    42
 E value
                    3.0e-14
 Match length
                    85
                    54
 % identity
 NCBI Description P.sativum GR gene
 Seq. No.
                    6644
                    7132 2.R1040
 Contig ID
 5'-most EST
                    g5605768
                    BLASTX
 Method
 NCBI GI
                    g2262156
 BLAST score
                    163
                    8.0e-12
 E value
 Match length
                    115
                    43
 % identity
                    (AC002329) hypothetical protein with weak similarity to S.
. NCBI Description
                    cerevisiae hypothetical protein PID:g1066493 [Arabidopsis
                    thaliana]
                    6645
 Seq. No.
                    7135 2.R1040
 Contig ID
 5'-most EST
                    sat7\overline{0}1003967.h1
                    BLASTX
 Method
                    g4204695
 NCBI GI
 BLAST score
                    153
                    5.0e-10
 E value
 Match length
                    98
 % identity
                    38
                    (AF117062) putative inositol polyphosphate 5-phosphatase
 NCBI Description
                    At5P1 [Arabidopsis thaliana]
                    6646
 Seq. No.
 Contig ID
                    7136 1.R1040
 5'-most EST
                    LIB3030-005-Q1-B1-D9
                    BLASTX
 Method
 NCBI GI
                    g2642153
 BLAST score
                    352
 E value
                    7.0e-33
 Match length
                    206
 % identity
 NCBI Description
                     (AC003000) unknown protein [Arabidopsis thaliana]
                    >gi 2795810 (AC003674) unknown protein [Arabidopsis
                    thaliana]
                    6647
 Seq. No.
                    7136 2.R1040
 Contig ID
```

jC-gmro02910044e04a1

NCBI Description

```
Seq. No.
                   6648
Contig ID
                   7138 1.R1040
5'-most EST
                   q5606078
Method
                   BLASTX
NCBI GI
                   g3023751
BLAST score
                   440
E value
                   2.0e-43
Match length
                   100
% identity
                   28
NCBI Description
                   70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
                   ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
                   peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                   >gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase
                   [Triticum aestivum]
                   6649
Seq. No.
                   7139 1.R1040
Contig ID
5'-most EST
                   LIB3030-005-Q1-B1-E11
                   BLASTX
Method
NCBI GI
                   g4371285
                   398
BLAST score
                   9.0e-39
E value
Match length
                   104
% identity
                   71
                   (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   6650
Seq. No.
                   7140 1.R1040
Contig ID
5'-most EST
                   q4282509
Method
                   BLASTX
NCBI GI
                   g3702368
BLAST score
                   1123
E value
                   1.0e-123
Match length
                   296
% identity
NCBI Description
                   (AJ001855) alpha subunit of F-actin capping protein
                   [Arabidopsis thaliana]
                   6651
Seq. No.
Contig ID
                   7141 1.R1040
5'-most EST
                   epx7\overline{0}1106727.h1
Seq. No.
                   6652
Contig ID
                   7146 1.R1040
5'-most EST
                   uC-gmronoir064d10b1
Seq. No.
                   6653
Contig ID
                   7147 1.R1040
5'-most EST
                   fde700874693.hl
Method
                   BLASTX
NCBI GI
                   q3080437
BLAST score
                   180
E value
                   6.0e-13
Match length
                   54
% identity
```

(AL022605) putative protein [Arabidopsis thaliana]

```
6654
Seq. No.
                   7152_1.R1040
Contig ID
5'-most EST
                   jC-gmst02400009e02a1
Method
                   BLASTX
                   q3269288
NCBI GI
BLAST score
                   800
                   2.0e-85
E value
                   199
Match length
                   78
% identity
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   6655
Seq. No.
                   7153 1.R1040
Contig ID
                   rca700996111.h1
5'-most EST
                   BLASTX
Method
                   g3450842
NCBI GI
BLAST score
                   624
                   4.0e-65
E value
                   159
Match length
                   68
% identity
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
                   6656
Seq. No.
Contig ID
                   7154 1.R1040
5'-most EST
                   LIB3030-005-Q1-B1-C4
Method
                   BLASTX
NCBI GI
                   q4455192
BLAST score
                   376
                   4.0e-36
E value
Match length
                   150
% identity
                   49
                   (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   6657
Seq. No.
                   7156 1.R1040
Contig ID
5'-most EST
                   xpa700792358.h1
Method
                   BLASTX
NCBI GI
                   g3142295
BLAST score
                   249
E value
                   4.0e-21
Match length
                   94
% identity
                   (AC002411) Strong similarity to phosphoribosylanthranilate
NCBI Description
                   transferase gb_D86180 from Pisum sativum. [Arabidopsis
                   thaliana]
                   6658
Seq. No.
Contig ID
                   7156_2.R1040
5'-most EST
                   vzy700754349.h1
Method
                   BLASTX
NCBI GI
                   g3142295
                   176
BLAST score
                   1.0e-12
E value
                   53
Match length
```

62

% identity

BLAST score

E value

421

4.0e-41

```
NCBI Description
                   (AC002411) Strong similarity to phosphoribosylanthranilate
                   transferase gb D86180 from Pisum sativum. [Arabidopsis
                   thaliana]
                   6659
Seq. No.
                   7160 1.R1040
Contig ID
                   jex700905076.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2924512
BLAST score
                   355
E value
                   1.0e-33
Match length
                   91
% identity
                   67
                   (AL022023) beta-galactosidase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   6660
Seq. No.
                   7164 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy0001h07b1
                   6661
Seq. No.
                   7167 1.R1040
Contig ID
5'-most EST
                   LIB3030-005-Q1-B1-A2
                   6662
Seq. No.
                   7170 1.R1040
Contig ID
5'-most EST
                   LIB3030-005-Q1-B1-A6
                   6663
Seq. No.
                   7174 1.R1040
Contig ID
5'-most EST
                   zhf700962284.h1
                   BLASTX
Method
                   g4467128
NCBI GI
BLAST score
                   897
E value
                   6.0e-97
Match length
                   228
% identity
                   76
NCBI Description
                   (AL035538) putative protein [Arabidopsis thaliana]
                   6664
Seq. No.
Contig ID
                   7176 1.R1040
5'-most EST
                  LIB3030-004-Q1-B1-G1
Method
                  BLASTX
NCBI GI
                  g4512652
BLAST score
                  169
E value
                   1.0e-11
Match length
                  221
% identity
NCBI Description
                   (AC007048) hypothetical protein [Arabidopsis thaliana]
                   6665
Seq. No.
                   7177 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy080c10b1
Method
                  BLASTX
NCBI GI
                  q2213590
```

BLAST score

```
158
Match length
% identity
                   51
                   (AC000348) T7N9.10 [Arabidopsis thaliana]
NCBI Description
                   6666
Seq. No.
                   7179 1.R1040
Contig ID
                   LIB3030-004-Q1-B1-G4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4455359
                   870
BLAST score
E value
                   1.0e-93
Match length
                   261
                   70
% identity
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   6667
Seq. No.
Contig ID
                   7182 1.R1040
5'-most EST
                   zsg7\overline{0}1123319.h1
                   6668
Seq. No.
Contig ID
                   7186_1.R1040
5'-most EST
                   epx701107104.h1
                   BLASTX
Method
                   g2213590
NCBI GI
BLAST score
                   178
                   6.0e-13
E value
Match length
                   86
% identity
                   41
                   (AC000348) T7N9.10 [Arabidopsis thaliana]
NCBI Description
                   6669
Seq. No.
                   7192 1.R1040
Contig ID
                   jC-gmle01810080f03a1
5'-most EST
                   6670
Seq. No.
                   7193 1.R1040
Contig ID
5'-most EST
                   LIB3109-042-Q1-K1-H1
Method
                   BLASTX
                   g1346766
NCBI GI
BLAST score
                   369
                   9.0e-35
E value
                   257
Match length
                   35
% identity
                   26S PROTEASOME REGULATORY SUBUNIT S14 (P31)
NCBI Description
                   >gi_1362741_pir__S56108 multicatalytic endopeptidase
complex (EC 3.4.99.46) regulatory chain 31 - human
                   >gi_1037164_dbj_BAA07237_ (D38047) 26S proteasome subunit
                   p31 [Homo sapiens] >gi_3702282 (AC005789) PP31_HUMAN [Homo
                   sapiens] >gi_4506233_ref_NP_002803.1_pPSMD8_ proteasome
                   (prosome, macropain) 26S subunit, non-ATPase,
                   6671
Seq. No.
Contig ID
                   7194 1.R1040
                   LIB3030-004-Q1-B1-E5
5'-most EST
Method
                   BLASTX
                   g3068705
NCBI GI
```

% identity

```
7.0e-19
E value
Match length
                   105
% identity
                   48
NCBI Description
                   (AF049236) unknown [Arabidopsis thaliana]
                   6672
Seq. No.
                   7196 1.R1040
Contig ID
5'-most EST
                   LIB3030-004-Q1-B1-E8
                   6673
Seq. No.
                   7197 1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1149726.h1
                   6674
Seq. No.
                   7203 1.R1040
Contig ID
5'-most EST
                   LIB3040-023-Q1-E1-A12
                   BLASTN
Method
                   g1272409
NCBI GI
BLAST score
                   240
                   1.0e-132
E value
Match length
                   384
                   91
% identity
                   Vicia faba immunophilin precursor (FKBP15) mRNA, complete
NCBI Description
                   cds
                   6675
Seq. No.
Contig ID
                   7209 1.R1040
5'-most EST
                   LIB3106-105-Q1-K1-E4
                   BLASTX
Method
                   g2275202
NCBI GI
BLAST score
                   178
E value
                   6.0e-13
Match length
                   60
% identity
                   (AC002337) acyl-CoA synthetase isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   6676
                   7213 1.R1040
Contig ID
                   bth7\overline{0}0843983.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1841475
BLAST score
                   353
                   2.0e-33
E value
Match length
                   80
                   75
% identity
NCBI Description
                   (Y11105) Myb26 [Pisum sativum]
Seq. No.
                   6677
                   7213 2.R1040
Contig ID
                   uC-gmflminsoy037e05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1002796
BLAST score
                   500
E value
                   9.0e-51
Match length
                   121
```

```
NCBI Description (U33915) Cpm10 [Craterostigma plantagineum]
                   6678
Seq. No.
Contig ID
                   7214 1.R1040
5'-most EST
                   rrt700646076.hl
                   BLASTX
Method
NCBI GI
                   q2130139
BLAST score
                   162
E value
                   5.0e-11
Match length
                   99
% identity
                   39
                   hypothetical protein - maize >gi_949980_emb_CAA61258_
NCBI Description
                   (X88779) orf [Zea mays]
Seq. No.
                   6679
Contig ID
                   7215 1.R1040
                   zhf700960909.hl
5'-most EST
Method
                   BLASTX
                   g2765366
NCBI GI
BLAST score
                   231
E value
                   3.0e-19
                   99
Match length
                   45
% identity
NCBI Description
                   (Y14038) putative Ole e 1 protein [Betula pendula]
                   6680
Seq. No.
                   7217 1.R1040
Contig ID
                   LIB3087-002-Q1-K1-D3
5'-most EST
Method
                   BLASTX
                   g2880048
NCBI GI
BLAST score
                   310
                   5.0e-28
E value
                   71
Match length
                   79
% identity
NCBI Description (AC002340) unknown protein [Arabidopsis thaliana]
Seq. No.
                   6681
                   7218 1.R1040
Contig ID
                   uC-gmflminsoy065f10b1
5'-most EST
Method
                   BLASTX
                   g3152605
NCBI GI
BLAST score
                   277
E value
                   2.0e-24
Match length
                   134
% identity
                   49
                   (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6682
Contig ID
                   7221 1.R1040
5'-most EST
                   V4R - \overline{0}2 - Q1 - B1 - C6
Method
                   BLASTX
NCBI GI
                   q4539335
BLAST score
                   1046
E value
                   1.0e-114
Match length
                   315
% identity
                   (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
```

% identity

```
6683 ·
Seq. No.
Contig ID
                  7222 1.R1040
5'-most EST
                  V4R-01-Q1-B1-G5
Method
                  BLASTX
NCBI GI
                  g1168470
BLAST score
                  1543
E value
                  1.0e-172
Match length
                   421
% identity
                  73
NCBI Description
                  PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase,
                  tyrosine/serine/threonine-specific (EC 2.7.1.-) -
                  Arabidopsis thaliana >gi_217829 dbj_BAA02092 (D12522)
                  protein tyrosine-serine-threonine kinase [Arabidopsis
                  thaliana]
Seq. No.
                   6684
                  7222 2.R1040
Contig ID
5'-most EST
                  zsg701117356.h1
                  BLASTX
Method
                  g3461835
NCBI GI
BLAST score
                  343
E value
                  5.0e-32
Match length
                  194
% identity
                   65
                   (AC005315) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  >gi 3927840 (AC005727) putative protein kinase [Arabidopsis
                  thaliana]
                  6685
Seq. No.
Contig ID
                  7222 5.R1040
5'-most EST
                  eep7\overline{0}0865844.h1
                  6686
Seq. No.
Contig ID
                  7226_1.R1040
5'-most EST
                  uC-gmflminsoy028g12b1
                                                      1
Method
                  BLASTX
                  g2493046
NCBI GI
BLAST score
                  735
                  9.0e-78
E value
                  197
Match length
% identity
                  75
                  ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_82297_pir__A41740 H+-transporting ATP synthase (EC
                  3.6.1.34) delta' chain precursor - sweet potato
                  >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                  delta subunit [Ipomoea batatas]
Seq. No.
                  6687
Contig ID
                  7229 1.R1040
5'-most EST
                  leu701156154.h1
Method
                  BLASTX
NCBI GI
                  q1848212
BLAST score
                  751
E value
                  7.0e-80
Match length
                  181
```

Contig ID

```
NCBI Description
                   (Y11209) protein disulfide-isomerase precursor [Nicotiana
                   tabacum]
                   6688
Seq. No.
                   7230 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400076d08a1
Method
                   BLASTN
NCBI GI
                   g1556445
BLAST score
                   224
                   1.0e-122
E value
                   608
Match length
                   84
% identity
                   Hordeum vulgare alpha tubulin (tubA) mRNA, complete cds
NCBI Description
                   6689
Seq. No.
                   7231 1.R1040
Contig ID
5'-most EST
                   asn701132470.hl
Method
                   BLASTX
NCBI GI
                   q2388580
BLAST score
                   1259
                   1.0e-139
E value
Match length
                   252
                   90
% identity
                   (AC000098) Similar to Sequence 10 from patent 5477002
NCBI Description
                   (gb_1253956). [Arabidopsis thaliana]
Seq. No.
                   6690
Contig ID
                   7233 1.R1040
5'-most EST
                   LIB3030-004-Q1-B1-C1
                   BLASTX
Method
NCBI GI
                   g542050
BLAST score
                   325
                   5.0e-30
E value
                   140
Match length
                   46
% identity
NCBI Description
                   catechol O-methyltransferase (EC 2.1.1.6) III - common
                   tobacco >gi_429114_emb_CAA50561_ (X71430) catechol
                   O-methyltransferase [Nicotiana tabacum]
Seq. No.
                   6691
Contig ID
                   7235 1.R1040
5'-most EST
                   gsv7\overline{0}1045787.h1
                   6692
Seq. No.
Contig ID
                   7239 1.R1040
5'-most EST
                   LIB3030-003-Q1-B1-G9
Seq. No.
                   6693
Contig ID
                   7240 1.R1040
5'-most EST
                   LIB3107-031-Q1-K1-F5
Seq. No.
                   6694
Contig ID
                   7240 2.R1040
5'-most EST
                   sat701007364.h2
                   6695
Seq. No.
```

7241 1.R1040

```
5'-most EST
                   ssr700559125.hl
Method
                  BLASTN
                  g887572
NCBI GI
BLAST score
                   74
E value
                   3.0e-33
                   206
Match length
% identity
                   84
NCBI Description
                  P.sativum mRNA for starch synthase (2988 bp)
Seq. No.
                   7245 1.R1040
Contig ID
                  bth700846389.h1
5'-most EST
                                                                9:-
Method
                  BLASTX
NCBI GI
                   q3023713
BLAST score
                   642
E value
                   3.0e-67
Match length
                   141
                   87
% identity
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
                   6697
                   7245 2.R1040
Contig ID
5'-most EST
                   uC-gmropic045a01b1
Method
                   BLASTX
NCBI GI
                   q3023713
BLAST score
                   478
E value
                   4.0e-48
Match length
                   110
% identity
                   85
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                   (U09450) enolase [Oryza sativa]
Seq. No.
Contig ID
                   7247 1.R1040
5'-most EST
                   LIB3170-043-Q1-J1-G7
Method
                   BLASTN
NCBI GI
                   q4159706
BLAST score
                   49
E value
                   2.0e-18
Match length
                   173
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGL6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   7247 2.R1040
Contig ID
                   leu7\overline{0}1149612.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                   g4159706
                  52
BLAST score
                   5.0e-20
E value
Match length
                   176
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
```

```
MGL6, complete sequence [Arabidopsis thaliana]
                   6700
Seq. No.
Contig ID
                   7247 3.R1040
                   LIB3106-110-Q1-K1-C9
5'-most EST
Method
                   BLASTN
                   g4159706
NCBI GI
BLAST score
                   41
E value
                   2.0e-13
Match length
                   125
                   83
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MGL6, complete sequence [Arabidopsis thaliana]
                   6701
Seq. No.
Contig ID
                   7247 4.R1040
5'-most EST
                   dpv7\overline{0}1097991.h1
                   BLASTN
Method
                   g4159706
NCBI GI
BLAST score
                   35
E value
                   5.0e-10
                   131
Match length
                   82
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MGL6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   6702
                   7247 5.R1040
Contig ID
5'-most EST
                   LIB3138-127-Q1-N1-D11
                   6703
Seq. No.
Contig ID
                   7250 1.R1040
                   LIB3040-002-Q1-E1-B3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3721856
BLAST score
                   208
E value
                   2.0e-16
Match length
                   54
                   65
% identity
NCBI Description
                   (AB014057) beta-Amyrin Synthase [Panax ginseng]
Seq. No.
                   6704
Contig ID
                   7251 1.R1040
5'-most EST
                   uC-gmropic091b10b1
                   6705
Seq. No.
Contig ID
                   7253 1.R1040
5'-most EST
                   uC-gmflminsoy068e02b1
Seq. No.
                   6706
Contig ID
                   7259 1.R1040
5'-most EST
                   uC-gmflminsoy044b04b1
Method
                   BLASTX
NCBI GI
                   q4049341
BLAST score
                   585
                   1.0e-60
E value
```

140

Match length

```
81
% identity
NCBI Description
                   (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                   6707
Contig ID
                   7260 1.R1040
5'-most EST
                  LIB3030-003-Q1-B1-F12
Method
                   BLASTX
NCBI GI
                   g99733
BLAST score
                   806
                   1.0e-96
E value
Match length
                   256
% identity
NCBI Description
                  hypothetical protein Hlflk - Arabidopsis thaliana
                   (fragment) >gi_16482_emb_CAA44318_ (X62461) H1flk
                   [Arabidopsis thaliana]
                   6708
Seq. No.
                   7262 1.R1040
Contig ID
                   sat701004636.hl
5'-most EST
Method
                   BLASTX
                   g2894607
NCBI GI
BLAST score
                   436
E value
                   5.0e-43
Match length
                   150
% identity
                   54.
NCBI Description
                   (ALO21889) NAM (no apical meristem) - like protein
                   [Arabidopsis thaliana]
                   6709
Seq. No.
                   7262 2.R1040
Contig ID
5'-most EST
                  LIB3051-059-Q1-K2-D5
Method
                  BLASTX
NCBI GI
                   g2894607
BLAST score
                   199
E value
                  2.0e-15
Match length
                   109
% identity
                   39
NCBI Description
                   (ALO21889) NAM (no apical meristem) - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   6710
Contig ID
                   7264 1.R1040
5'-most EST
                   LIB3107-041-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   g3747111
BLAST score
                   661
E value
                   6.0e-69
Match length
                  226
% identity
NCBI Description
                   (AF095641) MTN3 homolog [Arabidopsis thaliana]
Seq. No.
                   6711
                   7264 2.R1040
Contig ID
5'-most EST
                  LIB3170-082-Q1-J1-F1
Seq. No.
                   6712
```

7267 1.R1040

Contig ID

```
zzp700830203.h1
5'-most EST
                   6713
Seq. No.
Contig ID
                   7269 1.R1040
5'-most EST
                  jC-gmro02910059c03d1
Seq. No.
                   6714
                  7269 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy026g03b1
Seq. No.
                   6715
                  7271 1.R1040
Contig ID
                  LIB3138-125-Q1-N1-B7
5'-most EST
                  6716
Seq. No.
                  7271 2.R1040
Contig ID
                  LIB3030-003-Q1-B1-C12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1742187
BLAST score
                  185
E value
                   3.0e-13
Match length
                  150
% identity
                  30
NCBI Description
                   (D90771) ORF_ID:o260#14; similar to [SwissProt Accession
                  Number P11666] [Escherichia coli] >gi_1742198_dbj_BAA14933_
                   (D90772) ORF_ID:o260#14; similar to [SwissProt Accession
                  Number P11666] [Escherichia coli] >gi_1787591 (AE000231)
                  orf, hypothetical protein [Escherichia coli]
Seq. No.
                  6717
Contig ID
                  7276 1.R1040
5'-most EST
                  uC-gmrominsoy177g01b1
Method
                  BLASTX
                  g2832683
NCBI GI
BLAST score
                  673
E value
                  1.0e-70
Match length
                  160
% identity
                   (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
                   6718
Seq. No.
Contig ID
                  7277 1.R1040
                  jC-gmst02400055b10a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3298443
BLAST score
                  641
E value
                  5.0e-67
Match length
                  184
% identity
NCBI Description
                   (AB010880) chloroplast ribosomal protein L17 [Nicotiana
                  tabacum]
Seq. No.
                  6719
                  7277 2.R1040
Contig ID
5'-most EST
                  LIB3030-003-Q1-B1-D11
```

```
7277 3.R1040
Contig ID
                  LIB3106-072-P1-K1-G1
5'-most EST
                  BLASTX
Method
                  g3298443
NCBI GI
BLAST score
                  155
E value
                  2.0e-10
                  57
Match length
                  61
% identity
                   (AB010880) chloroplast ribosomal protein L17 [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  6721
                  7278 2.R1040
Contig ID
5'-most EST
                  LIB3030-003-Q1-B1-D12
Seq. No.
                  6722
Contig ID
                  7280 1.R1040
5'-most EST
                  LIB3030-003-Q1-B1-D5
Method
                  BLASTX
NCBI GI
                  q4206122
BLAST score
                  419
E value
                  3.0e-41
                  146
Match length
% identity
NCBI Description
                   (AF097667) protein phosphatase 2C homolog [Mesembryanthemum
                  crystallinum]
Seq. No.
                  6723
                  7281 1.R1040
Contig ID
5'-most EST
                  uC-gmropic050b08b1
Method
                  BLASTX
NCBI GI
                  g399333
BLAST score
                  489
                  2.0e-49
E value
                  128
Match length
                  75
% identity
NCBI Description
                  CYSTEINE SYNTHASE CHLOROPLAST PRECURSOR (O-ACETYLSERINE
                  SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                  >gi_322740_pir__A43407 cysteine synthase (EC 4.2.99.8)
                  precursor - pepper >gi_17944_emb_CAA46086_ (X64874)
                  O-acetylserine (thiol)-lyase [Capsicum annuum]
Seq. No.
                  6724
Contig ID
                  7281 2.R1040
5'-most EST
                  LIB3030-003-Q1-B1-D7
                  6725
Seq. No.
Contig ID
                  7286_1.R1040
5'-most EST
                  jC-gmle01810055g05a1
Method
                  BLASTX
NCBI GI
                  g4006865
BLAST score
                  817
E value
                  2.0e-87
Match length
                  227
% identity
                  67
```

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Match length

```
6726
Seq. No.
                   7286 3.R1040
Contig ID
                   zpv700761628.h1
5'-most EST
Method
                   BLASTX
                   q2190551
NCBI GI
BLAST score
                   163
                   2.0e-11
E value
                   39
Match length
                   85
% identity
NCBI Description
                   (AC001229) Similar to C. elegans hypothetical protein
                   K07C5.6 (gb_Z71181). ESTs gb_H36844,gb_AA394956 come from
                   this gene. [Arabidopsis thaliana]
                  6727
Seq. No.
                   7287 1.R1040
Contig ID
                   leu7\overline{0}1147472.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q541944
BLAST score
                   632
E value
                   1.0e-65
Match length
                   181
                   71
% identity
NCBI Description
                   nodulin-26 - soybean
Seq. No.
                   6728
                   7287 2.R1040
Contig ID
5'-most EST
                   asn701134248.hl
Method
                   BLASTX
                   g1076748
NCBI GI
BLAST score
                   379
E value
                   8.0e-37
                   93
Match length
                   77
% identity
                   major intrinsic protein - rice >gi_440869_dbj_BAA04257_
NCBI Description
                   (D17443) major intrinsic protein [Oryza sativa]
Seq. No.
                   6729
                   7289 1.R1040
Contig ID
                   bnh700764511.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   a1076668
BLAST score
                   650
                   4.0e-68
E value
Match length
                   158
                   79
% identity
                   NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                   >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
                   6730
Seq. No.
                   7289 2.R1040
Contig ID
5'-most EST
                   leu701151520.h1
Method
                   BLASTX
                   g1076668
NCBI GI
BLAST score
                   153
E value
                   2.0e-10
```

6738

```
% identity
                         60
      NCBI Description
                         NADH dehydrogenase (EC 1.6.99.3) - potato
                         >gi_639834_emb_CAA58823 (X83999) NADH dehydrogenase
                         [Solanum tuberosum]
      Seq. No.
                         6731
      Contig ID
                         7290 1.R1040
      5'-most EST
                         dpv7\overline{0}1097134.h1
      Seq. No.
                         6732
      Contig ID
                         7290 2.R1040
      5'-most EST
                         LIB3093-015-Q1-K1-C8
                         6733
      Seq. No.
      Contig ID
                         7291 1.R1040
      5'-most EST
                         k11701207653.h1
      Seq. No.
                         6734
                         7291 2.R1040
      Contig ID
      5'-most EST
                         pmv700894835.h1
      Seq. No.
                         6735
                         7294 1.R1040
     Contig ID
                         jex7\overline{0}0906742.h1
      5'-most EST
                         BLASTX
     Method
     NCBI GI
                         q2529703
     BLAST score
                         300
                         6.0e-27
     E value
     Match length
                         159
      % identity
     NCBI Description
                         (AF000142) class II knotted-like homeodomain protein
                         [Lycopersicon esculentum]
                         6736
     Seq. No.
     Contig ID
                         7294 2.R1040
      5'-most EST
                         sat701003783.hl
Method
                         BLASTX
     NCBI GI
                         q1805618
     BLAST score
                         190
     E value
                         4.0e-14
     Match length
                         126
      % identity
     NCBI Description
                         (D49704) OSH45 transcript [Oryza sativa]
     Seq. No.
                         6737
     Contig ID
                         7295 1.R1040
      5'-most EST
                         wvk7\overline{0}0684662.h1
     Method
                         BLASTX
     NCBI GI
                         g2462781
     BLAST score
                         748
     E value
                         2.0e-79
     Match length
                         219
      % identity
                         69
                         (U73175) carbamoyl phosphate synthetase small subunit
     NCBI Description
                         [Arabidopsis thaliana]
```

NCBI GI

```
7295 2.R1040
Contig ID
5'-most EST
                   vwf700675431.hl
Method
                   BLASTX
NCBI GI
                   g2462781
BLAST score
                   522
E value
                   4.0e-53
Match length
                   142
% identity
                   75
NCBI Description
                   (U73175) carbamoyl phosphate synthetase small subunit
                   [Arabidopsis thaliana]
Seq. No.
                   6739
                   7296 1.R1040
Contig ID
5'-most EST
                   txt700734315.h1
Method
                   BLASTX
NCBI GI
                   q465740
BLAST score
                   261
E value
                   7.0e-22
Match length
                   374
% identity
NCBI Description
                   HYPOTHETICAL 54.9 KD PROTEIN CO2F5.7 IN CHROMOSOME III
                   >gi_630513_pir__S44609 hypothetical protein C02F5.7 -
                   Caenorhabditis elegans >gi_289614 (L14745) homology with
                   glucose induced repressor, GRR1; putative [Caenorhabditis
                   elegans]
Seq. No.
                   6740
                   7296 2.R1040
Contig ID
5'-most EST
                   fua701037212.hl
Seq. No.
                   6741
                   7297 1.R1040
Contig ID
5'-most EST
                   LIB3030-003-Q1-B1-B10
Method
                   BLASTX
NCBI GI
                   q4538975
BLAST score
                   289
E value
                   7.0e-26
Match length
                   62
% identity
NCBI Description
                   (AL049487) putative protein [Arabidopsis thaliana]
Seq. No.
                   6742
Contig ID
                   7305 1.R1040
5'-most EST
                   LIB3139-080-P1-N1-E7
Method
                   BLASTX
NCBI GI
                   q4432839
BLAST score
                   454
E value
                   3.0e-45
Match length
                   90
% identity
                   52
NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   6743
                   7305 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy108b05b1
Method
                   BLASTN
```

q4432829

```
38
BLAST score
E value
                   6.0e-12
Match length
                   94
% identity
                   Arabidopsis thaliana chromosome II BAC T1B3 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   6744
Seq. No.
Contig ID
                   7308 1.R1040
                   LIB3049-037-Q1-E1-F1
5'-most EST
Method
                   BLASTX
                   g4235430
NCBI GI
BLAST score
                   752
E value
                   1.0e-147
Match length
                   418
% identity
                   64
NCBI Description
                   (AF098458) latex-abundant protein [Hevea brasiliensis]
                   6745
Seq. No.
                   7308 2.R1040
Contig ID
                   fde7\overline{0}0875009.h1
5'-most EST
Method
                   BLASTX
                   g4235430
NCBI GI
BLAST score
                   748
E value
                   2.0e-79
Match length
                   231
% identity
                   65
NCBI Description
                   (AF098458) latex-abundant protein [Hevea brasiliensis]
                   6746
Seq. No.
                   7315 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy200b02b1
                   BLASTX
Method
NCBI GI
                   g2827529
BLAST score
                   793
E value
                   1.0e-84
Match length
                   304
% identity
                   (AL021633) putative protein [Arabidopsis thaliana]
NCBI Description
                   6747
Seq. No.
Contig ID
                   7317 1.R1040
5'-most EST
                   LIB3049-052-Q1-E1-H5
                   6748
Seq. No.
                   7319 1.R1040
Contig ID
5'-most EST
                   hrw701057579.h1
Method
                   BLASTX
NCBI GI
                   q2244898
BLAST score
                   327
E value
                   4.0e-30
Match length
                   201
% identity
                   48
NCBI Description
                   (Z97338) strong similarity to protein phosphatase 2A
                   regulatory chain, 74K [Arabidopsis thaliana]
```

5'-most EST

```
Contig ID
                   7324 1.R1040 · ·
5'-most EST
                   LIB3106-040-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   q120663
BLAST score
                   1928
E value
                   0.0e+00
Match length
                   442
% identity
                   83
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,
                   CHLOROPLAST >gi_66027_pir__DEPMNB
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast -
                   garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate
                   dehydrogenase B subunit [Pisum sativum]
Seq. No.
                   6750
                   7324 2.R1040
Contig ID
                   jC-gmle01810045f02d1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q20732
BLAST score
                   232
                   1.0e-127
E value
Match length
                   432
% identity
NCBI Description
                   Pea chloroplast GAPB mRNA encoding
                  glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit B
                   (EC 1.2.1.13)
                   6751
Seq. No.
Contig ID
                  7324 3.R1040
5'-most EST
                  LIB3106-059-Q1-K1-E4
Method
                  BLASTN
NCBI GI
                  q20732
BLAST score
                  146
E value
                   3.0e-76
Match length
                   374
% identity
                  85
NCBI Description
                  Pea chloroplast GAPB mRNA encoding
                  qlyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit B
                   (EC 1.2.1.13)
Seq. No.
                  6752
Contig ID
                  7324 5.R1040
5'-most EST
                  kmv700739659.h1
Method
                  BLASTN
NCBI GI
                  q20732
BLAST score
                  37
E value
                  2.0e-11
Match length
                  89
% identity
NCBI Description
                  Pea chloroplast GAPB mRNA encoding
                  glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit B
                  (EC 1.2.1.13)
Seq. No.
                  6753
                  7324 6.R1040
Contig ID
```

 $zhf7\overline{0}0961332.h1$

```
Method
                  BLASTX
NCBI GI
                  g2213610
BLAST score
                   146
E value
                   1.0e-09
Match length
                   47
                   32
% identity
NCBI Description
                   (AC000103) F21J9.4 [Arabidopsis thaliana]
Seq. No.
                   6754
                   7324 7.R1040
Contig ID
5'-most EST
                   zhf700961396.h1
                  BLASTN
Method
NCBI GI
                  q20732
BLAST score
                   43
E value
                   4.0e-15
Match length
                   63
                   92
% identity
                  Pea chloroplast GAPB mRNA encoding
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit B
                   (EC 1.2.1.13)
                   6755
Seq. No.
Contig ID
                   7326 1.R1040
5'-most EST
                  LIB3039-015-Q1-E1-E2
Method
                  BLASTX
                  g4218120
NCBI GI
BLAST score
                   739
                   2.0e-99
E value
                  260
Match length
                   72
% identity
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                   thaliana]
                   6756
Seq. No.
Contig ID
                   7327 1.R1040
5'-most EST
                  LIB3092-007-Q1-K1-D7
                   6757
Seq. No.
Contig ID
                   7331 1.R1040
5'-most EST
                   iex700904224.hl
Method
                  BLASTX
NCBI GI
                   q2505940
BLAST score
                  551
E value
                   1.0e-56
Match length
                  130
% identity
NCBI Description
                  (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]
Seq. No.
                   6758
                   7331 2.R1040
Contig ID
5'-most EST
                  LIB3087-012-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2505940
BLAST score
                  387
                  2.0e-37
E value
Match length
                  103
% identity
                  77
```

NCBI GI

```
NCBI Description (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]
Seq. No.
                   6759
Contig ID
                   7336 1.R1040
5'-most EST
                   zhf700956360.hl
Method
                   BLASTX
                   g2828292
NCBI GI
BLAST score
                   1556
E value
                   1.0e-174
Match length
                   404
% identity
                   71
NCBI Description
                   (AL021687) neoxanthin cleavage enzyme-like protein.
                   [Arabidopsis thaliana]
Seq. No.
                   6760
Contig ID
                   7342 1.R1040
                   LIB3056-013-Q1-N1-F6
5'-most EST
Method
                   BLASTX
                   g2500715
NCBI GI
BLAST score
                   526
                   1.0e-53
E value
Match length
                   105
% identity
                   83
NCBI Description
                   PATHOGENESIS-RELATED PROTEIN PR-1 PRECURSOR
                   >gi_629627_pir__S47171 gene PR-1 protein - barrel medic
                   >gi_505553_emb_CAA56174_ (X79778) PR-1 [Medicago
                   truncatula]
                   6761
Seq. No.
                   7343 1.R1040
Contig ID
5'-most EST
                   LIB3039-045-Q1-E1-D3
                   6762
Seq. No.
                   7348 1.R1040
Contig ID
5'-most EST
                   gsf700698427.hl
Seq. No.
                   6763
                   7351 1.R1040
Contig ID
                   pxt7\overline{0}0942441.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3702102
BLAST score
                   259
E value
                   4.0e-30
Match length
                   134
% identity
NCBI Description
                   (AL031765) 1-evidence=predicted by match;
                   1-match_accession=SPTREMBL:Q14105;
                   1-match_description=D1075-LIKE GENE (FRAGMENT).;
                   1-match_species=HOMO SAPIENS (HUMAN).;
                   1-method=blastx;1.4.9; 1-method_score=101.00; 56.00;
                   180.00; 2
                   6764
Seq. No.
                   7355 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy032b07b1
Method
                   BLASTN
```

q4220637

Match length

```
BLAST score
                   54
                   5.0e-21
E value
Match length
                   390
% identity
                   83
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MIE1, complete sequence [Arabidopsis thaliana]
Seq. No.
Contig ID
                   7355 2.R1040
5'-most EST
                   ncj7\overline{0}0980967.h1
                   6766
Seq. No.
Contig ID
                   7356 1.R1040
5'-most EST
                   gsv701044894.hl
Method
                   BLASTX
NCBI GI
                   q3695388
BLAST score
                   185
E value
                   2.0e-13
Match length
                   42
% identity
                   69
                   (AF096371) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6767
Contig ID
                   7356 2.R1040
5'-most EST
                   jex700907890.h1
                   6768
Seq. No.
                   7358 1.R1040
Contig ID
5'-most EST
                   pxt700944366.h1
Seq. No.
                   6769
                   7361 1.R1040
Contig ID
5'-most EST
                   leu701148420.h1
                   6770
Seq. No.
Contig ID
                   7362 1.R1040
5'-most EST
                   jex700909523.hl
Method
                   BLASTN
NCBI GI
                   q758249
BLAST score
                   427
E value
                   0.0e + 00
Match length
                   543
% identity
                   95
NCBI Description
                   P.vulgaris mRNA for plasma membrane H+ ATPase
                   6771
Seq. No.
Contig ID
                   7364 1.R1040
5'-most EST
                   LIB3138-128-Q1-N1-A2
Seq. No.
                   6772
                   7366 1.R1040
Contig ID
5'-most EST
                   LIB3030-002-Q1-B1-B9
Method
                   BLASTX
NCBI GI
                   g2444178
BLAST score
                   509
E value
                   1.0e-51
```

```
% identity
                   (U94784) unconventional myosin [Helianthus annuus]
NCBI Description
Seq. No.
                  7369 1.R1040
Contig ID
5'-most EST
                  LIB3106-054-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2961346
BLAST score
                  387
E value
                   2.0e-37
Match length
                   96
                  70
% identity
NCBI Description
                   (AL022140) pectinesterase like protein [Arabidopsis
                  thaliana]
                   6774
Seq. No.
                  7370 1.R1040
Contig ID
5'-most EST
                   trc700566871.h1
                  BLASTX
Method
NCBI GI
                  q173419
BLAST score
                  253
                   2.0e-36
E value
Match length
                   118
% identity
                   67
                   (L11574) p68 RNA helicase [Schizosaccharomyces pombe]
NCBI Description
                  >gi 3810840 emb CAA21801 (AL032684) p68-like protein.
                   [Schizosaccharomyces pombe]
                   6775
Seq. No.
                   7376 1.R1040
Contig ID
5'-most EST
                  LIB3030-001-Q1-B1-H4
Method
                  BLASTX
NCBI GI
                  q2459438
BLAST score
                  248
                   5.0e-21
E value
Match length
                  133
% identity
                   51
NCBI Description
                   (AC002332) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  7377 1.R1040
5'-most EST
                  LIB3030-001-Q1-B1-H5
Seq. No.
Contig ID
                  7378 1.R1040
5'-most EST
                  LIB3092-044-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2257756
BLAST score
                   450
E value
                   3.0e-44
Match length
                   302
                  39
% identity
                   (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
NCBI Description
                  >gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea
                  mays]
```

```
7378 2.R1040
Contig ID
5'-most EST
                   LIB3052-001-Q1-B1-H2
Method
                   BLASTX
                   g2257756
NCBI GI
BLAST score
                   238
E value
                   1.0e-19
Match length
                   101
                   58
% identity
NCBI Description
                   (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
                   >gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea
                   mays]
                   6779
Seq. No.
                   7378_3.R1040
Contig ID
5'-most EST
                   uC-gmropic115a01b1
Method .
                   BLASTX
                   g2257756
NCBI GI
BLAST score
                   295
E value
                   3.0e-26
Match length
                   242
% identity
                   35
NCBI Description
                   (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
                   >gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea
                   mays]
                   6780
Seq. No.
Contig ID
                   7379 1.R1040
                   LIB3030-001-Q1-B1-H7
5'-most EST
                   6781
Seq. No.
Contig ID
                   7380 1.R1040
5'-most EST
                   jC-gmle01810084e03a1
Seq. No.
                   6782
                   7380 2.R1040
Contig ID
5'-most EST
                   zhf700963876.h1
Seq. No.
                   6783
                   7380 3.R1040
Contig ID
5'-most EST
                   epx7\overline{0}1105982.h1
Seq. No.
                   6784
                   7384 1.R1040
Contig ID
5'-most EST
                   sat7\overline{0}1004583.h1
Method
                   BLASTX
NCBI GI
                   q1170508
BLAST score
                   2019
E value
                   0.0e + 00
Match length
                   413
% identity
NCBI Description
                   EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)
                   >gi_2119931_pir__S60244 translation initiation factor
                   eIF-4A.8, anther-specific - common tobacco
                   >gi_475219_emb_CAA55639_ (X79004) translation initiation
                   factor (eIF-4A) [Nicotiana tabacum]
                   >gi_475221_emb_CAA55640_ (X79005) translation initiation
```

factor (eIF-4A) [Nicotiana tabacum]

```
6785
Seq. No.
                   7384_3.R1040
Contig ID
5'-most EST
                  LIB3106-106-Q1-K1-G7
Method
                  BLASTX
                   g1170503
NCBI GI
BLAST score
                   608
E value
                   4.0e-63
Match length
                  122
% identity
NCBI Description
                  EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
                   >gi_322503_pir__JC1452 translation initiation factor
                   eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188
                   (X65052) eukaryotic translation initiation factor 4A-1
                   [Arabidopsis thaliana]
                   6786
Seq. No.
                   7384 4.R1040
Contig ID
                   trc700561210.hl
5'-most EST
                   6787
Seq. No.
                   7384_5.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy043d12b1
                   BLASTX
Method
                   g2500521
NCBI GI
BLAST score
                   584
E value
                   2.0e-60
Match length
                   120
                   93
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-15 (EIF-4A-15)
NCBI Description
                   >gi 485945 emb CAA55739 (X79138) NeIF-4A15 [Nicotiana
                   tabacum]
                   6788
Seq. No.
Contig ID
                   7384 6.R1040
5'-most EST
                   LIB3039-022-Q1-E1-H6
Method
                   BLASTN
NCBI GI
                   g485986
                   108
BLAST score
                   1.0e-53
E value
                   224
Match length
                   87
% identity
NCBI Description
                  N.tabacum NeIF-4A11 mRNA
                   6789
Seq. No.
                   7384 8.R1040
Contig ID
5'-most EST
                   fde700876750.hl
Method
                   BLASTN
NCBI GI
                   g485944
BLAST score
                   69
                   2.0e-30
E value
Match length .
                   157
% identity
                   86
NCBI Description
                  N.tabacum NeIF-4A15 mRNA
                   6790
Seq. No.
```

7385_1.R1040

Contig ID

5'-most EST

```
5'-most EST
                   LIB3030-002-Q1-B1-A2
Method
                   BLASTX
                   q1935021
NCBI GI
BLAST score
                   535
                   1.0e-54
E value
                   145
Match length
% identity
                   64
                   (Z93775) monosaccharid transport protein [Vicia faba]
NCBI Description
Seq. No.
                   6791
Contig ID
                   7390 1.R1040
                   yza700764039.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2245131
BLAST score
                   499
                   6.0e-50
E value
Match length
                   255
                   45
% identity
NCBI Description
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   6792
                   7391 1.R1040
Contig ID
5'-most EST
                   LIB3087-002-Q1-K1-C6
Method
                   BLASTX
NCBI GI
                   q3402701
BLAST score
                   182
E value
                   4.0e-13
Match length
                   75
                   56
% identity
                   (AC004261) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6793
                   7393_1.R1040
Contig ID
                   uC-gmflminsoy063d12b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3047083
BLAST score
                   795
                   7.0e-85
E value
                   199
Match length
% identity
                   (AF058914) similar to FLAP endonuclease-1 (SW:P39748)
NCBI Description
                   [Arabidopsis thaliana]
                   6794
Seq. No.
                   7393 2.R1040
Contig ID
5'-most EST
                   vwf700674123.h1
Method
                   BLASTX
NCBI GI
                   q4454052
BLAST score
                   163
E value
                   8.0e-11
Match length
                   200
% identity
                   (AL035394) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   6795
Seq. No.
                   7396 1.R1040
Contig ID
```

kl1701213446.hl

Method

BLASTN

```
6796
Seq. No.
Contig ID
                  .7397 1.R1040
5'-most EST
                  LIB3030-001-Q1-B1-G12
Method
                  BLASTX
                  g2129740
NCBI GI
BLAST score
                  300
E value
                  8.0e-27
Match length
                  105
% identity
                  59
NCBI Description
                  small nuclear ribonucleoprotein - Arabidopsis thaliana
                  >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis
                  thaliana >gi_1255711 (M93439) small nuclear
                  ribonucleoprotein [Arabidopsis thaliana] >gi 1354469
                   (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]
Seq. No.
                  6797
                  7397 2.R1040
Contig ID
5'-most EST
                  jC-gmro02910048h03a1
Method
                  BLASTX
                  g2129740
NCBI GI
BLAST score
                  388
E value
                  6.0e-38
Match length
                  88
% identity
                  81
NCBI Description
                  small nuclear ribonucleoprotein - Arabidopsis thaliana
                  >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis
                  thaliana >gi 1255711 (M93439) small nuclear
                  ribonucleoprotein [Arabidopsis thaliana] >gi_1354469
                   (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]
Seq. No.
                  6798
Contig ID
                  7398 1.R1040
                  fC-gmro7000748475f1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3820531
BLAST score
                  592
                  3.0e-61
E value
                  169
Match length
% identity
                   (AF072736) beta-glucosidase [Pinus contorta]
NCBI Description
                  6799
Seq. No.
                  7401 1.R1040
Contig ID
5'-most EST
                  epx7\overline{0}1106660.h1
                  BLASTX
Method
NCBI GI
                  q1946359
BLAST score
                  361
E value
                  2.0e-34
Match length
                  89
% identity
                  73
NCBI Description
                  (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  7403 1.R1040
                  hrw701060631.h1
5'-most EST
```

Contig ID

6806

7409 2.R1040

```
q2274858
NCBI GI
BLAST score
                   113
E value
                   2.0e-56
Match length
                   233
% identity
                  87
NCBI Description
                  Arabidopsis thaliana mRNA for Cks1/Suc1 protein homologue
Seq. No.
Contig ID
                  7404 1.R1040
5'-most EST
                  ncj700987926.h1
Seq. No.
                   6802
                  7406 1.R1040
Contig ID
5'-most EST
                   trc700565644.h1
Method
                  BLASTX
NCBI GI
                  q3004547
BLAST score
                  795
E value
                   1.0e-84
Match length
                   210
% identity
                   (AC003673) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4185150 (AC005724) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                   6803
Contig ID
                  7408 1.R1040
5'-most EST
                  uC-qmrominsoy071d11b1
Method
                  BLASTX
NCBI GI
                  q1894771
BLAST score
                   434
E value
                   3.0e-42
Match length
                   326
                   32
% identity
NCBI Description
                   (Z92954) product highly similar to metabolite transport
                  proteins [Bacillus subtilis] >gi_2636109_emb_CAB15600.1
                   (Z99122) similar to metabolite transport protein [Bacillus
                  subtilis]
Seq. No.
                   6804
                  7408 2.R1040
Contig ID
5'-most EST
                  LIB3109-043-Q1-K1-F4
Seq. No.
                   6805
Contig ID
                  7409 1.R1040
5'-most EST
                  LIB3139-072-P1-N1-F12
Method
                  BLASTX
NCBI GI
                  g729668
BLAST score
                  397
E value
                  3.0e-38
Match length
                  140
% identity
                  59
NCBI Description
                  HISTONE H1 >gi 2147479 pir S65059 histone H1,
                  drought-inducible - Lycopersicon pennellii >qi 436823
                   (U01890) Solanum pennellii histone H1 [Solanum pennellii]
```

5'-most EST

```
5'-most EST
                   LIB3170-067-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                   q729668
BLAST score
                   348
E value
                   2.0e-32
Match length
                   136
% identity
                   56
NCBI Description
                   HISTONE H1 >gi 2147479 pir S65059 histone H1,
                   drought-inducible - Lycopersicon pennellii >gi 436823
                   (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.
Contig ID
                   7410 1.R1040
5'-most EST
                   LIB3106-062-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   g2642158
BLAST score
                   324
E value
                   1.0e-52
Match length
                   136
% identity
                   71
NCBI Description
                   (AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   6808
Contig ID
                   7410 2.R1040
5'-most EST
                   uaw7\overline{0}0663338.h1
                   6809
Seq. No.
                   7411 1.R1040
Contig ID
5'-most EST
                   LIB3030-001-Q1-B1-E12
                   BLASTX
Method
NCBI GI
                   q2924509
BLAST score
                   666
E value
                   9.0e-70
Match length
                  229
                   54
% identity
NCBI Description
                   (AL022023) subtilisin proteinase - like [Arabidopsis
                   thaliana]
                   6810
Seq. No.
                   7412 1.R1040
Contig ID
5'-most EST
                   vwf700676026.hl
Seq. No.
                   6811
Contig ID
                   7413 1.R1040
5'-most EST
                   LIB3030-001-Q1-B1-E3
Method
                   BLASTX
NCBI GI
                   q3738339
BLAST score
                   314
E value
                   2.0e-28
Match length
                   123
% identity
                   54
NCBI Description
                   (AC005170) putative kinase [Arabidopsis thaliana]
Seq. No.
                   7413 2.R1040
Contig ID
```

LIB3049-006-Q1-E1-C6

Contig ID

5'-most EST

```
۵.
                   6813
Seq. No.
Contig ID
                   7414 1.R1040
5'-most EST
                   dpv701097016.hl
Method
                   BLASTX
NCBI GI
                   q1076344
BLAST score
                   156
E value
                   3.0e-10
Match length
                   111
% identity
                   42
NCBI Description
                   kinase-associated protein phosphatase precursor -
                   Arabidopsis thaliana
                   6814
Seq. No.
                   7415_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910064f09a1
                   6815
Seq. No.
Contig ID
                   7415 2.R1040
5'-most EST
                   uC-gmflminsoy097f06b1
Seq. No.
                   6816
Contig ID
                   7416_1.R1040
5'-most EST
                   LIB3093-058-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   g4138583
BLAST score
                   2250
E value
                   0.0e + 00
Match length
                   613
% identity
                   75
NCBI Description
                   (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
Seq. No.
                   6817
Contig ID
                   7416 2.R1040
5'-most EST
                   LIB3092-002-Q1-K1-H1
Method
                   BLASTX
NCBI GI
                   g4138583
BLAST score
                   346
E value
                   2.0e-32
Match length
                   103
% identity
                   71
NCBI Description
                   (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
                   6818
Seq. No.
                   7416 3.R1040
Contig ID
5'-most EST
                   LIB3051-001-Q1-E1-A12
Method
                   BLASTX
NCBI GI
                   g4138583
                   534
BLAST score
E value
                   1.0e-54
Match length
                   117
% identity
                   91
NCBI Description
                   (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
                   6819
Seq. No.
```

7418 1.R1040

 $sat7\overline{0}1009519.h1$

NCBI GI

```
6820
Seq. No.
                   7422 1.R1040
Contig ID
5'-most EST
                   LIB3051-017-Q1-E1-H2
Method
                   BLASTX
NCBI GI
                   g3075391
BLAST score
                   1716
E value
                   0.0e+00
Match length
                   596
% identity
                   59
NCBI Description
                   (AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   7422 2.R1040
5'-most EST
                   jC-qmro02910010q05a1
Seq. No.
Contig ID
                   7422 3.R1040
5'-most EST
                   jC-gmle01810073c05a1
Method
                   BLASTX
NCBI GI
                   g3075391
BLAST score
                   187
                   1.0e-13
E value
Match length
                   88
% identity
                   49
                   (AC004484) unknown protein [Arabidopsis thaliana].
NCBI Description
                   6823
Seq. No.
                   7422 4.R1040
Contig ID
5'-most EST
                   jC-gmf102220052b07a1
                   BLASTX
Method
NCBI GI
                   q3075391
BLAST score
                   552
E value
                   9.0e-57
Match length
                   147
                   75
% identity
NCBI Description
                   (AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.
                   6824
Contig ID
                   7422 7.R1040
5'-most EST
                   uC-gmropic088h02b1
Seq. No.
                   6825
                   7428 1.R1040
Contig ID
5'-most EST
                   LIB3109-005-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   g2342735
BLAST score
                   463
E value
                   4.0e-46
Match length
                   130
% identity
NCBI Description
                   (AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.
                   6826
                   7428 2.R1040
Contig ID
                   kmv7\overline{0}0738733.h1
5'-most EST
Method
                   BLASTX
```

g2342735

```
BLAST score
                   227
E value
                   9.0e-19
Match length
                   57
% identity
                   81
                   (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                   6827
Seq. No.
                   7430 1.R1040
Contig ID
5'-most EST
                   jex7\overline{0}0904532.h1
                   6828
Seq. No.
                   7433_1.R1040
Contig ID
5'-most EST
                   g4290321
                   6829
Seq. No.
Contig ID
                   7442 1.R1040
                   LIB3\overline{0}40-040-Q1-E1-B3
5'-most EST
Method
                   BLASTX
                   g2135841
NCBI GI
BLAST score
                   184
                   7.0e-13
E value
                   78
Match length
                   46
% identity
NCBI Description
                   nucleic acid-binding protein E5.1 - human >gi_598231
                   (L37368) RNA-binding protein [Homo sapiens]
                   6830
Seq. No.
                   7448 1.R1040
Contig ID
5'-most EST
                   LIB3030-001-Q1-B1-B5
Method
                   BLASTX
NCBI GI
                   g3915022
BLAST score
                   768
E value
                   5.0e-82
Match length
                   178
                   83
% identity
NCBI Description
                   SUCROSE-PHOSPHATE SYNTHASE 2
                   (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 2)
                   >gi_2190350_emb_CAA72491_ (Y11795) sucrose-phosphate
                   synthase [Craterostigma plantagineum]
                   6831
Seq. No.
Contig ID
                   7449 1.R1040
5'-most EST
                   g5606523
                   6832
Seq. No.
                   7450 1.R1040
Contig ID
5'-most EST
                   LIB3\overline{1}06-101-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   g3915665
BLAST score
                   236
E value
                   3.0e-27
Match length
                   143
% identity
NCBI Description
                   ELONGATION FACTOR G (EF-G) >gi 2688449 (AE001155)
```

burgdorferi]

translation elongation factor G (fus-1) [Borrelia

Match length

```
6833
  Seq. No.
                      7456 1.R1040
  Contig ID
  5'-most EST
                      uxk700667188.hl
  Method
                      BLASTX
  NCBI GI
                      g4490733
  BLAST score
                      574
  E value
                      5.0e-59
  Match length
                      249
  % identity
                      49
  NCBI Description
                      (AL035709) putative protein [Arabidopsis thaliana]
  Seq. No.
                      7458 1.R1040
  Contig ID
  5'-most EST
                      zsg701119169.hl
  Seq. No.
                      7459 1.R1040
  Contig ID
  5'-most EST
                      jC-gmf102220079b07a1
  Seq. No.
                      7465 1.R1040
  Contig ID
                      fde7\overline{0}0875880.h1
  5'-most EST
  Method
                      BLASTX
                      q1169586
  NCBI GI
                      582
  BLAST score
  E value
                      4.0e-60
                      127
  Match length
  % identity
                      FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
  NCBI Description
                      (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                      (CY-F1) >gi_542079_pir__S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi_440591_emb_CAA54265_ (X76946)
                      fructose-1,6-bisphosphatase [Solanum tuberosum]
  Seq. No.
                      6837
  Contig ID
                      7465 2.R1040
  5'-most EST
                      LIB3106-095-Q1-K1-H11
                      BLASTX
- Method
  NCBI GI
                      q1169586
  BLAST score
                      273
  E value
                      4.0e-24
  Match length
                      57
  % identity
  NCBI Description
                      FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
                       (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                      (CY-F1) >gi_542079_pir__S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi_440591_emb_CAA54265_ (X76946)
                      fructose-1,6-bisphosphatase [Solanum tuberosum]
  Seq. No.
                      6838
                      7466 1.R1040
  Contig ID
  5'-most EST
                      smc700747854.hl
  Method
                      BLASTX
                      g3107931
  NCBI GI
  BLAST score
                      1876
                      0.0e + 00
  E value
```

```
% identity
                   (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
NCBI Description
Seq. No.
                   6839
                   7466 2.R1040
Contig ID
                   pmv700893276.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                   q3107930
BLAST score
                  99
E value
                   4.0e-48
Match length
                   316
% identity
                   83
NCBI Description
                  Pyrus pyrifolia mRNA for UDP-glucose pyrophosphorylase,
                   complete cds
Seq. No.
                   6840
                   7466 3.R1040
Contig ID
5'-most EST
                   jC-gmst02400062h08d1
Method
                   BLASTX
NCBI GI
                   q136739
BLAST score
                   232
E value
                   3.0e-19
Match length
                  59
% identity
NCBI Description
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
                   PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir_XNPOU
                   UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                   potato >gi 218001 dbj_BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                   6841
                   7466 5.R1040
Contig ID
5'-most EST
                   pxt700946288.h1
Method
                  BLASTX
NCBI GI
                   q3107931
BLAST score
                   175
E value
                   1.0e-12
Match length
                   43
% identity
                   72
NCBI Description
                   (AB013353) UDP-qlucose pyrophosphorylase [Pyrus pyrifolia]
Seq. No.
                   6842
                   7466 9.R1040
Contig ID
5'-most EST
                   ncj700981983.hl
Method
                  BLASTX
NCBI GI
                   g136739
BLAST score
                   123
E value
                   3.0e-14
                  55
Match length
% identity
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                   PYROPHOSPHORYLASE) (UDPGP) >qi 67061 pir XNPOU
                   UTP--glucose-1-phosphate uridy\overline{l}yltransfe\overline{rase} (EC 2.7.7.9) -
                  potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
```

```
7467 1.R1040
 Contig ID
                     leu7\overline{0}1153852.h1
  5'-most EST
                     BLASTX
 Method
                     g461498
 NCBI GI
 BLAST score
                     1244
                     1.0e-137
 E value
 Match length
                     293
  % identity
                     80
                     ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
 NCBI Description
                     TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                     (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC
                     2.6.1.2) - proso millet >gi 296204 emb CAA49199 (X69421)
                     alanine aminotransferase [Panicum miliaceum]
                     6844
  Seq. No.
                     7467 4.R1040
  Contig ID
                     kmv7\overline{0}0740452.h1
  5'-most EST
                     BLASTX
 Method
 NCBI GI
                     q461498
 BLAST score
                     184
                     8.0e-14
 E value
 Match length
                     47
                     72
  % identity
                     ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
 NCBI Description
                     TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                     (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421)
                     alanine aminotransferase [Panicum miliaceum]
, Seq. No.
                     6845
                     7470 1.R1040
  Contig ID
                     LIB3030-005-Q1-B1-E5
  5'-most EST
 Method
                     BLASTX
 NCBI GI
                     q3914940
 .BLAST score
                     1579
 E value
                     1.0e-176
 Match length
                     378
  % identity
                     SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
 NCBI Description
                      (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                     >gi 2529376 (L76556) sedoheptulose-1,7-bisphosphatase
                     [Spinacia oleracea]
  Seq. No.
                     6846
                     7470 2.R1040
  Contig ID
                     LIB3092-013-Q1-K1-D11
  5'-most EST
  Seq. No.
                     6847
                     7474 1.R1040
  Contig ID
                     fua701041768.hl
  5'-most EST
 Method
                     BLASTX
                     g2492952
 NCBI GI
  BLAST score
                     1304
  E value
                     1.0e-144
 Match length
                     312
                     78
  % identity
```

NCBI Description CHORISMATE SYNTHASE 1 PRECURSOR

Contig ID

Šŝ.

6853

7479 1.R1040

```
precursor - tomato >gi_410482_emb_CAA79859_ (Z21796) chorismate synthase 1 [Lycopersicon esculentum]
Seq. No.
                    6848
                    7477 1.R1040
Contig ID
5'-most EST
                    jC-qmf102220131g06a1
Method
                    BLASTX
NCBI GI
                    g1871192 .
BLAST score
                    1127
E value
                    1.0e-147
Match length
                    485
% identity
                    (U90439) Cys3His zinc finger protein isolog [Arabidopsis
NCBI Description
                    thaliana]
                    6849
Seq. No.
Contig ID
                    7478 1.R1040
5'-most EST
                    LIB3139-045-P1-N1-B6
Method
                    BLASTX
NCBI GI
                    q1763063
BLAST score
                    328
E value
                    4.0e-30
Match length
                    178
% identity
                    43
                    (U68763) SCOF-1 [Glycine max]
NCBI Description
                    6850
Seq. No.
                    7478 2.R1040
Contig ID
5'-most EST
                    LIB3092-049-Q1-K1-G5
                    BLASTX
Method
NCBI GI
                    q1763063
BLAST score
                    272
E value
                    8.0e-24
Match length
                    112
% identity
                    58
NCBI Description
                    (U68763) SCOF-1 [Glycine max]
                    6851
Seq. No.
Contig ID
                    7478 3.R1040
5'-most EST
                    LIB3107-036-Q1-K1-B11
Method.
                    BLASTX
NCBI GI
                    g439489
BLAST score
                    219
E value
                    9.0e-18
Match length
                    113
% identity
                    35
                    (D26084) zinc-finger DNA binding protein [Petunia x
NCBI Description
                    hybrida]
Seq. No.
                    6852
                    7478 4.R1040
Contig ID
5'-most EST
                    LIB3050-022-Q1-K1-F11
```

(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)

>gi_542026_pir__\$40410 chorismate synthase (EC 4.6.1.4) 1

% identity

```
5'-most EST
                   uC-qmrominsoy040h09b1
Method
                   BLASTX
NCBI GI
                   q100226
BLAST score
                   332
E value
                    6.0e-31
Match length
                   143
% identity
                   51
NCBI Description
                   hypothetical protein - tomato >gi 19275 emb CAA78112_
                    (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi_445619_prf__1909366A Leu zipper protein
                    [Lycopersicon esculentum]
Seq. No.
                   6854
Contig ID
                   7481 1.R1040
5'-most EST
                   zsq701127164.h1
Method
                   BLASTX
NCBI GI
                   q4433048
BLAST score
                   635
E value
                   9.0e-66
Match length
                   146
% identity
NCBI Description
                    (D26578) DNA-binding protein [Daucus carota]
Seq. No.
                   6855
                   7481 2.R1040
Contig ID
5'-most EST
                   LIB3065-014-Q1-N1-F3
Method
                   BLASTX
NCBI GI
                   a1168547
BLAST score
                   176
E value
                   3.0e-12
Match length
                   188
                   33
% identity
NCBI Description
                   HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-6 (HD-ZIP PROTEIN
                   ATHB-6) >gi_629505_pir__S47136 homeotic protein Athb-6 - Arabidopsis thaliana >gi_499162_emb_CAA47427_ (X67034)
                   Athb-6 [Arabidopsis thaliana]
Seq. No.
                   6856
Contig ID
                   7481 3.R1040
5'-most EST
                   LIB3050-023-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   g4433048
BLAST score
                   274
E value
                   6.0e-24
Match length
                   68
% identity
NCBI Description
                   (D26578) DNA-binding protein [Daucus carota]
Seq. No.
                   6857
                   7483 1.R1040
Contig ID
5'-most EST
                   sat701010763.hl
Method
                   BLASTN
NCBI GI
                   q2318116
BLAST score
                   392
                   0.0e+00
E value
Match length
                   675
```

```
Pisum sativum Mq-chelatase subunit D (ChlD) mRNA, complete
NCBI Description
                   cds
                   6858
Seq. No.
                   7491 1.R1040
Contig ID
                   LIB3030-001-Q1-B1-H10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4468990
BLAST score
                   496
E value
                   7.0e-50
Match length
                   245
% identity
                   45
                   (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6859
Contig ID
                   7492 1.R1040
5'-most EST
                   LIB3030-002-Q1-B1-B3
Method
                   BLASTX
NCBI GI
                   q2688830
BLAST score
                   180
E value
                   5.0e-13
Match length
                   52
% identity
NCBI Description
                   (AF000952) putative sugar transporter [Prunus armeniaca]
Seq. No.
                   6860
Contig ID
                   7497 1.R1040
5'-most EST
                  LIB3030-003-Q1-B1-G3
Method
                  BLASTX
NCBI GI
                   g1213629
BLAST score
                   367
E value
                   5.0e-35
Match length
                  113
% identity
                   60
NCBI Description
                  (X95991) pectinesterase [Prunus persica]
Seq. No.
                   6861
                   7497 2.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy041b10b1
Method
                  BLASTX
NCBI GI
                   g1213629
BLAST score
                  164
                   2.0e-11
E value
Match length
                  82
                   39
% identity
NCBI Description
                   (X95991) pectinesterase [Prunus persica]
Seq. No.
                   7499 1.R1040
Contig ID
                  bth700846254.h1
5'-most EST
Seq. No.
                   6863
                   7500 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220073a09d1
                   6864
Seq. No.
```

7501_1.R1040

Contig ID

5'-most EST

```
5'-most EST
                   q5753413
Method
                   BLASTX
NCBI GI
                   q2129564
BLAST score
                   2107
E value
                   0.0e+00
Match length
                   585
                   68
% identity
NCBI Description
                   cryptochrome 2 apoprotein - Arabidopsis thaliana
Seq. No.
                   7501 2.R1040
Contig ID
5'-most EST
                   LIB3094-102-Q1-K1-H6
Method
                   BLASTX
NCBI GI
                   q730324
BLAST score
                   276
E value
                   2.0e-24
Match length
                   55
% identity
                   DEOXYRIBODIPYRIMIDINE PHOTOLYASE (DNA PHOTOLYASE)
NCBI Description
                   (PHOTOREACTIVATING ENZYME) >gi_1084356_pir__S48120
                   deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - white
                   mustard >gi_414196_emb_CAA50898_ (X72019) photolyase
                   [Sinapis alba]
                   6866
Seq. No.
                   7501 3.R1040
Contig ID
5'-most EST
                   jC-qmle01810030c10a2
                   BLASTX
Method
NCBI GI
                   g730324
BLAST score
                   161
E value
                   1.0e-10
Match length
                   37
                   70
% identity
NCBI Description
                   DEOXYRIBODIPYRIMIDINE PHOTOLYASE (DNA PHOTOLYASE)
                   (PHOTOREACTIVATING ENZYME) >gi_1084356_pir__S48120
                   deoxyribodipyrimidine photo-lyase (EC \overline{4}.1.\overline{99}.3) - white
                   mustard >gi 414196 emb CAA50898 (X72019) photolyase
                   [Sinapis alba]
Seq. No.
                   6867
Contig ID
                   7501 4.R1040
5'-most EST
                   LIB3030-004-Q1-B1-B2
Method
                   BLASTX
NCBI GI
                   g2129564
BLAST score
                   219
E value
                   2.0e-17
Match length
                   170
% identity
                   39
NCBI Description
                   cryptochrome 2 apoprotein - Arabidopsis thaliana
                   6868
Seq. No.
                   7501 5.R1040
Contig ID
                   k11701203603.h2
5'-most EST
                   6869
Seq. No.
                   7502 1.R1040
Contig ID
```

jC-gmro02800040g05d1

```
6870
Seq. No.
Contig ID
                   7504 1.R1040
5'-most EST
                   LIB3030-004-Q1-B1-G3
Method
                   BLASTX
NCBI GI
                   g2769566
BLAST score
                   494
E value
                   1.0e-49
Match length
                   156
% identity
                   (Y10477) chloroplast thylakoidal processing peptidase
NCBI Description
                   [Arabidopsis thaliana]
                   6871
Seq. No.
Contig ID
                   7506 1.R1040
5'-most EST
                   uC-gmronoir038a04b1
Method
                   BLASTX
                   g3819710
NCBI GI
BLAST score
                   265
E value
                   6.0e-23
Match length
                   60
% identity
NCBI Description
                   (AJ224161) delta-8 sphingolipid desaturase [Arabidopsis
                   thaliana]
Seq. No.
                   6872
                   7506 4.R1040
Contig ID
5'-most EST
                   zzp700834013.hl
Method
                   BLASTX
NCBI GI
                   g3702328
BLAST score
                   309
E value
                   2.0e-28
                   70
Match length
% identity
NCBI Description
                   (AC005397) putative cytochrome b5 [Arabidopsis thaliana]
Seq. No.
                   6873
                   7508 1.R1040
Contig ID
5'-most EST
                   LIB3138-042-Q1-N1-A5
Seq. No.
                   6874
                   7508 2.R1040
Contig ID
5'-most EST
                   zzp700833303.hl
Method
                   BLASTN
NCBI GI
                   g1750375
BLAST score
                   65
E value
                   8.0e-28
Match length
                   161
% identity
                   85
                   Arabidopsis thaliana ubiquitin activating enzyme (UBA1)
NCBI Description
                   gene, complete cds
                   6875
Seq. No.
                   7511 1.R1040
Contig ID
5'-most EST
                   k117\overline{0}1212848.h1
```

A 1786

```
7514 1.R1040
Contig ID
5'-most EST
                    jC-gmro02910061a04a1
                   BLASTX
Method
NCBI GI
                   g4314365
                   191
BLAST score
                   3.0e-14
E value
Match length
                   142
% identity
                    39
                    (AC006340) putative copia-like retrotransposon Hopscotch
NCBI Description
                    [Arabidopsis thaliana]
                    6877
Seq. No.
                   7516 1.R1040
Contig ID
5'-most EST
                   LIB3030-007-Q1-B1-A9
Method
                   BLASTX
NCBI GI
                   q4337175
BLAST score
                   501
                   2.0e-50
E value
Match length
                   161
                    60
% identity
                    (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
NCBI Description
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                   gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                    6878
                   7518 1.R1040
Contig ID
                   LIB3051-026-Q1-K1-F9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2689720
BLAST score
                   249
                    3.0e-21
E value
                   83
Match length
% identity
NCBI Description
                    (AF037168) DnaJ homologue [Arabidopsis thaliana]
                    6879
Seq. No.
                   7519 1.R1040
Contig ID
5'-most EST
                   LIB3030-007-Q1-B1-G4
Seq. No.
                   6880
                   7520 1.R1040
Contig ID
                   LIB3106-112-Q1-K1-C7
5'-most EST
                   6881
Seq. No.
                   7522 1.R1040
Contig ID
5'-most EST
                   LIB3030-008-Q1-B1-A9
                   6882
Seq. No.
                   7523 1.R1040
Contig ID
5'-most EST
                   LIB3030-008-Q1-B1-B4
                   6883
Seq. No.
                   7525 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400055g12d1
                    6884
Seq. No.
```

BLAST score

```
7527 1.R1040
Contig ID
5'-most EST
                   LIB3030-008-Q1-B1-G2
Method
                   BLASTX
NCBI GI
                   g3757523
BLAST score
                   894
E value
                   1.0e-96
Match length
                   225
 % identity
                   75
NCBI Description
                   (AC005167) putative transportin [Arabidopsis thaliana]
Seq. No.
                   6885
Contig ID
                   7530 1.R1040
 5'-most EST
                   uC-gmropic096d09b1
Method
                   BLASTX
NCBI GI
                   a3033374
BLAST score
                   192
E value
                   1.0e-14
Match length
                   137
 % identity
                   39
NCBI Description
                   (AC004238) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   7532 1.R1040
5'-most EST
                   uC-gmronoir044e01b1
Seq. No.
Contig ID
                   7532 2.R1040
5'-most EST
                   uC-qmflminsoy032g03b1
                   6888
Seq. No.
Contig ID
                   7535 1.R1040
5'-most EST
                   fC-gmst700664572d3
Method
                   BLASTX
NCBI GI
                   g3925363
BLAST score
                   1011
E value
                   1.0e-110
Match length
                   267
% identity
NCBI Description
                   (AF067961) homeodomain protein [Malus domestica]
Seq. No.
                   6889
Contig ID
                   7535 2.R1040
 5'-most EST
                   fC-gmst700664572d5
Method
                   BLASTX
NCBI GI
                   q3925363
BLAST score
                   670
E value
                   3.0e-70
Match length
                   161
% identity
NCBI Description
                   (AF067961) homeodomain protein [Malus domestica]
Seq. No.
                   7536 1.R1040
Contig ID
                   LIB3030-009-Q1-B1-C10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3047124
```

Contig ID

```
2.0e-14
E value
Match length
                   62
% identity
                   55
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7538 1.R1040
Contig ID
5'-most EST
                   fC-gmro700797913a1
Method
                   BLASTX
NCBI GI
                   g2627181
BLAST score
                   682
E value
                   6.0e-72
Match length
                   153
% identity
                   80
                   (D89619) cycloartenol synthase [Pisum sativum]
NCBI Description
Seq. No.
                   6892
Contig ID
                   7540 1.R1040
5'-most EST
                   epx701107112.h1
Method
                   BLASTX
NCBI GI
                   q4454471
BLAST score
                   685
E value
                   8.0e-72
Match length
                   315
% identity
NCBI Description
                   (AC006234) putative G protein coupled receptor [Arabidopsis
                   thaliana]
Seq. No.
                   6893
Contig ID
                   7541 1.R1040
5'-most EST
                   LIB3030-009-Q1-B1-C4
Method
                   BLASTX
NCBI GI
                   g3522950
BLAST score
                   228
E value
                   1.0e-18
Match length
                   99
% identity
                   49
NCBI Description
                   (AC004411) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   7545 1.R1040
                   LIB3030-009-Q1-B1-E1
5'-most EST
Seq. No.
                   6895
                   7551 1.R1040
Contig ID
5'-most EST
                   k117\overline{0}1207181.h1
Method
                   BLASTN
NCBI GI
                   g1044939
BLAST score
                   226
E value
                   1.0e-124
Match length
                   432
% identity
                   91
                   Z.mays mRNA for ubiquitin/ribosomal protein S27a fusion
NCBI Description
                   protein
                   6896
Seq. No.
```

7551 3.R1040

Contig ID

```
taw700660412.h1
5'-most EST
                    BLASTN
Method
NCBI GI
                    q967984
BLAST score
                    142
                    7.0e-74
E value
Match length
                    285
% identity
                    88
NCBI Description
                    Oryza sativa (clone rma630) ribosomal protein-linked
                    ubiquitin mRNA, complete cds
Seq. No.
                    6897
                    7551 6.R1040
Contig ID
5'-most EST
                    jC-qmst02400060a06d1
Method
                    BLASTN
NCBI GI
                    q967984
BLAST score
                    126
E value
                    2.0e-64
Match length
                    221
% identity
                    89
                    Oryza sativa (clone rma630) ribosomal protein-linked
NCBI Description
                    ubiquitin mRNA, complete cds
Seq. No.
                    6898
Contig ID
                    7552 1.R1040
5'-most EST
                    LIB3055-004-Q1-N1-G8
Method
                    BLASTX
NCBI GI
                    q2500079
BLAST score
                    166
E value
                    2.0e-16
Match length
                    296
% identity
                    13
NCBI Description
                    X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR >gi 1314871
                    (U57629) retinitis pigmentosa GTPase regulator [Homo
                    sapiens] >gi_2204218_emb_CAA66258_ (X97668) XLRP3 [Homo
sapiens] >gi_4506581_ref_NP_000319.1_pRP3_ retinitis
pigmentosa 3 (X-linked recessive)
Seq. No.
                    6899
                    7552 2.R1040
Contig ID
                    fde700876589.h1
5'-most EST
                    6900
Seq. No.
                    7552 3.R1040
Contig ID
                    LIB3138-090-P1-N1-B6
5'-most EST
Method
                    BLASTX
NCBI GI
                    g1477565
BLAST score
                    162
                    6.0e-11
E value
Match length
                    112
% identity
                    (U50078) p532 [Homo sapiens]
NCBI Description
                    >gi 4557026 ref NP 003913.1 pHERC1 hect (homologous to the
                    E6-AP (UBE3A) carboxyl terminus) domain and RCC1
                    (CHC1)-like domain (RLD)
                    6901
Seq. No.
```

7556 1.R1040

```
5'-most EST
                  LIB3030-009-01-B1-G9
Method
                  BLASTX
NCBI GI
                  g2244856
BLAST score
                  292
E value
                  4.0e-26
Match length
                  128
% identity
NCBI Description (Z97337) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                  7556 2.R1040
Contig ID
5'-most EST
                  ssr700556456.hl
                  6903
Seq. No.
Contig ID
                  7557 1.R1040
                  LIB3107-006-Q1-K1-B11
5'-most EST
Method
                  BLASTX
                  g3860333
NCBI GI
BLAST score
                  449
E value
                  3.0e-44
Match length
                  124
% identity
                  69
NCBI Description (AJ012693) basic blue copper protein [Cicer arietinum]
                  6904
Seq. No.
Contig ID
                  7557 2.R1040
                  leu701152331.h1
5'-most EST
Method
                  BLASTX
                  g3860333
NCBI GI
BLAST score
                  432
E value
                  2.0e-42
                  127
Match length
% identity
                  65
NCBI Description
                  (AJ012693) basic blue copper protein [Cicer arietinum]
Seq. No.
Contig ID
                  7558 1.R1040
5'-most EST
                  uC-qmflminsoy028b03b1
Seq. No.
Contig ID
                  7562 1.R1040
5'-most EST
                  LIB3030-010-Q1-B1-A12
Seq. No.
                  7562 2.R1040
Contig ID
5'-most EST
                  LIB3094-074-Q1-K1-H5
Seq. No.
                  6908
Contig ID
                  7565 1.R1040
5'-most EST
                  LIB3030-010-Q1-B1-C12
Method
                  BLASTX
NCBI GI
                  q2191175
BLAST score
                  472
E value
                  7.0e-47
Match length
                  264
% identity
                  47
NCBI Description (AF007270) A IG002P16.24 gene product [Arabidopsis
```

BLAST score

E value

594

3.0e-61

thaliana]

```
Seq. No.
                   6909
                   7565 2.R1040
Contig ID
5'-most EST
                   jC-gmf102220056e09a1
                   6910
Seq. No.
Contig ID
                   7566 1.R1040
5'-most EST
                   uC-gmronoir047b10b1
                   6911
Seq. No.
                   7567 1.R1040
Contig ID
5'-most EST
                   LIB3053-006-Q1-N1-G4
Method
                   BLASTX
NCBI GI
                   q3721926
BLAST score
                   2332
E value
                   0.0e+00
Match length
                   543
% identity
                   87
NCBI Description
                   (AB017480) chloroplast FtsH protease [Nicotiana tabacum]
                   6912
Seq. No.
                   7567 2.R1040
Contig ID
5'-most EST
                   rca700998469.hl
Method
                   BLASTX
NCBI GÍ
                   q2492515
BLAST score
                   540
E value
                   6.0e-55
Match length
                   191
% identity
NCBI Description
                   CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
                   >gi_2129924_pir__S58298 ATPase - pepper (fragment)
                   >gi_929013_emb_CAA62084_ (X90472) ATPase [Capsicum annuum]
Seq. No.
                   6913
Contig ID
                   7570 1.R1040
5'-most EST
                   LIB3030-010-Q1-B1-D9
                   6914
Seq. No.
                   7575 1.R1040
Contig ID
5'-most EST
                   zzp700836238.h1
Seq. No.
                   6915
                   7576 1.R1040
Contig ID
5'-most EST
                   zsg701130230.hl
Seq. No.
                   6916
                   7577 1.R1040
Contig ID
                   LIB3030-010-Q1-B1-F12
5'-most EST
                   6917
Seq. No.
                   7581 1.R1040
Contig ID
                   LIB3030-010-Q1-B1-G11
5'-most EST
Method
                  BLASTX
                   g2245108
NCBI GI
```

Seq. No.

```
Match length
                   203
% identity
                   57
NCBI Description
                   (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
                   6918
Seq. No.
                   7583 1.R1040
Contig ID
5'-most EST
                   LIB3040-014-Q1-E1-E10
Method
                   BLASTX
NCBI GI
                   g3122386
BLAST score
                   1798
E value
                   0.0e + 00
Match length
                   356
                   91
% identity
                   WD-40 REPEAT PROTEIN MSI1 >gi 2394227 (AF016845) WD-40
NCBI Description
                   repeat protein [Lycopersicon esculentum]
                   6919
Seq. No.
                   7583 2.R1040
Contig ID
5'-most EST
                   epx701106768.h1
                   6920
Seq. No.
                   7583 3.R1040
Contig ID
5'-most EST
                   hrw701063160.h1
                   6921
Seq. No.
Contig ID
                   7583 4.R1040
                   LIB3109-029-Q1-K1-G10
5'-most EST
                   6922
Seq. No.
                   7586 1.R1040
Contig ID
5'-most EST
                   LIB3030-012-Q1-B1-A2
Method
                   BLASTX
NCBI GI
                   g4218120
BLAST score
                   757
E value
                   1.0e-85
Match length
                   219
% identity
                   70
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   6923
Seq. No.
                   7586 2.R1040
Contig ID
5'-most EST
                   wrg7\overline{0}0790986.h1
                   BLASTX
Method
NCBI GI
                   g4218120
BLAST score
                   321
E value
                   7.0e-30
Match length
                   84
% identity
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   6924
Contig ID
                   7591 1.R1040
5'-most EST
                   LIB3030-012-Q1-B1-D1
```

```
Contig ID
                   7592 1.R1040
5'-most EST
                   q5606539
Method
                   BLASTX
NCBI GI
                   g4510373
BLAST score
                   623
E value
                   2.0e-64
Match length
                   171
% identity
NCBI Description
                   (AC007017) putative harpin-induced protein [Arabidopsis
                   thaliana]
                   6926
Seq. No.
                   7592 2.R1040
Contig ID
5'-most EST
                   qsv701052671.hl
Method
                   BLASTX
NCBI GI
                   g4510373
BLAST score
                   241
E value
                   5.0e-20
Match length
                   92
% identity
                   (AC007017) putative harpin-induced protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   6927
                   7595 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220062e05a1
Method
                   BLASTX
NCBI GI
                   q1255951
BLAST score
                   1926
E value
                   0.0e+00
Match length
                   515
                   69
% identity
NCBI Description
                   (X96932) PS60 [Nicotiana tabacum]
Seq. No.
                   6928
Contig ID
                   7598 1.R1040
5'-most EST
                   fC-qmf1700904909f4
Method
                   BLASTX
NCBI GI
                   q4098246
BLAST score
                   1035
E value
                   1.0e-113
Match length
                   282
% identity
                   86
                   (U76410) homeobox 2 protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   7598 2.R1040
Contig ID
                   jC-gmst02400067a07a1
5'-most EST
                   BLASTX
Method
                   g1170191
NCBI GI
BLAST score
                   583
                   3.0e-60
E value
                   150
Match length
                   77
% identity
                   HOMEOBOX PROTEIN HD1 >gi_1076449_pir__S47535
NCBI Description
                   homeodomain-containing protein - rape
                   >gi_453949_emb_CAA82314_ (Z29073) homeodomain-containing
```

Seq. No.

6935

```
protein [Brassica napus]
Seq. No.
                    6930
Contig ID
                    7598 3.R1040
5'-most EST
                    uC-gmropic045e12b1
Method
                    BLASTX
NCBI GI
                    q4098246
BLAST score
                    479
                    4.0e-48
E value
Match length
                    118
% identity
                    (U76410) homeobox 2 protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                    6931
                    7598 4.R1040
Contig ID
                    wrg7\overline{0}0790517.h2
5'-most EST
Method
                    BLASTX
                    q4098246
NCBI GI
BLAST score
                    359
                    5.0e-34
E value
                    66
Match length
% identity
                    (U76410) homeobox 2 protein [Lycopersicon esculentum]
NCBI Description
                    6932
Seq. No.
                    7598 5.R1040
Contig ID
                    leu701145388.h1
5'-most EST
                    BLASTX
Method
                    q1170191
NCBI GI
BLAST score
                    245
                    3.0e-21
E value
Match length
                    78
% identity
NCBI Description
                    HOMEOBOX PROTEIN HD1 >gi_1076449_pir__S47535
                    homeodomain-containing protein - rape
                    >gi_453949_emb_CAA82314 (Z29073) homeodomain-containing
protein [Brassica napus] >gi_1090522_prf__2019252A homeobox
                    protein [Brassica napus]
Seq. No.
                    6933
Contig ID
                    7604 1.R1040
5'-most EST
                    leu7\overline{0}1155424.h1
Seq. No.
                    6934
Contig ID
                    7607 1.R1040
5'-most EST
                    k11701202720.h1
Method
                    BLASTN
NCBI GI
                    g2760170
BLAST score
                    34
E value
                    2.0e-09
                    97
Match length
% identity
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                    MIO24, complete sequence [Arabidopsis thaliana]
```

protein [Brassica napus] >gi 1090522 prf 2019252A homeobox

NCBI Description

```
Contig ID
                   7607 2.R1040
5'-most EST
                   zhf7\overline{0}0962831.h1
                   6936
Seq. No.
Contig ID
                   7611 1.R1040
5'-most EST
                   LIB3170-003-Q1-K1-F8
Method
                   BLASTN
                   g3869254
NCBI GI
BLAST score
                   152
E value
                   1.0e-79
Match length
                   328
% identity
                   87
NCBI Description
                   Pisum sativum defender against death homolog Peadad
                   (PEADAD) mRNA, complete cds
                   6937
Seq. No.
                   7612 1.R1040
Contig ID
5'-most EST
                   LIB3170-056-Q1-K1-C12
                   6938
Seq. No.
Contig ID
                   7616_1.R1040
5'-most EST
                   LIB3170-001-Q1-K1-E10
                   BLASTN
Method
NCBI GI
                   g498788
BLAST score
                   195
E value
                   1.0e-105
Match length
                   499
                   85
% identity
                  S.tuberosum (Desiree) cycl II mRNA. for cytochrome cl
NCBI Description
                   6939
Seq. No.
Contig ID
                   7616 2.R1040
5'-most EST
                   uC-gmflminsoy035g09b1
Method
                   BLASTX
                   g440953
NCBI GI
BLAST score
                   418
E value
                   5.0e-41
                   93
Match length
                   83
% identity
                   (S66866) cytochrome c1 [Solanum tuberosum=potatoes,
NCBI Description
                   Desiree, monohaploid line AM 80/5793, Peptide
                   Mitochondrial, 320 aa] [Solanum tuberosum]
                   6940
Seq. No.
                   7616 3.R1040
Contig ID
5'-most EST
                   zhf700963832.h1
Seq. No.
                   6941
Contig ID
                   7616 4.R1040
                   jex7\overline{0}0906970.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q498788
BLAST score
                   48
E value
                   7.0e-18
Match length
                   108
% identity
```

S.tuberosum (Desiree) cycl II mRNA. for cytochrome cl

5'-most EST

```
6942
  Seq. No.
  Contig ID
                     7621 1.R1040
  5'-most EST
                     LIB3107-056-Q1-K1-A8
  Method
                     BLASTX
  NCBI GI
                     q445612
  BLAST score
                     595
  E value
                     2.0e-61
  Match length
                     122
  % identity
                     93
  NCBI Description
                    ribosomal protein S19 [Solanum tuberosum]
                     6943
  Seq. No.
                     7624 1.R1040
  Contig ID
  5'-most EST
                     LIB3039-054-Q1-E1-D4
  Method
                     BLASTX
                     g2583135
  NCBI GI
  BLAST score
                     239
  E value
                     6.0e-20
  Match length
                     86
  % identity
                     56
                     (AC002387) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                     >gi_3822216 (AF074948) FIL [Arabidopsis thaliana]
                     >gi_4322477_gb_AAD16053 (AF087015) abnormal floral organs
                     protein [Arabidopsis thaliana]
                                                         Seq. No.
                     6944
  Contig ID
                     7626 1.R1040
                     bnc7\overline{0}0605624.h2
  5'-most EST
                     6945
  Seq. No.
  Contig ID
                     7627 1.R1040
                     fC-gmro7000746976f1
  5'-most EST
  Method
                     BLASTX
  NCBI GI
                     g2501433
  BLAST score
                     542
  E value
                     5.0e-55
  Match length
                     172
                     59
  % identity
                     UBIQUITIN-CONJUGATING ENZYME E2-24 KD (UBIQUITIN-PROTEIN
  NCBI Description
                     LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-EPF5) >gi 181916
                     (M91670) ubiquitin carrier protein [Homo sapiens]
                     6946
  Seq. No.
                     7627 2.R1040
  Contig ID
  5'-most EST
                     leu701146523.h1
  Method
                     BLASTX
NCBI GI
                     q345829
  BLAST score
                     381
  E value
                     1.0e-36
  Match length
                     108
  % identity
  NCBI Description
                    ubiquitin carrier protein E2 - human
  Seq. No.
                     6947
                     7627 3.R1040
  Contig ID
```

fC-gmro7000746976r1

NCBI Description

```
6948
Seq. No.
Contig ID
                   .7634 1.R1040
5'-most EST
                   epx7\overline{0}1108179.h1
Method
                   BLASTX
                   g4455293
NCBI GI
BLAST score
                   211
E value
                   1.0e-16
Match length
                   57
% identity
                   72
                    (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   6949
Seq. No.
                   7636 1.R1040
Contig ID
5'-most EST
                   LIB3039-054-Q1-E1-B6
                   6950
Seq. No.
                   7637 1.R1040
Contig ID
5'-most EST
                   LIB3049-016-Q1-E1-F11
                   6951
Seq. No.
                   7637 2.R1040
Contig ID
5'-most EST
                   LIB3093-010-Q1-K1-C1
                   6952
Seq. No.
                   7638 1.R1040
Contig ID
5'-most EST
                   LIB3039-010-Q1-E1-D2
                    6953
Seq. No.
                   7638 2.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0981237.h1
                    6954
Seq. No.
                   7643_1.R1040
Contig ID
                   LIB3106-073-Q1-K1-C6
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4263782
BLAST score
                   146
E value
                    5.0e-09
Match length
                   47
                    53
% identity
NCBI Description
                    (AC006068) hypothetical protein [Arabidopsis thaliana]
                    6955
Seq. No.
Contig ID
                   7645 1.R1040
5'-most EST
                    jsh701067491.h1
Seq. No.
                    6956
Contig ID
                   7647 1.R1040
5'-most EST
                   LIB3049-046-Q1-E1-F3
Method
                   BLASTX
NCBI GI
                    g3341443
BLAST score
                    376
E value
                    4.0e-36
Match length
                    130
% identity
```

(AJ223074) acid phosphatase [Glycine max]

```
6957
Seq. No.
                   7648_1.R1040
Contig ID
5'-most EST
                   LIB3039-026-Q1-E1-D11
Method
                   BLASTX
NCBI GI
                   g4220524
BLAST score
                   291
E value
                   7.0e-26
Match length
                   148
% identity
                   47
                   (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   6958
                   7648 2.R1040
Contig ID
5'-most EST
                   LIB3039-016-Q1-E1-H4
                   6959
Seq. No.
                   7652 1.R1040
Contig ID
5'-most EST
                   LIB3074-025-Q1-E1-E11
                   BLASTN
Method
                   g2852444
NCBI GI
BLAST score
                   119
E value
                   6.0e-60
Match length
                   319
% identity
                   84
                   Salix bakko mRNA for SUI1 homolog, complete cds
NCBI Description
                   6960
Seq. No.
                   7652 2.R1040
Contig ID
5'-most EST
                   LIB3106-061-Q1-K1-C2
Seq. No.
                   6961
Contig ID
                   7657 1.R1040
5'-most EST
                   g4296782
Method
                   BLASTX
NCBI GI
                   g3947719
BLAST score
                   237
E value
                   9.0e-20
                   51
Match length
% identity
                   92
                   (AJ012653) ribosomal protein S28 [Prunus persica]
NCBI Description
                   >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28
[Prunus persica] >gi_3947723_emb_CAA10103_ (AJ012655)
                   ribosomal protein S28 [Prunus persica]
                   6962
Seq. No.
Contig ID
                   7657 2.R1040
5'-most EST
                   LIB3039-001-Q1-E1-D7
                   BLASTN
Method
                   g3947720
NCBI GI
BLAST score
                   66
E value
                   1.0e-28
Match length
                   182
% identity
NCBI Description
                   Prunus persica mRNA for ribosomal protein S28 (rps28.2)
```

6963

Seq. No.

Match length

```
Contig ID
                  7657 3.R1040
5'-most EST
                  jsh701070119.hl
Method
                  BLASTN
NCBI GI
                  g3947720
BLAST score
                  66
E value
                  1.0e-28
Match length
                  182
                  84
% identity
NCBI Description
                  Prunus persica mRNA for ribosomal protein S28 (rps28.2)
Seq. No.
                   6964
                  7657 4.R1040
Contig ID
                  LIB3049-049-01-E1-E3
5'-most EST
Method
                  BLASTX
NCBI GI
                  a3947719
BLAST score
                  237
                   1.0e-19
E value
                  51
Match length
% identity
NCBI Description
                   (AJ012653) ribosomal protein S28 [Prunus persica]
                  >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28
                   [Prunus persica] >gi_3947723_emb_CAA10103_ (AJ012655)
                  ribosomal protein S28 [Prunus persica]
                   6965
Seq. No.
Contig ID
                  7657 7.R1040
                  qsv701050725.h1
5'-most EST
Method
                  BLASTX
                  q3947719
NCBI GI
                   229
BLAST score
E value
                   7.0e-19
                   51
Match length
% identity
                   (AJ012653) ribosomal protein S28 [Prunus persica]
NCBI Description
                  >gi 3947721 emb CAA10102 (AJ012654) ribosomal protein S28
                   [Prunus persica] >gi_3947723_emb_CAA10103 (AJ012655)
                   ribosomal protein S28 [Prunus persica]
                   6966
Seq. No.
                   7659 1.R1040
Contig ID
                  LIB3170-051-Q1-K2-F2
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4510379
BLAST score
                   387
E value
                   5.0e-37
Match length
                   182
% identity
NCBI Description
                   (AC007017) hypothetical protein [Arabidopsis thaliana]
                   6967
Seq. No.
                  7665 1.R1040
Contig ID
5'-most EST
                  LIB3170-034-Q1-K1-H12
Method
                  BLASTN
NCBI GI
                  g19572
BLAST score
                  150
E value
                   2.0e-78
```

% identity NCBI Description M.sativa C29 mRNA for snRNP-related protein Seq. No. 6968 Contig ID 7665 2.R1040 5'-most EST LIB3072-007-Q1-E1-G1 Method BLASTN NCBI GI g19572 BLAST score 137 E value 5.0e-71 Match length 229 90 % identity NCBI Description M.sativa C29 mRNA for snRNP-related protein Seq. No. 6969 Contig ID 7666 1.R1040 5'-most EST LIB3073-015-Q1-K1-B9 Method BLASTN NCBI GI g313026 BLAST score 86 E value 2.0e-40 Match length 210 % identity 85 NCBI Description L.esculentum rpl38 mRNA for ribosomal protein L38 6970 Seq. No. Contig ID 7667 1.R1040 $qsv7\overline{0}1054182.h1$ 5'-most EST Method BLASTX g1587206 NCBI GI BLAST score 961 1.0e-104 E value 203 Match length % identity NCBI Description T complex protein [Cucumis sativus] Seq. No. 6971 7667 2.R1040 Contig ID 5'-most EST LIB3138-126-Q1-N1-C12 Method BLASTX NCBI GI q3024697 BLAST score 1420 1.0e-158 E value Match length 325 84 % identity T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) NCBI Description (CCT-EPSILON) >gi_2213618 (AC000103) F21J9.12 [Arabidopsis

thaliana]

Seq. No. 6972

Contig ID 7667_3.R1040 5'-most EST pcp700992489.h1

Method BLASTX
NCBI GI g1587206
BLAST score 530
E value 4.0e-54
Match length 127

NCBI GI

```
% identity
                   8.4
NCBI Description
                   T complex protein [Cucumis sativus]
Seq. No.
                   6973
                   7668 1.R1040
Contig ID
5'-most EST
                   LIB3138-028-Q1-N1-E1
Method
                   BLASTX
NCBI GI
                   q4469025
BLAST score
                   488
E value
                   4.0e-49
Match length
                   106
% identity
                   67
NCBI Description
                   (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   6974
                   7668 2.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1147156.h1
Method
                   BLASTX
NCBI GI
                   q4469025
BLAST score
                   408
E value
                   8.0e-40
Match length
                   98
% identity
NCBI Description
                   (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   6975
                   7668 3.R1040
Contig ID
5'-most EST
                   dpv701101316.hl
Method
                   BLASTX
NCBI GI
                   q4469025
BLAST score
                   200
E value
                   2.0e-15
Match length
                   43
% identity
NCBI Description
                   (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   6976
                   7669 1.R1040
Contig ID
5'-most EST
                   uC-gmropic091g08b1
Method
                   BLASTX
NCBI GI
                   g730463
BLAST score
                   319
E value
                   4.0e-29
Match length
                   105
% identity
                   58
NCBI Description
                   60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
                   >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                   (Saccharomyces cerevisiae) >gi 484241 (L23923) ribosomal
                   protein L37 [Saccharomyces cerevisiae]
                   >gi 1420537_emb_CAA99454_ (Z75142) ORF YOR234c
                   [Saccharomyces cerevisiae]
                   6977
Seq. No.
                   7669 2.R1040
Contig ID
                   LIB3040-052-Q1-E1-B9
5'-most EST
Method
                   BLASTX
```

g730463

Match length

```
BLAST score
                  319
E value
                  3.0e-29
Match length
                  105
% identity
                  57
                  60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
NCBI Description
                  >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                  (Saccharomyces cerevisiae) >gi 484241 (L23923) ribosomal
                  protein L37 [Saccharomyces cerevisiae]
                  >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c
                  [Saccharomyces cerevisiae]
                  6978
Seq. No.
                  7672 1.R1040
Contig ID
                  LIB3040-048-01-E1-D2
5'-most EST
Method
                  BLASTN
                  q643073
NCBI GI
                  222
BLAST score
                  1.0e-121
E value
                  430
Match length
                  88
% identity
                  Fragaria x ananassa putative 40S ribosomal protein s12
NCBI Description
                  mRNA, complete cds
                  6979
Seq. No.
                  7672 2.R1040
Contig ID
5'-most EST
                  LIB3055-004-Q1-N1-H6
Method
                  BLASTN
                  q643073
NCBI GI
BLAST score
                  188
                  1.0e-101
E value
Match length
                  428
% identity
                  Fragaria x ananassa putative 40S ribosomal protein s12
NCBI Description
                  mRNA, complete cds
                  6980
Seq. No.
Contig ID
                  7672 4.R1040
                  sat701013854.hl
5'-most EST
                  BLASTX
Method
                  a1173187
NCBI GI
BLAST score
                  279
E value
                  4.0e-44
Match length
                  139
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                  6981
Seq. No.
Contig ID
                  7672 5.R1040
5'-most EST
                  sat701010376.h1
Method
                  BLASTN
NCBI GI
                  g643073
BLAST score
                  73
E value
                  9.0e-33
```

% identity

```
% identity
                   88
NCBI Description
                   Fragaria x ananassa putative 40S ribosomal protein s12
                   mRNA, complete cds
                   6982
Seq. No.
                   7677 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220068c02a1
Method
                   BLASTX
NCBI GI
                   g4335750
BLAST score
                   252
E value
                   2.0e-21
Match length
                   76
                   54
% identity
                   (AC006284) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                   thaliana]
                   6983
Seq. No.
                   7677 2.R1040
Contig ID
5'-most EST
                   sat701009283.hl
                   6984
Seq. No.
Contig ID
                   7678 1.R1040
5'-most EST
                   LIB3039-053-Q1-E1-E9
                   6985
Seq. No.
Contig ID
                   7681 1.R1040
                   gsv7\overline{0}1054724.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4406372
BLAST score
                   1532
E value
                   1.0e-171
Match length
                   378
% identity
                   76
                   (AF109156) thiosulfate sulfurtransferase [Datisca
NCBI Description
                   glomerata]
Seq. No.
                   6986
                   7683 1.R1040
Contig ID
5'-most EST
                   uC-gmropic046a05b1
Method
                   BLASTX
NCBI GI
                   q4558661
BLAST score
                   1198
E value
                   1.0e-132
Match length
                   294
                   78
% identity
NCBI Description
                   (AC007063) putative malate oxidoreductase (NAD)
                   [Arabidopsis thaliana]
                   6987
Seq. No.
Contig ID
                   7684 1.R1040
5'-most EST
                   LIB3049-004-Q1-E1-G7
Method
                   BLASTX
NCBI GI
                   q3668082
BLAST score
                   619
E value
                   4.0e-64
Match length
                   204
```

NCBI GI

E value

BLAST score

```
NCBI Description (AC004667) putative DAL1 protein [Arabidopsis thaliana]
                   6988
Seq. No.
                   7684 2.R1040
Contig ID
5'-most EST
                   LIB3039-033-Q1-E1-D9
Method
                   BLASTX
NCBI GI
                   g2459425
BLAST score
                   300
E value
                   4.0e-27
Match length
                   90
                   67
% identity
NCBI Description
                   (AC002332) plastid protein [Arabidopsis thaliana]
Seq. No.
                   6989
                   7690 1.R1040
Contig ID
5'-most EST
                  LIB3073-023-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                   g294060
BLAST score
                  192
E value
                   3.0e-14
Match length.
                  127
% identity
                   33
NCBI Description
                   (L06467) major latex protein [Papaver somniferum]
Seq. No.
                   6990
                   7691_1.R1040
Contig ID
5'-most EST
                  LIB3039-053-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                   g99755
BLAST score
                   341
E value
                   4.0e-32
Match length
                  128
% identity
NCBI Description
                  RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis
                   thaliana retrotransposon Tal-1 (fragment)
                  >gi_16356_emb_CAA37917_ (X53973) reverse transcriptase
                   [Arabidopsis thaliana]
                  6991
Seq. No.
                  7692 1.R1040
Contig ID
5'-most EST
                  LIB3039-053-Q1-E1-C1
Method
                  BLASTX
NCBI GI
                  g4185140
BLAST score
                  410
E value
                  4.0e-40
Match length
                  88
% identity
                  92
NCBI Description
                   (AC005724) putative small nuclear ribonucleoprotein E
                   (snRNP-E) [Arabidopsis thaliana]
                  6992
Seq. No.
Contig ID
                 7692 2.R1040
5'-most EST
                  LIB3072-008-Q1-E1-E1
Method
                  BLASTX
```

g4185140

4.0e-40

% identity

```
88
Match length
% identity
                    91
NCBI Description
                    (AC005724) putative small nuclear ribonucleoprotein E
                    (snRNP-E) [Arabidopsis thaliana]
Seq. No.
                    6993
                    7692 3.R1040
Contig ID
5'-most EST
                    LIB3170-080-Q1-K1-A12
Method
                    BLASTX
NCBI GI
                    q4185140
                    378
BLAST score
E value
                    2.0e-36
Match length
                    81
                    93
% identity
NCBI Description
                    (AC005724) putative small nuclear ribonucleoprotein E
                    (snRNP-E) [Arabidopsis thaliana]
Seq. No.
                    7696 1.R1040
Contig ID
5'-most EST
                    LIB3056-003-Q1-N1-G2
Method
                    BLASTX
NCBI GI
                    q1730035
BLAST score
                    231
E value
                    7.0e-19
Match length
                    121
% identity
                    PROTEIN KE2 >gi_2137410_pir__I53651 hydrophilic protein -
NCBI Description
                    mouse >gi_198574 (M65255) hydrophilic protein [Mus
                   musculus] >gi_198576 (M65256) hydrophilic protein [Mus musculus] >gi_3811379 (AF100956) KE2 [Mus musculus]
                    >gi 4050102 (AF110520) KE2 [Mus musculus]
Seq. No.
                    6995
Contig ID
                    7696 2.R1040
5'-most EST
                    6HC-\overline{0}1-Q1-B1-B12 BLASTX
Method
NCBI GI
                    q2344898
BLAST score
                    571
E value
                    1.0e-58
Match length
                    168
% identity
NCBI Description
                    (AC002388) 60S ribosomal protein L30 isolog [Arabidopsis
                    thaliana]
Seq. No.
                    6996
Contig ID
                    7698 1.R1040
5'-most EST
                    LIB3039-053-Q1-E1-C8
                    6997
Seq. No.
                    7699 1.R1040
Contig ID
5'-most EST
                    LIB3040-018-Q1-E1-G4
Method
                    BLASTX
NCBI GI
                    q2431771
BLAST score
                    248
                    7.0e-21
E value
Match length
                    114
```

```
NCBI Description (U62753) acidic ribosomal protein P2b [Zea mays]
                   6998
Seq. No.
Contig ID
                   7699 2.R1040
5'-most EST
                   LIB3106-077-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g2431771
BLAST score
                   226
E value
                   2.0e-18
Match length
                   114
% identity
                   45
NCBI Description
                   (U62753) acidic ribosomal protein P2b [Zea mays]
                   6999
Seq. No.
Contig ID
                   7699 3.R1040
                   gsv7\overline{0}1048437.h1
5'-most EST
Method
                   BLASTX
                   g2431771
NCBI GI
BLAST score
                   162
E value
                   2.0e-11
Match length
                   47
                   68
% identity
NCBI Description (U62753) acidic ribosomal protein P2b [Zea mays]
                   7000
Seq. No.
                   7699 4.R1040
Contig ID
                   wrg7\overline{0}0792224.h1
5'-most EST
Method
                   BLASTX
                   g2431771
NCBI GI
BLAST score
                   251
E value
                   1.0e-21
                   70
Match length
                   70
% identity
                   (U62753) acidic ribosomal protein P2b [Zea mays]
NCBI Description
                   7001
Seq. No.
Contig ID
                   7700 1.R1040
5'-most EST
                   LIB3109-002-Q1-K1-B11
                   BLASTX
Method
NCBI GI
                   q3175990
BLAST score
                   2186
E value
                   0.0e + 00
Match length
                   436
% identity
NCBI Description
                   (AJ005836) GDP dissociation inhibitor [Cicer arietinum]
Seq. No.
                   7002
Contig ID
                   7700 2.R1040
5'-most EST
                   wvk700685939.h1
Method
                   BLASTN
NCBI GI
                   q3175989
BLAST score
                   247
E value
                   1.0e-136
Match length
                   430
% identity
                   90
```

NCBI Description Cicer arietinum mRNA for GDP dissociation inhibitor (gdi)

NCBI Description

```
Seq. No.
                   7003
                   7700 3.R1040
Contig ID
                   LIB3049-032-Q1-E1-A9
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3175989
BLAST score
                   147
                   7.0e-77
E value
Match length
                   294
% identity
                   88
NCBI Description
                   Cicer arietinum mRNA for GDP dissociation inhibitor (gdi)
Seq. No.
                   7704 1.R1040
Contiq ID
5'-most EST
                   LIB3073-024-Q1-K1-H9
Seq. No.
                   7005
                   7706 1.R1040
Contig ID
5'-most EST
                   LIB3065-001-Q1-N1-G12
Method
                   BLASTX
NCBI GI
                   g4263521
BLAST score
                   351
E value
                   3.0e-33
Match length
                   87
% identity
NCBI Description
                   (AC004044) putative WD-repeat protein [Arabidopsis
                   thaliana]
Seq. No.
                   7006
                   7708 1.R1040
Contig ID
5'-most EST
                   LIB3039-053-Q1-E1-B3
Seq. No.
Contig ID
                   7713 1.R1040
5'-most EST
                   LIB3039-041-Q1-E1-C12
Seq. No.
                   7008
Contig ID
                   7715 1.R1040
5'-most EST
                   uC-gmflminsoy077b08b1
Method
                   BLASTX
NCBI GI
                   q3785986
BLAST score
                   154
                   7.0e-10
E value
Match length
                   65
% identity
NCBI Description
                   (AC005560) RGA1 protein [Arabidopsis thaliana]
Seq. No.
                   7009
                   7727 1.R1040
Contig ID
5'-most EST
                   fC-gmse700753078a2
Method
                   BLASTX
NCBI GI
                   g3702326
BLAST score
                   839
E value
                   7.0e-90
Match length
                   194
% identity
                   81
```

(AC005397) hypothetical protein [Arabidopsis thaliana]

```
7010
Seq. No.
                   7727 2.R1040
Contig ID
                   qsv7\overline{0}1055260.h1
5'-most EST
Method
                   BLASTX
                   g3702326
NCBI GI
BLAST score
                   237
E value
                   2.0e-26
Match length
                   104
% identity
                   62
                   (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   7011
Seq. No.
Contig ID
                   7729 1.R1040
                   LIB3040-021-Q1-E1-D10
5'-most EST
                   BLASTX
Method
                   g3320379
NCBI GI
BLAST score
                   924
E value
                   1.0e-100
Match length
                   204
                   88
% identity
                   (AF014375) putative JUN kinase activation domain binding
NCBI Description
                   protein [Medicago sativa]
                   7012
Seq. No.
Contig ID
                   7733 1.R1040
5'-most EST
                   LIB3039-052-Q1-E1-G12
                   BLASTX
Method
                   g2583108
NCBI GI
BLAST score
                   651
E value
                   9.0e-68
Match length
                   308
% identity
                   44
                   (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
                   7013
Seq. No.
Contig ID
                   7737 1.R1040
5'-most EST
                   LIB3107-056-Q1-K1-G7
                   7014
Seq. No.
                   7746 1.R1040
Contig ID
5'-most EST
                   LIB3049-001-Q1-E1-F6
Method
                   BLASTX
NCBI GI
                   q3687237
BLAST score
                   885
E value
                   1.0e-107
Match length
                   354
% identity
                   59
NCBI Description
                   (AC005169) putative Cys3His zinc-finger protein
                   [Arabidopsis thaliana]
                   7015
Seq. No.
                   7746 2.R1040
Contig ID
5'-most EST
                   LIB3049-048-Q1-E1-C7
Method
                   BLASTX
NCBI GI
                   g3687237
BLAST score
                   383
```

1301

1.0e-36

E value

% identity

```
186
Match length
% identity
                   50
NCBI Description
                   (AC005169) putative Cys3His zinc-finger protein
                   [Arabidopsis thaliana]
                   7016
Seq. No.
                   7748 1.R1040 ·
Contig ID
5'-most EST
                   LIB3039-052-Q1-E1-C1
Seq. No.
                   7017
                   7757 1.R1040
Contiq ID
                   seb7\overline{0}0652631.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4335725
BLAST score
                   280 -
E value
                   2.0e-24
Match length
                   142
                   46
% identity
NCBI Description
                   (AC006248) hypothetical protein [Arabidopsis thaliana]
                   7018
Seq. No.
                   7757 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810001h12d1
                   7019
Seq. No.
Contig ID
                   7758 1.R1040
5'-most EST
                   LIB3039-052-Q1-E1-C9
Method
                   BLASTX
NCBI GI
                   q4263704
BLAST score
                   280
E value
                   9.0e-25
Match length
                   103
                   48
% identity
NCBI Description
                   (AC006223) putative sugar starvation-induced protein
                   [Arabidopsis thaliana]
Seq. No.
                   7020
Contig ID
                   7774 1.R1040
5'-most EST
                   LIB3039-051-Q1-E1-G10
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   183
E value
                   1.0e-98
Match length
                   287
% identity
                   92
NCBI Description
                   Glycine max vegetative storage protein (vspB) gene,
                   complete cds
                   7021
Seq. No.
                   7776 1.R1040
Contig ID
                   LIB3049-047-Q1-E1-G5
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1531753
BLAST score
                   140
                   2.0e-72
E value
                   400
Match length
                   84
```

NCBI Description A.officinalis mRNA for Histone H3

Method BLASTX
NCBI GI g19611
BLAST score 467
E value 1.0e-46
Match length 96

% identity 99

NCBI Description (X13675) histone H3 (AA 1-123) [Medicago sativa]

>gi_2916748_emb_CAA05554_ (AJ002555) histone H3 [Pisum

satīvum]

Seq. No. 7023

Contig ID 7776 3.R1040

5'-most EST LIB3170-015-Q1-J1-E5

Seq. No. 7024

Contig ID 7783 1.R1040

5'-most EST LIB3039-047-Q1-E1-B8

Seq. No. 7025

Contig ID 7796_1.R1040 5'-most EST wrg700791377.h1

Method BLASTX
NCBI GI g3885513
BLAST score 425
E value 1.0e-41
Match length 88

% identity 88

NCBI Description (AF084201) similar to chloroplast 50S ribosomal protein L31

[Medicago sativa]

Seq. No. 7026

Contig ID 7803_1.R1040 5'-most EST epx701109040.h1

Seq. No. 7027

Contig ID 7806 1.R1040

5'-most EST LIB3039-051-Q1-E1-D4

Method BLASTX
NCBI GI g4226129
BLAST score 175
E value 2.0e-12
Match length 155
% identity 30

NCBI Description (AF125459) No definition line found [Caenorhabditis

elegans]

Seq. No. 7028

Contig ID 7807_1.R1040

5'-most EST LIB3039-051-Q1-E1-C10

Seq. No. 7029

Contig ID 7808_1.R1040

```
sat701006613.hl
5'-most EST
                   7030
Seq. No.
                   7809 1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1150109.h1
                   7031
Seq. No.
                   7811 1.R1040
Contig ID
                   leu701146266.hl
5'-most EST
                   7032
Seq. No.
Contig ID
                   7811 2.R1040
                   ncj7\overline{0}0978210.h1
5'-most EST
                   7033
Seq. No.
                   7812 1.R1040
Contig ID
5'-most EST
                   LIB3039-020-Q1-E1-B8
Method
                   BLASTX
NCBI GI
                   q1708464
                   257
BLAST score
                   3.0e-22
E value
                   90
Match length
                   57
% identity
                   PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD)
NCBI Description
                   (2,3-DIHYDROXY ACID HYDROLYASE) >gi_1213255_emb_CAA93689_
                   (Z69795) unknown [Schizosaccharomyces pombe]
Seq. No.
                   7034
                   7814 1.R1040
Contig ID
                   leu7\overline{0}1144777.h1
5'-most EST
                   BLASTX
Method
                   g400649
NCBI GI
BLAST score
                   145
E value
                   8.0e-09
                   65
Match length
                   40
% identity
                   NADH-UBIQUINONE OXIDOREDUCTASE 12 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-12KD) (CI-12KD) >gi_479205_pir__S32568 gene
                   NUO-12.3 protein - Neurospora crassa >gi 3040 emb_CAA48768_
                   (X68965) NUO-12.3 [Neurospora crassa]
                   7035
Seq. No.
Contig ID
                   7815 1.R1040
5'-most EST
                   uxk7\overline{0}0670174.h1
                   7036
Seq. No.
                   7820 1.R1040
Contig ID
5'-most EST
                   LIB3039-051-Q1-E1-B9
Method
                   BLASTX
NCBI GI
                   q2827888
                   594
BLAST score
                   2.0e-61
E value
Match length
                   197
% identity
                   (AF016621) ATP-dependent Clp protease proteolytic subunit
NCBI Description
```

[Arabidopsis thaliana]

Contig ID

```
Seq. No.
                    7037
                    7829 1.R1040
Contig ID
5'-most EST
                    k11701205406.h1
Seq. No.
                    7038
                    7837 1.R1040
Contig ID
                    zhf7\overline{0}0964782.h1
5'-most EST
Seq. No.
                    7039
                    7841 1.R1040
Contig ID
5'-most EST
                    LIB3039-050-Q1-E1-G12
Method
                    BLASTX
NCBI GI
                    q3821254
BLAST score
                    1529
E value
                    0.0e + 00
Match length
                    463
% identity
NCBI Description
                    (AJ007789) geranylgeranyl reductase [Nicotiana tabacum]
Seq. No.
Contig ID
                    7846 1.R1040
5'-most EST
                    LIB3039-050-Q1-E1-E2
Seq. No.
Contig ID
                    7852 1.R1040
5'-most EST
                    uC-gmflminsoy057c11b1
Seq. No.
Contig ID
                    7855 1.R1040
5'-most EST
                    LIB3039-035-Q1-E1-G1
Method
                    BLASTX
NCBI GI
                    g464621
BLAST score
                    819
E value
                    1.0e-87
Match length
                    224
% identity
                    71
                    60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586
NCBI Description
                    ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                    [Mesembryanthemum crystallinum]
                    7043
Seq. No.
                    7855 2.R1040
Contig ID
5'-most EST
                    g5676862
Method
                    BLASTX
NCBI GI
                    g464621
BLAST score
                    323
E value
                    7.0e-58
                    199
Match length
                    78
% identity
NCBI Description
                    60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586
                    ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                    [Mesembryanthemum crystallinum]
Seq. No.
                    7044
```

7855 4.R1040

```
5'-most EST
                  LIB3040-060-01-E1-G2
Method
                  BLASTX
NCBI GI
                  g464621
BLAST score
                   233
E value
                   2.0e-19
Match length
                  56
                   80
% identity
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__$28586
NCBI Description
                   ribosomal protein ML16 - common ice plant
                  >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                   7045
Seq. No.
                   7856 1.R1040
Contig ID
5'-most EST
                  LIB3106-058-Q1-K1-F4
                  BLASTX
Method
                  q3097266
NCBI GI
BLAST score
                   1042
E value
                   0.0e + 00
Match length
                   407
% identity
                   88
NCBI Description
                   (Y17186) translation initiation factor [Pisum sativum]
                   7046
Seq. No.
Contig ID
                   7858 1.R1040
5'-most EST
                  LIB3039-050-Q1-E1-D10
Method
                  BLASTX
                  g3036807
NCBI GI
BLAST score
                   664
E value
                   4.0e-85
Match length
                  269
% identity
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                   7047
Seq. No.
Contig ID
                   7860 1.R1040
5'-most EST
                  LIB3039-050-Q1-E1-D12
Method
                  BLASTN
                  g3980263
NCBI GI
BLAST score
                   355
                   0.0e + 00
E value
Match length
                  814
                  89
% identity
NCBI Description
                  Cicer arietinum mRNA for 20S proteasome beta subunit
                   7048
Seq. No.
Contig ID
                   7860 2.R1040
5'-most EST
                   seb700652801.hl
Method
                  BLASTN
NCBI GI
                  q3980263
BLAST score
                  136
E value
                   3.0e-70
Match length
                  456
% identity
NCBI Description
                  Cicer arietinum mRNA for 20S proteasome beta subunit
```

7049

Seq. No.

BLAST score

495

```
7868 1.R1040
Contig ID
5'-most EST
                   LIB3093-035-Q1-K1-A8
                   BLASTX
                                                                .
Method
NCBI GI
                   g3063454
BLAST score
                   148
E value
                   4.0e-09
                   136
Match length
                   46
% identity
                    (AC003981) F22013.16 [Arabidopsis thaliana]
NCBI Description
                   7050
Seq. No.
                   7868 2.R1040
Contig ID
5'-most EST
                   kmv700739710.h1
                   7051
Seq. No.
Contig ID
                   7875 1.R1040
                   awf700839764.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4567302
BLAST score
                   148
E value
                   4.0e-09
                   86
Match length
                   45
% identity
                   (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7052
Contig ID
                   7877 1.R1040
5'-most EST
                   gsv701047796.hl
Method
                   BLASTX
                   g2497543
NCBI GI
BLAST score
                   2263
E value
                   0.0e + 00
Match length
                   493
                   89
% identity
                   PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__$41379
NCBI Description
                   pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
                   7053
Seq. No.
Contig ID
                   7877 2.R1040
5'-most EST
                   jC-gmst02400055d10a1
Method
                   BLASTX
                   q4033431
NCBI GI
BLAST score
                   570
                   8.0e-59
E value
Match length
                   126
% identity
                   87
                   PROBABLE PYRUVATE KINASE, CYTOSOLIC ISOZYME (PK) >gi_2982467_emb_CAA18231_ (AL022223) pyruvate kinase like
NCBI Description
                   protein [Arabidopsis thaliana]
                   7054
Seq. No.
Contig ID
                   7877 3.R1040
5'-most EST
                   LIB3170-061-Q1-K2-D11
Method
                   BLASTX
NCBI GI
                   g2497543
```

1.3

Seq. No.

```
5.0e-50
E value
Match length
                   104
% identity
                   89
NCBI Description
                   PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir S41379
                   pyruvate kinase - common tobacco >gi 444023 emb CAA82628_
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
                   7055
Seq. No.
Contig ID
                   7877 4.R1040
                   sat701010766.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2497543
BLAST score
                   436
                   6.0e-43
E value
Match length
                   143
% identity
                   75
                   PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir S41379
NCBI Description
                   pyruvate kinase - common tobacco >gi 444023 emb CAA82628
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
                   7056
Seq. No.
                   7880 1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1146874.h1
Seq. No.
                   7057
                   7880 2.R1040
Contig ID
5'-most EST
                   LIB3170-012-Q1-J1-C11
                   7058
Seq. No.
                   7883 1.R1040
Contig ID
5'-most EST
                   taw7\overline{0}0655766.h1
                   7059
Seq. No.
Contig ID
                   7883 2.R1040
5'-most EST
                   g5510176
Seq. No.
                   7060 .
Contig ID
                   7883 3.R1040
5'-most EST
                   LIB3073-015-Q1-K1-B1
Seq. No.
                   7061
Contig ID
                   7883 4.R1040
5'-most EST
                   ssr7\overline{0}0557657.h1 .
                   7062
Seq. No.
                   7884_1.R1040
Contig ID
5'-most EST
                   LIB3039-049-Q1-E1-H9
Method
                   BLASTX
NCBI GI
                   g4204294
BLAST score
                   202
                   7.0e-16
E value
Match length
                   71
% identity
                   66
NCBI Description
                   (AC003027) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
```

```
7892 1.R1040
 Contig ID
 5'-most EST
                   LIB3109-048-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   g3063449
BLAST score
                   1364
E value
                   1.0e-151
Match length
                   347
 % identity
                   74
NCBI Description
                   (AC003981) F22013.11 [Arabidopsis thaliana]
Seq. No.
                   7064
                   7892 2.R1040
Contig ID
 5'-most EST
                   LIB3039-049-Q1-E1-H10
Method
                   BLASTX
NCBI GI
                   q3063449
BLAST score
                   436
E value
                   3.0e-43
Match length
                   109
                   78
 % identity
NCBI Description
                   (AC003981) F22013.11 [Arabidopsis thaliana]
Seq. No.
                   7065
Contig ID
                   7896_1.R1040
5'-most EST
                   jC-qmst02400015c11a1
Method
                   BLASTX
NCBI GI
                   a3668097
BLAST score
                   649
E value
                   7.0e-68
Match length
                   155
% identity
NCBI Description
                   (AC004667) putative glycine cleavage system protein H
                   precursor [Arabidopsis thaliana]
                   7066
Seq. No.
                   7896 2.R1040
Contig ID
5'-most EST
                   LIB3170-035-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   q3668097
BLAST score
                   571
E value
                   7.0e-59
Match length
                   138
% identity
NCBI Description
                   (AC004667) putative glycine cleavage system protein H
                   precursor [Arabidopsis thaliana]
Seq. No.
Contig ID
                   7900 1.R1040
5'-most EST
                   LIB3106-010-Q1-K1-G1
Method
                   BLASTX
NCBI GI
                   q1717755
BLAST score
                   829
E value
                   1.0e-88
Match length
                   263
% identity
                   60
                   TROPINONE REDUCTASE HOMOLOG (P29X) >gi 539028_pir__C48674
NCBI Description
                   tropinone reductase homolog - jimsonweed >gi 424158
                   (L20475) 29kDa protein; high homology to aa sequence of
```

tropinone reductases [Datura stramonium]

7068 Seq. No. Contig ID 7900 3.R1040 5'-most EST LIB3049-008-Q1-E1-F4 Method BLASTX q1717755 NCBI GI BLAST score 279 E value 5.0e-27 .100 Match length % identity 64 NCBI Description TROPINONE REDUCTASE HOMOLOG (P29X) >gi_539028_pir__C48674 tropinone reductase homolog - jimsonweed >gi_424158 (L20475) 29kDa protein; high homology to aa sequence of tropinone reductases [Datura stramonium] Seq. No. 7069 7904 1.R1040 Contig ID 5'-most EST LIB3049-020-Q1-E1-A8 Method BLASTX g1922938 NCBI GI BLAST score 152 E value 7.0e-10 Match length 66 % identity .52 (AC000106) Similar to Caenorhabditis hypothetical protein NCBI Description CO7A9.11 (gb Z29094). [Arabidopsis thaliana] Seq. No. 7070 Contig ID 7908 1.R1040 5'-most EST LIB3039-049-Q1-E1-E4 BLASTX Method g1532163 NCBI GI BLAST score 191 E value 2.0e-29 Match length 94 % identity NCBI Description (U63815) similar to glutaredoxin encoded by GenBank Accession Number Z49699; localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop c Seq. No. 7071 Contig ID 7910 1.R1040 $1eu7\overline{0}1155340.h1$ 5'-most EST Method BLASTX NCBI GI q3914999 BLAST score 420 3.0e-41 E value Match length 110 % identity 71

Seq. No. 7072

NCBI Description

dismutase precursor [Solidago canadensis]

SUPEROXIDE DISMUTASE, CHLOROPLAST [CU-ZN] PRECURSOR

>gi_1944326_dbj_BAA19675_ (D49486) copper/zinc-superoxide

% identity

```
Contig ID
                   7912 1.R1040
5'-most EST
                   gsv701046882.h1
Method
                   BLASTX
NCBI GI
                   q4337176
BLAST score
                   198
E value
                   3.0e-15
Match length
                   136
% identity
NCBI Description
                   (AC006416) T31J12.4 [Arabidopsis thaliana]
Seq. No.
                   7073
                   7912 2.R1040
Contig ID
5'-most EST
                   LIB3039-049-Q1-E1-E8
                   BLASTX
Method
                   q4337176
NCBI GI
BLAST score
                   182
E value
                   2.0e-13
Match length
                   133
                   16
% identity
NCBI Description
                   (AC006416) T31J12.4 [Arabidopsis thaliana]
Seq. No.
                   7074
Contig ID
                   7916 1.R1040
5'-most EST
                   zpv700757882.h1
Method
                   BLASTX
NCBI GI
                   g2245108
BLAST score
                   530
                   7.0e-54
E value
Match length
                   188
                   53
% identity
NCBI Description
                   (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
                   7075
Seq. No.
                   7918 1.R1040
Contig ID
5'-most EST
                   hrw7\overline{0}1060365.h1
Method
                   BLASTX
NCBI GI
                   q3122703
BLAST score
                   624
E value
                   6.0e-65
Match length
                   151
                   85
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L23A >qi 2641201 (AF031542) ribosomal
                   protein L23a [Fritillaria agrestis]
Seq. No.
                   7076
Contig ID
                   7918 2.R1040
5'-most EST
                   LIB3094-047-Q1-K1-B3
                   7077
Seq. No.
Contig ID
                   7919 1.R1040
5'-most EST
                   LIB3039-049-Q1-E1-C8
Method
                   BLASTX
NCBI GI
                   q2330833
BLAST score
                   251
E value
                   3.0e-21
Match length
                   104
```

BLAST score

```
NCBI Description
                    (298531) hypothetical protein [Schizosaccharomyces pombe]
                    7078
Seq. No.
                    7919 2.R1040
Contig ID
5'-most EST
                    leu701155674.hl
                    7079
Seq. No.
Contig ID
                    7922 1.R1040
5'-most EST
                    LIB3039-049-Q1-E1-D11
Method
                    BLASTX
NCBI GI
                    q1708971
BLAST score
                    381
E value
                    2.0e-36
Match length
                    160
% identity
                    43
NCBI Description
                    (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
                    (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
                    >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) -
black cherry >gi_288116_emb_CAA51194_ (X72617)
mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
                    (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
                    serotina] >gi_1090776_prf_ 2019441A mandelonitrile lyase
                    [Prunus serotina]
Seq. No.
                    7080
Contig ID
                    7934 1.R1040
5'-most EST
                    LIB3039-049-01-E1-C11
Method
                    BLASTX
NCBI GI
                    q416731
BLAST score
                    141
E value
                    7.0e-09
Match length
                    67
% identity
NCBI Description
                    POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107
                    18.3K protein precursor, pollen - maize
                    >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea
                    mays=corn, Peptide, 170 aa] [Zea mays]
                    >gi 1588669 prf 2209273A Zm13 [Zea mays]
Seq. No.
                    7081
Contig ID
                    7938 1.R1040
5'-most EST
                    ncj7\overline{0}0983184.h1
Method
                    BLASTX
NCBI GI
                    g1653702
BLAST score
                    275
E value
                    3.0e-24
Match length
                    81
% identity
                    (D90915) dihydrolipoamide acetyltransferase component (E2)
NCBI Description
                    of pyruvate dehydrogenase complex [Synechocystis sp.]
Seq. No.
                    7082
                    7938 2.R1040
Contig ID
5'-most EST
                    uC-gmropic073g06b1
Method
                    BLASTX
NCBI GI
                    g1653702
```

% identity

```
9.0e-17
E value
Match length
                   50
% identity
                   82
NCBI Description
                   (D90915) dihydrolipoamide acetyltransferase component (E2)
                   of pyruvate dehydrogenase complex [Synechocystis sp.]
                   7083
Seq. No.
                   7939 1.R1040
Contig ID
5'-most EST
                   LIB3072-010-Q1-E1-A5
Method
                   BLASTX
NCBI GI
                   g4324409
BLAST score
                   233
                   7.0e-19
E value
                   206
Match length
                   31
% identity
                   (AF104119) intracellular chloride ion channel protein p64H1
NCBI Description
                   [Rattus norvegicus]
                   7084
Seq. No.
Contig ID
                   7943_1.R1040
                   LIB3\overline{0}39-049-Q1-E1-B1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3193284
BLAST score
                   390
E value
                   1.0e-37
Match length
                   154
% identity
                   55
                   (AF069298) No definition line found [Arabidopsis thaliana]
NCBI Description
                   7085
Seq. No.
Contig ID
                   7944 1.R1040
                   LIB3039-049-Q1-E1-B10
5'-most EST
                   BLASTN
Method
NCBI GI
                   g703230
BLAST score
                   47
E value
                   2.0e-17
Match length
                   71
% identity
                  Pisum sativum (clone HW54) gene fragment
NCBI Description
Seq. No.
                   7086
Contig ID
                   7947 1.R1040
5'-most EST
                   LIB3039-048-Q1-E1-G12
Seq. No.
                   7087
Contig ID
                   7953 1.R1040
5'-most EST
                   LIB3039-048-Q1-E1-G9
                   7088
Seq. No.
Contig ID
                   7955 1.R1040
5'-most EST
                   LIB3049-008-Q1-E1-A7
Method
                   BLASTX
NCBI GI
                   g2252866
BLAST score
                   352
                   1.0e-32
E value
Match length
                   194
```

```
NCBI Description
                   (AF013294) contains region of similarity to SYT
                   [Arabidopsis thaliana]
Seq. No.
                   7955 2.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0978551.h1
                   BLASTX
Method
NCBI GI
                   g2252866
BLAST score
                   266
                   4.0e-23
E value
Match length
                   56
                   95
% identity
                   (AF013294) contains region of similarity to SYT
NCBI Description
                   [Arabidopsis thaliana]
                   7090
Seq. No.
                   7957 1.R1040
Contig ID
                   LIB3039-048-Q1-E1-F6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4467111
BLAST score
                   173
E value
                   5.0e-12
Match length
                   63
% identity
                   (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   7091
Seq. No.
                   7961 1.R1040
Contig ID
                   LIB3039-048-Q1-E1-E5
5'-most EST
                   7092
Seq. No.
Contig ID
                   7961 2.R1040
5'-most EST
                   gsv7\overline{0}1048205.h1
                   7093
Seq. No.
Contig ID
                   7964_1.R1040
5'-most EST
                   uC-gmropic113a06b1
Method
                   BLASTX
                   g729704
NCBI GI
                   339
BLAST score
                   3.0e-31
E value
Match length
                   223
% identity
                   12
                   DNA-BINDING PROTEIN HEXBP (HEXAMER-BINDING PROTEIN)
NCBI Description
                   >gi 1078700 pir__A47156 hexamer-binding protein HEXBP -
                   Leishmania major >gi_159342 (M94390) HEXBP DNA binding
                   protein [Leishmania major]
Seq. No.
                   7094
                   7975 1.R1040
Contig ID
                   LIB3039-048-Q1-E1-C6
5'-most EST
Method
                   BLASTX
                   g2341024
NCBI GI
BLAST score
                   254
E value
                   5.0e-22
Match length
                   84
```

56

% identity

NCBI Description

```
(AC000104) F19P19.1 [Arabidopsis thaliana]
NCBI Description
                  7095
Seq. No.
                  7979 1.R1040
Contig ID
                  fC-gmle700557018f3
5'-most EST
                  BLASTX
Method
                  g1351271
NCBI GI
BLAST score
                  1246
E value
                  1.0e-137
                  270
Match length
                  87
% identity
                  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                  >gi 1084309_pir S52032 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - spinach >gi_806312
                  (L36387) triosephosphate isomerase, chloroplast isozyme
                  [Spinacia oleracea]
                  7096
Seq. No.
                  7979 2.R1040
Contig ID
                  LIB3040-059-Q1-E1-H10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1351271
BLAST score
                  701
E value
                  5.0e-74
Match length
                  182
% identity
                  76
                  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                  >gi 1084309 pir S52032 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - spinach >gi_806312
                  (L36387) triosephosphate isomerase, chloroplast isozyme
                  [Spinacia oleracea]
                  7097
Seq. No.
                  7979 3.R1040
Contig ID
5'-most EST
                  fC-qmle7000739771d1
Method
                  BLASTX
NCBI GI
                  q1351271
BLAST score
                  347
E value
                  1.0e-32
                  78
Match length
% identity
                  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                  >gi_1084309_pir__S52032 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - spinach >gi 806312
                  (L36387) triosephosphate isomerase, chloroplast isozyme
                  [Spinacia oleracea]
                  7098
Seq. No.
                  7979 4.R1040
Contig ID
                  LIB3107-068-Q1-K1-G9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1174745
BLAST score
                  192
                  1.0e-14
E value
                  41
Match length
% identity
                  83
```

TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)

```
>gi_609262_emb_CAA83533 (Z32521) triosephosphate isomerase
[Secale cereale] >gi_1095494_prf__2109226B triosephosphate
                    isomerase [Secale cereale]
Seq. No.
                    7099
Contig ID
                    7989 1.R1040
5'-most EST
                    LIB3039-048-Q1-E1-B11
Method
                    BLASTX
NCBI GI
                    q3080450
BLAST score
                    575
E value
                    3.0e-59
Match length
                    187
% identity
NCBI Description
                    (AL022605) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                    7995 1.R1040
5'-most EST
                    LIB3040-055-Q1-E1-E8
Seq. No.
Contig ID
                    7996 1.R1040
5'-most EST
                    LIB3039-047-Q1-E1-G4
Seq. No.
                    7997 1.R1040
Contig ID
5'-most EST
                    leu7\overline{0}1145158.h1
Method
                    BLASTX
NCBI GI
                    q3687243
BLAST score
                    251
E value
                    3.0e-21
Match length
                    61
% identity
NCBI Description
                    (AC005169) putative ribosomal protein [Arabidopsis
                    thaliana]
Seq. No.
                    7103
                    7997 2.R1040
Contig ID
                    sat7\overline{0}1002975.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3687243
BLAST score
                    146
E value
                    5.0e-09
Match length
                    32
% identity
NCBI Description
                    (AC005169) putative ribosomal protein [Arabidopsis
                    thaliana]
                    7104
Seq. No.
                    8002 1.R1040
Contig ID
5'-most EST
                    LIB3039-047-Q1-E1-H2
Method
                    BLASTX
NCBI GI
                    g1071924
BLAST score
                    147
E value
                    1.0e-12
                    72
Match length
```

>gi_1363523_pir__S53761 triose-phosphate isomerase (EC

5.3.1.1) precursor, chloroplast - rye

```
% identity
NCBI Description
                   Kunitz trypsin inhibitor precursor - soybean
                   >gi 510515 emb CAA56343 (X80039) Kunitz trypsin inhibitor
                   [Glycine max]
Seq. No.
                   7105
                   8004 1.R1040
Contig ID
5'-most EST
                   LIB3039-047-Q1-E1-H7
Method
                   BLASTX
NCBI GI
                   g3747050
BLAST score
                   491
E value
                   2.0e-49
Match length
                   118
% identity
                   81
NCBI Description
                   (AF093540) ribosomal protein L26 [Zea mays]
Seq. No.
                   7106
                   8004 2.R1040
Contig ID
5'-most EST
                   LIB3170-077-Q1-J1-H5
Method
                   BLASTN
NCBI GI
                   q3747049
BLAST score
                   67
E value
                   3.0e-29
Match length
                   143
% identity
                   87
NCBI Description
                  Zea mays ribosomal protein L26 mRNA, partial cds
Seq. No.
Contig ID
                   8006 1.R1040
5'-most EST
                   q5509188
Method
                   BLASTX
NCBI GI
                   g294845
BLAST score
                   637
E value
                   3.0e-66
Match length
                   262
% identity
                   49
NCBI Description
                   (L13655) membrane protein [Saccharum hybrid cultivar
                  H65-7052]
Seq. No.
                   7108
Contig ID
                   8006 2.R1040
5'-most EST
                   uC-gmropic058e08b1
Method
                  BLASTX
NCBI GI
                   g294845
BLAST score
                  248
E value
                   4.0e-21
Match length
                  87
% identity
                   (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                  H65-70521
Seq. No.
                   7109
                   8013 1.R1040
Contig ID
5'-most EST
                   zhf700960701.h1
                  BLASTX
Method
NCBI GI
                   g2914706
```

719

BLAST score

```
E value
                   7.0e-76
Match length
                   238
% identity
                   56
NCBI Description
                   (AC003974) putative homeobox protein [Arabidopsis thaliana]
Seq. No.
                   8013 2.R1040
Contig ID
5'-most EST
                   LIB3109-044-Q1-K1-A5
Method
                   BLASTX
NCBI GI
                   q3298555
BLAST score
                   176
                   1.0e-12
E value
Match length
                   48
                   62
% identity
NCBI Description
                   (AC004681) putative homeobox protein, 3' partial
                   [Arabidopsis thaliana]
Seq. No.
                   7111
                   8016 1.R1040
Contig ID
5'-most EST
                   uC-gmropic065a06b1
Method
                   BLASTX
NCBI GI
                   g1669601
BLAST score
                   581
E value
                   6.0e-60
Match length
                   190
% identity
                   63
                   (D88747) AR401 [Arabidopsis thaliana]
NCBI Description
                   7112
Seq. No.
                   8020 1.R1040
Contig ID
5'-most EST
                   LIB3039-047-Q1-E1-D6
Method
                   BLASTX
NCBI GI
                   q3341443
BLAST score
                   330
E value
                   8.0e-31
Match length
                   115
% identity
NCBI Description
                   (AJ223074) acid phosphatase [Glycine max]
Seq. No.
Contig ID
                   8031 1.R1040
                   vwf700678476.hl
5'-most EST
Seq. No.
                   8044 1.R1040
Contig ID
```

5'-most EST LIB3039-047-Q1-E1-A7

Method BLASTX
NCBI GI g731852
BLAST score 274
E value 3.0e-24
Match length 90
% identity 58

NCBI Description HYPOTHETICAL 48.3 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION >gi 626372 pir S48469 probable membrane protein YIL103w -

yeast (Saccharomyces cerevisiae) >gi_558703_emb_CAA86277_

(Z38125) orf, len: 425, CAI: 0.19 [Saccharomyces

cerevisiae]

```
Seq. No.
                  7115
Contig ID
                  8048 1.R1040
5'-most EST
                  LIB3039-047-Q1-E1-B11
Seq. No.
Contig ID
                  8053 1.R1040
5'-most EST
                  bth700843962.h1
Method
                  BLASTX
NCBI GI
                  q3834325
BLAST score
                  1145
E value
                  1.0e-125
Match length
                  316
% identity
NCBI Description
                  (AC005679) Strong similarity to gb AF067141 gamma-glutamyl
                  hydrolase from Arabidopsis thaliana. ESTs gb_R83955,
                  gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and
                  gb AI00672 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  8054 1.R1040
Contig ID
5'-most EST
                  LIB3049-041-01-E1-B4
Seq. No.
                  7118
Contig ID
                  8069 1.R1040
5'-most EST
                  kl1701211702.hl
Method
                  BLASTX
NCBI GI
                  a3212112
BLAST score
                  355
E value
                  2.0e-33
Match length
                  163
% identity
NCBI Description
                  (Y17394) prefoldin subunit 3 [Homo sapiens]
                  >gi_4507873_ref_NP_003363.1_pVBP1_ von Hippel-Lindau
                  binding protein
Seq. No.
                  7119
                  8069 2.R1040
Contig ID
5'-most EST
                  LIB3039-046-Q1-E1-G11
Method
                  BLASTX
NCBI GI
                  g3915477
BLAST score
                  170
E value
                  4.0e-12
Match length
                  92
                  37
% identity
NCBI Description
                  HYPOTHETICAL 20.9 KD PROTEIN TOGG6.9 IN CHROMOSOME I
                  >gi 3879580 emb CAB04707 (Z81587) Similarity to Human VHL
                  binding protein-1 (TR:Q15765); cDNA EST EMBL:C13429 comes
                  from this gene; cDNA EST EMBL:C10456 comes from this gene;
                  cDNA EST yk486h8.3 comes from this gene [Caenorhabditis
                  elegans]
Seq. No.
                  7120
                  8069 3.R1040
Contig ID
                  sat701008639.h1
5'-most EST
Method
                  BLASTX
                  q3915477
NCBI GI
```

BLAST score 145 E value 2.0e-09 Match length 71 % identity 41

HYPOTHETICAL 20.9 KD PROTEIN TOGG6.9 IN CHROMOSOME I NCBI Description >gi 3879580 emb CAB04707 (Z81587) Similarity to Human VHL binding protein-1 (TR:Q15765); cDNA EST EMBL:C13429 comes from this gene; cDNA EST EMBL:C10456 comes from this gene; cDNA EST yk486h8.3 comes from this gene [Caenorhabditis

elegans]

Seq. No. 7121

8080 1.R1040 Contig ID

LIB3039-046-Q1-E1-E6 5'-most EST

Method BLASTX NCBI GI q1169199 BLAST score 634 E value 5.0e-66 Match length 171 70 % identity

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT102

>gi_479739_pir__S35271 hypothetical protein - Arabidopsis

thaliana >gi_166928 (L11368) [Arabidopsis thaliana

unidentified mRNA sequence, complete cds.], gene product

[Arabidopsis thaliana]

Seq. No. 7122

Contig ID 8088 1.R1040 $jex7\overline{0}0904890.h1$ 5'-most EST

Method BLASTN NCBI GI g3982595 BLAST score 209 E value 1.0e-114

Match length 221 99 % identity

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 7123

Contig ID 8091 1.R1040

5'-most EST LIB3039-046-Q1-E1-C8

7124 Seq. No.

8093 1.R1040 Contig ID

LIB3049-012-Q1-E1-B2 5'-most EST

Method BLASTX NCBI GI g122087 BLAST score 673 E value 1.0e-70 Match length 136 % identity

NCBI Description

HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964__(X13673) histone H3 (AA 1-136) [Medicago satīva] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago satīva] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi 488565 (U09459)

histone H3.1 [Medicago sativa] >gi 2565419 (AF026803)

histone H3 [Onobrychis viciifolia]

Seq. No. 7125 Contig ID 8102 1.R1040 5'-most EST pmv700890295.h1Method BLASTX NCBI GI q3021409 BLAST score 668 E value 5.0e-70 Match length 244 % identity 25 NCBI Description (Y12781) transducin (beta) like 1 protein [Homo sapiens] Seq. No. Contig ID 8111 1.R1040 5'-most EST LIB3039-045-Q1-E1-H1 Seq. No. 8117 1.R1040 Contig ID 5'-most EST LIB3039-045-Q1-E1-H8 7128 Seq. No. Contig ID 8122 1.R1040 5'-most EST $sat7\overline{0}1014331.h1$ BLASTX Method q1871185 NCBI GI BLAST score 231 8.0e-19 E value Match length 115 % identity NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana] 7129 Seq. No. 8126 1.R1040 Contig ID 5'-most EST LIB3039-045-Q1-E1-F6 Method BLASTX NCBI GI q125722 BLAST score 284 E value 4.0e-25 Match length 176 % identity 47 NCBI Description KUNITZ-TYPE TRYPSIN INHIBITOR KTI1 PRECURSOR >gi_81814_pir__JQ1091 trypsin inhibitor KTi1 (Kunitz) soybean > gi 256635 bbs 115028 (S45035) Kunitz trypsin inhibitor KTil [soybeans, Peptide, 203 aa] [Glycine max] Seq. No. 7130 8127 1.R1040 Contig ID leu701149923.h1 5'-most EST BLASTX Method q4007792 NCBI GI BLAST score 246 9.0e-21 E value Match length 65 71 % identity (AL034463) Xenopus 14s cohesin smc1 subunit homolog NCBI Description

[Schizosaccharomyces pombe]

5'-most EST

```
Seq. No.
                    7131
Contig ID
                    8129 1.R1040
5'-most EST
                    g5676949
Method
                    BLASTN
NCBI GI
                    g303838
BLAST score
                    72
E value
                    7.0e-32
Match length
                    208
% identity
                    84
NCBI Description
                    Rice mRNA for 40S subunit ribosomal protein, complete cds
Seq. No.
                    7132
                    8129 2.R1040
Contig ID
5'-most EST
                    jC-gmf102220076f03d1
Seq. No.
                    7133
                    8129 3.R1040
Contig ID
5'-most EST
                    jC-gmst02400007d04d1
Method
                    BLASTX
NCBI GI
                    g2129648
BLAST score
                    160
E value
                    2.0e-10
Match length
                    189
% identity
                    34
NCBI Description
                    MYB-related protein 33,3K - Arabidopsis thaliana
                    >gi_1263095_emb_CAA90809 (Z54136) MYB-related protein
                    [Arabidopsis thaliana]
                    7134
Seq. No.
Contig ID
                    8129 4.R1040
5'-most EST
                    LIB3040-034-Q1-E1-F5
Method
                    BLASTX
NCBI GI
                    q548852
BLAST score
                    368
E value
                    3.0e-35
Match length
                    82
% identity
                    40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
NCBI Description
                    subunit ribosomal protein [Oryza sativa]
Seq. No.
                    7135
                    8131 1.R1040
Contig ID
5'-most EST
                    9440\overline{5}656
Seq. No.
                    7136
                    8136 1.R1040
Contig ID
5'-most EST
                    ssr700557227.hl
Seq. No.
                    7137
                    8136 2.R1040
Contig ID
5'-most EST
                    kl1701213934.h1
                    7138
Seq. No.
Contig ID
                    8136 3.R1040
```

xpa700792412.h1

```
7139
Seq. No.
Contig ID
                   8139 1.R1040
5'-most EST
                   LIB3051-030-Q1-K1-D10
Seq. No.
                   7140
                   8147 1.R1040
Contig ID
                   rrt700645919.hl
5'-most EST
                   7141
Seq. No.
                   8150 1.R1040
Contig ID
5'-most EST
                   trc700565861.hl
                   7142
Seq. No.
Contig ID
                   8151 1.R1040
5'-most EST
                   ssr700556967.h1
Method
                   BLASTX
NCBI GI
                   g3150402
BLAST score
                   1329
                   1.0e-147
E value
Match length
                   339
% identity
                   (AC004165) putative malonyl-CoA:Acyl carrier protein
NCBI Description
                   transacylase [Arabidopsis thaliana]
Seq. No.
                   7143
Contig ID
                   8151 2.R1040
                   qsv7\overline{0}1052805.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2347187
BLAST score
                   239
E value
                   6.0e-20
                   90
Match length
% identity
                   (AC002338) putative malonyl-CoA:Acyl carrier protein
NCBI Description
                   transacylase, 3' partial [Arabidopsis thaliana]
Seq. No.
                   7144
                   8151 3.R1040
Contig ID
                   trc700567853.h1
5'-most EST
                   7145
Seq. No.
Contig ID
                   8153 1.R1040
5'-most EST
                   LIB3087-010-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g1350720
BLAST score
                   456
E value
                   2.0e-45
Match length
                   111
% identity
                   77
NCBI Description
                   60S RIBOSOMAL PROTEIN L32
Seq. No.
                   7146
                   8154 2.R1040
Contig ID
5'-most EST
                   LIB3039-045-Q1-E1-C5
```

7147

Seq. No.

NCBI GI

```
8158 1.R1040
Contig ID
5'-most EST
                   LIB3040-030-Q1-E1-E5
Method
                   BLASTX
NCBI GI
                   q122003
BLAST score
                   404
                   4.0e-39
E value
Match length
                   115
% identity
                   72
NCBI Description
                   HISTONE H2A >gi_82089_pir__JQ1182 histone H2A.1 - tomato
                   7148
Seq. No.
Contig ID
                   8173 1.R1040
                   LIB3\overline{0}39-021-Q1-E1-H8
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2262151
                   374
BLAST score
                   2.0e-35
E value
                   198
Match length
% identity
                   46
                   (AC002330) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   7149
Seq. No.
                   8173 2.R1040
Contig ID
                   bth700846442.h1
5'-most EST
                   7150
Seq. No.
Contig ID
                   8178 1.R1040
5'-most EST
                   jex700909126.h1
Seq. No.
                   7151
                   8189 1.R1040
Contig ID
5'-most EST
                   LIB3039-044-Q1-E1-F4
Method
                   BLASTX
NCBI GI
                   q4314388
BLAST score
                   475
E value
                   1.0e-47
Match length
                   129
% identity
NCBI Description
                   (AC006232) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   8189 2.R1040
Contig. ID
5'-most EST
                   sat701006251.h2
Method
                   BLASTX
NCBI GI
                   q4314388
BLAST score
                   394
E value
                   3.0e - 38
Match length
                   117
% identity
NCBI Description
                   (AC006232) hypothetical protein [Arabidopsis thaliana]
                   7153
Seq. No.
                   8198 1.R1040
Contig ID
5'-most EST
                   LIB3039-044-Q1-E1-G6
Method
                   BLASTX
```

g2281094

```
508
BLAST score
E value
                   2.0e-51
Match length
                   132
% identity
                   71
NCBI Description
                   (AC002333) molybdenum cofactor biosynthesis protein E
                   isolog [Arabidopsis thaliana] >gi_4469121_emb_CAB38428_
                   (AJ133519) molybdopterin synthase large subunit
                   [Arabidopsis thaliana]
Seq. No.
                   7154
Contig ID
                   8204 1.R1040
                   kmv700738093.h1
5'-most EST
Method
                   BLASTX
                   g2339980
NCBI GI
BLAST score
                   380
E value
                   2.0e-36
Match length
                   164
                   55
% identity
                   (Y11337) RGA2 protein [Arabidopsis thaliana]
NCBI Description
                   7155
Seq. No.
                   8204_2.R1040
Contig ID
5'-most EST
                   jex700904794.h1
                   BLASTX
Method
                   g2339978
NCBI GI
BLAST score
                   247
E value
                   5.0e-21
Match length
                   100
                   60
% identity
NCBI Description
                   (Y11336) RGA1 protein [Arabidopsis thaliana]
Seq. No.
                   7156
Contig ID
                   8217 1.R1040
5'-most EST
                   LIB3039-044-Q1-E1-D10
                   7157
Seq. No.
                   8223 1.R1040
Contig ID
5'-most EST
                   pmv700893311.h1
Method
                   BLASTX
NCBI GI
                   q3421123
BLAST score
                   1060
E value
                   1.0e-116
Match length
                   227
% identity
NCBI Description
                   (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis
                   thaliana]
Seq. No.
                   7158
Contig ID
                   8226 1.R1040
5'-most EST
                   epx701109794.hl
Method
                   BLASTX
NCBI GI
                   q2832686
BLAST score
                   240
E value
                   6.0e-20
Match length
                   138
% identity
NCBI Description
                   (AL021712) putative protein [Arabidopsis thaliana]
```

7159 Seq. No. 8226 2.R1040 Contig ID 5'-most EST uC-gmflminsoy053e06b1 Seq. No. 7160 8236 1.R1040 Contig ID LIB3039-043-Q1-E1-H8 5'-most EST Method BLASTX NCBI GI g3122861 BLAST score 157 3.0e-10 E value Match length 114 34 % identity D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PGDH) >gi 2649798 NCBI Description (AE001048) phosphoglycerate dehydrogenase (serA) [Archaeoglobus fulgidus] 7161 Seq. No. 8240_1.R1040 Contig ID 5'-most EST LIB3039-041-Q1-E1-E11 Method BLASTX g299370 NCBI GI BLAST score 216 E value 4.0e-17 Match length 118 % identity 42 NCBI Description (S58039) zeta-crystallin/quinone reductase [human, liver, Peptide, 328 aa] [Homo sapiens] >gi 4503067 ref NP 001880.1 pCRYZ crystallin, zeta (quinone reductase) 7162 Seq. No. 8245_1.R1040 Contig ID LIB3039-008-Q1-E1-A7 5'-most EST Method BLASTX g3108209 NCBI GI BLAST score 809 1.0e-86 E value 172 Match length 85 % identity NCBI Description (AF028809) eukaryotic cap-binding protein [Arabidopsis thaliana] Seq. No. 7163 Contig ID 8245 2.R1040 5'-most EST g5058009 Method BLASTX g3108209 NCBI GI BLAST score 298 6.0e-27 E value Match length 62 % identity 85 (AF028809) eukaryotic cap-binding protein [Arabidopsis NCBI Description thaliana]

7164

Seq. No.

E value

6.0e-24

```
8246 1.R1040
Contiq ID
5'-most EST
                   LIB3040-008-01-E1-A8
Seq. No.
                   7165
Contig ID
                   8249 1.R1040
5'-most EST
                   LIB3039-043-Q1-E1-G12
Method
                   BLASTX
NCBI GI
                   q3309170
BLAST score
                   269
E value ·
                   3.0e-23
Match length
                   130
                   45
% identity
NCBI Description
                   (AF071314) COP9 complex subunit 4 [Mus musculus]
Seq. No.
                   7166
                   8249 2.R1040
Contig ID
5'-most EST
                   LIB3109-005-Q1-K1-H3
                   BLASTX
Method
NCBI GI
                   q3309170
BLAST score
                   721
                   4.0e-76
E value
Match length
                   284
% identity
                   53
NCBI Description
                   (AF071314) COP9 complex subunit 4 [Mus musculus]
Seq. No.
                   7167
                   8258 1.R1040
Contig ID
5'-most EST
                   LIB3039-043-Q1-E1-D6
Method
                   BLASTX
NCBI GI
                   g4432835
BLAST score
                   406
E value
                   3.0e-39
Match length
                   141
                   52
% identity
NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   7168
Contig ID
                   8263 1.R1040
5'-most EST
                   zsq701127333.h1
Method
                   BLASTX
NCBI GI
                   g232031
BLAST score
                   589
E value
                   1.0e-60
Match length
                   224
% identity
                   54
                  ELONGATION FACTOR 1 BETA' >gi_322851_pir__$29224
NCBI Description
                   translation elongation factor eEF-1 beta chain - rice
                   >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                   [Oryza sativa]
                   7169
Seq. No.
                   8263 3.R1040
Contig ID
                   smc700749004.h1
5'-most EST
Method
                  BLASTX
                   g232031
NCBI GI
BLAST score
                   273
```

```
Match length
                  . 76
                  66
% identity
                  ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224
NCBI Description
                  translation elongation factor eEF-1 beta chain - rice
                  >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta'
                  [Oryza sativa]
                  7170
Seq. No.
                  8263 4.R1040
Contig ID
                  jC-gmro02800025g06d1
5'-most EST
                  BLASTN
Method
                  g398607
NCBI GI
BLAST score
                  35
                  3.0e-10
E value
                  59
Match length
                  90
% identity
NCBI Description A.thaliana mRNA for elongation factor 1 beta
                  7171
Seq. No.
                  8269 1.R1040
Contig ID
5'-most EST
                  eep700867383.hl
Method
                  BLASTX
NCBI GI
                  g2559012
BLAST score
                  1412
E value
                  1.0e-157
Match length
                  373
% identity
                  73
NCBI Description
                   (AF026293) chaperonin containing t-complex polypeptide 1,
                  beta subunit; CCT-beta [Homo sapiens] >gi 4090929
                   (AF026166) chaperonin-containing TCP-1 beta subunit homolog
                   [Homo sapiens]
                  7172
Seq. No.
                  8278_1.R1040
Contig ID
                  ncj7\overline{0}0979022.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3618214
BLAST score
                  215
                  8.0e-17
E value
Match length
                  189
                  31
% identity
                   (AL031579) dihydrofolate reductase [Schizosaccharomyces
NCBI Description
                  pombe]
                  7173
Seq. No.
                  8287 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy113h05b1
Method
                  BLASTX
                  g2129742
NCBI GI
                  295
BLAST score
E value
                  1.0e-26
                  75
Match length
% identity
                  73
NCBI Description
                  stress-induced protein OZI1 precursor - Arabidopsis
                  thaliana >gi 790583 (U20347) mRNA corresponding to this
                  gene accumulates in response to ozone stress and pathogen
                   (bacterial) infection; putative pathogenesis-related
```

protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No. 717

Contig ID 8287_2.R1040 5'-most EST gsv701050369.h1

Method BLASTX
NCBI GI g2129742
BLAST score 302
E value 2.0e-27
Match length 75
% identity 73

NCBI Description stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi 790583 (U20347) mRNA corresponding to this

gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No

definition line found [Arabidopsis thaliana]

Seq. No. 7175

Contig ID 8287_3.R1040

5'-most EST LIB3040-050-Q1-E1-F7

Method BLASTX
NCBI GI g2129742
BLAST score 295
E value 1.0e-26
Match length 75
% identity 72

NCBI Description stress-induced protein OZI1 precursor - Arabidopsis

thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No

definition line found [Arabidopsis thaliana]

Seq. No. 7176

Contig ID 8287 4.R1040

5'-most EST uC-gmflminsoy035e03b1

Method BLASTX
NCBI GI g2129742
BLAST score 299
E value 3.0e-27
Match length 75
% identity 73

NCBI Description stress-induced protein OZI1 precursor - Arabidopsis

thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi 2252869 (AF013294) No

definition line found [Arabidopsis thaliana]

Seq. No. 7177

Contig ID 8287_5.R1040 5'-most EST g4313658 Method BLASTX NCBI GI g2129742 BLAST score 283 E value 4.0e-25 Match length 75 69 % identity NCBI Description stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi 790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No definition line found [Arabidopsis thaliana] Seq. No. 7178 Contig ID 8289 1.R1040 $leu7\overline{0}1154286.h1$ 5'-most EST 7179 Seq. No. 8292 1.R1040 Contig ID leu701151247.h1 5'-most EST Method BLASTX NCBI GI g2529662 BLAST score 534 E value 2.0e-54 Match length 108 94 % identity NCBI Description (AC002535) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana] >gi_3738278 (AC005309) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana] 7180 Seq. No. 8292 2.R1040 Contig ID 5'-most EST LIB3072-008-Q1-E1-F11 Method BLASTX NCBI GI g2529662 BLAST score 533 E value 2.0e-54 Match length 108 % identity NCBI Description (AC002535) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana] >gi_3738278 (AC005309) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana] 7181 Seq. No. 8292 3.R1040 Contig ID LIB3040-057-Q1-E1-G6 5'-most EST Method BLASTX NCBI GI q2529662 BLAST score 405 E value 1.0e-39 Match length 87 % identity (AC002535) putative small nuclear ribonucleoprotein, Sm D2 NCBI Description [Arabidopsis thaliana] >qi 3738278 (AC005309) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis

Seq. No. 7182

thaliana]

Contig ID

5'-most EST

```
8294 1.R1040
Contig ID
5'-most EST
                  LIB3039-043-Q1-E1-A4
Method
                  BLASTX
NCBI GI
                  q3759184
BLAST score
                  165
E value
                  1.0e-11
Match length
                  66
                  47
% identity
                  (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
                  7183
Seq. No.
                  8295 1.R1040
Contig ID
5'-most EST
                  leu701155106.h1
                  BLASTX
Method
NCBI GI
                  q232024
BLAST score
                  163
                  2.0e-10
E value
                  247
Match length
                  34
% identity
                  PROTEIN E6 >gi 421806 pir A46130 fiber protein - upland
NCBI Description
                  cotton >gi 2129498 pir__S65061 fiber protein E6 (clone
                  CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site
                  is putative; putative [Gossypium hirsutum] >gi_1000084
                  (U30505) E6 [Gossypium hirsutum]
Seq. No.
                  7184
Contig ID
                  8295 2.R1040
5'-most EST
                  jC-gmro02910020g09a1
                  7185
Seq. No.
                  8300 1.R1040
Contig ID
5'-most EST
                  LIB3039-043-Q1-E1-B2
                  BLASTX
Method
                  g4097547
NCBI GI
BLAST score
                  171
E value
                  8.0e-12
Match length
                  77
% identity
                  35
                  (U64906) ATFP3 [Arabidopsis thaliana]
NCBI Description
                  7186
Seq. No.
                  8301 1.R1040
Contig ID
                  LIB3039-043-Q1-E1-B4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3367593
BLAST score
                  312
E value
                  3.0e-28
Match length
                  129
% identity
                  45
                  (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3805841_emb_CAA21461_ (AL031986) putative protein
                  [Arabidopsis thaliana]
                  7187
Seq. No.
```

8304 1.R1040

LIB3039-042-Q1-E1-G5

5'-most EST

```
Seq. No.
                   7188
Contig ID
                   8309 1.R1040
5'-most EST
                   g5677411
                   7189
Seq. No.
                   8318 1.R1040
Contig ID
5'-most EST
                   LIB3049-043-Q1-E1-C1
Method
                   BLASTX
NCBI GI
                   q1707074
BLAST score
                   253
E value
                   2.0e-21
Match length
                   209
                   34
% identity
                   (U80450) M01E11.2 [Caenorhabditis elegans]
NCBI Description
Seq. No.
                   7190
                   8325 1.R1040
Contig ID
5'-most EST
                   LIB3039-021-Q1-E1-H6
Method
                   BLASTX
NCBI GI
                   g1169782
BLAST score
                   437
E value
                   4.0e-43
Match length
                   149
% identity
                   63
NCBI Description
                   FUSCA PROTEIN FUS6 >gi 432446 (L26498) FUS6 [Arabidopsis
                   thaliana]
                   7191
Seq. No.
                   8331 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910029g06a1
Seq. No.
                   7192
                   8331 2.R1040
Contig ID
5'-most EST
                   g5607075
Seq. No.
                   7193
Contig ID
                   8331 3.R1040
5'-most EST
                   vzy700753608.hl
                   7194
Seq. No.
Contig ID
                   8331 4.R1040
5'-most EST
                   LIB3039-042-Q1-E1-C7
Seq. No.
                   7195
Contig ID
                   8340 1.R1040
5'-most EST
                   pmv700889160.hl
Method
                   BLASTX
NCBI GI
                   q2832642
BLAST score
                   407
E value
                   5.0e-39
                   463
Match length
% identity
NCBI Description
                   (AL021710) putative protein [Arabidopsis thaliana]
                   7196
Seq. No.
                   8344 1.R1040
Contig ID
```

LIB3107-031-Q1-K1-C4

Seq. No. Contig ID

```
Method
                   BLASTX
NCBI GI
                   g2982283
BLAST score
                   382
E value
                   2.0e-36
Match length
                   148
% identity
                   51
                   (AF051226) PREG-like protein [Picea mariana]
NCBI Description
Seq. No.
                   7197
                   8344 2.R1040
Contig ID
5'-most EST
                   LIB3107-072-Q1-K1-C8
                   7198
Seq. No.
                   8349 1.R1040
Contig ID
5'-most EST
                   LIB3170-011-Q1-J1-E1
Method
                   BLASTX
NCBI GI
                   q459009
BLAST score
                   236
E value
                   1.0e-19
Match length
                   79 -
% identity
                   54
NCBI Description
                   (U00037) similar to multifunctional aminoacyl-tRNA
                   synthetase, especially to the prolyl-tRNA synthetase region
                   [Caenorhabditis elegans]
                   7199
Seq. No.
Contig ID
                   8349 2.R1040
5'-most EST
                   LIB3072-025-Q1-E1-A6
Method
                   BLASTX
                   g459009
NCBI GI
BLAST score
                   211
E value
                   8.0e-17
                   80
Match length
                   49
% identity
NCBI Description
                   (U00037) similar to multifunctional aminoacyl-tRNA
                   synthetase, especially to the prolyl-tRNA synthetase region
                   [Caenorhabditis elegans]
                   7200
Seq. No.
                   8349 3.R1040
Contig ID
5'-most EST
                   taw700657102.h1
                   7201
Seq. No.
                   8353 1.R1040
Contig ID
                   asn7\overline{0}1131479.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2911060
BLAST score
                   154
E value
                   5.0e-10
Match length
                   88
                   29
% identity
NCBI Description
                   (AL021961) putative protein [Arabidopsis thaliana]
                   >gi_3297826_emb_CAA19884.1_ (AL031032) putative protein
                   [Arabidopsis thaliana]
```

8361_1.R1040

5'-most EST

```
5'-most EST
                  LIB3039-041-Q1-E1-F12
Seq. No.
                  7203
Contig ID
                  8370 1.R1040
5'-most EST
                  ncj700981540.hl
Method
                  BLASTX
NCBI GI
                  g3335337
BLAST score
                  446
E value
                  5.0e-44
Match length
                  119
% identity
NCBI Description
                   (AC004512) Similar to acyl carrier protein, mitochondrial
                  precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD
                  subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs
                  gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330
                  come from this gene
Seq. No.
                  7204
Contig ID
                  8370 2.R1040
5'-most EST
                  LIB3039-033-Q1-E1-E11
Method
                  BLASTX
NCBI GI
                  q3335337
BLAST score
                  327
E value
                  2.0e-30
Match length
                  115
% identity
NCBI Description
                   (AC004512) Similar to acyl carrier protein, mitochondrial
                  precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD
                  subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs
                  gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330
                  come from this gene
                  7205
Seq. No.
Contig ID
                  8376 1.R1040
5'-most EST
                  LIB3049-018-Q1-E1-D1
Method
                  BLASTX
NCBI GI
                  g3135265
BLAST score
                  354
E value
                  3.0e-33
Match length
                  101
% identity
                  68
                  (AC003058) unknown protein [Arabidopsis thaliana]
NCBI Description
                                                           â.
                  7206
Seq. No.
                  8376 2.R1040
Contig ID
5'-most EST
                  LIB3109-034-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q3135265
BLAST score
                  441
                  1.0e-43
E value
Match length
                  101
% identity
                  81
NCBI Description
                  (AC003058) unknown protein [Arabidopsis thaliana]
                  7207
Seq. No.
                  8378 1.R1040
Contig ID
```

LIB3109-006-Q1-K1-B12

```
Method
                   BLASTX
NCBI GI
                   g746510
BLAST score
                   454
E value
                   1.0e-44
Match length
                   213
% identity
                   43
                   (U23517) similar to ubiquitin conjugating enzyme
NCBI Description
                   [Caenorhabditis elegans]
                   7208
Seq. No.
                   8378 3.R1040
Contig ID
                   LIB3072-010-Q1-E1-D9 ·
5'-most EST
Method
                   BLASTX
NCBI GI
                   g746510
BLAST score
                   325
E value
                   3.0e - 30
                   97
Match length
% identity
                   57
NCBI Description
                   (U23517) similar to ubiquitin conjugating enzyme
                   [Caenorhabditis elegans]
                   7209
Seq. No.
                   8378 5.R1040
Contig ID
5'-most EST
                   LIB3138-007-Q1-N1-A10
                   7210
Seq. No.
Contig ID
                   8378 6.R1040
5'-most EST
                   zzp700831760.h1
Method
                   BLASTX
NCBI GI
                   g746510
BLAST score
                   171
                   2.0e-12
E value
Match length
                   44
                   64
% identity
                   (U23517) similar to ubiquitin conjugating enzyme
NCBI Description
                   [Caenorhabditis elegans]
Seq. No.
                   7211
                   8387 1.R1040
Contig ID
5'-most EST
                   LIB3039-041-Q1-E1-D6
Method
                   BLASTX
NCBI GI
                   q3461813
BLAST score
                   382
E value
                   2.0e-40
Match length
                   125
% identity
NCBI Description
                   (AC004138) putative sucrose/H+ symporter [Arabidopsis
                   thaliana]
                   7212
Seq. No.
Contig ID
                   8397 1.R1040
5'-most EST
                   LIB3106-020-Q1-K1-B1
Seq. No.
                   7213
Contig ID
                   8408 1.R1040
```

 $ncj7\overline{0}0984619.h1$

BLASTX

5'-most EST Method

```
NCBI GI
                   g2586127
BLAST score
                   309
E value
                   4.0e-28
Match length
                   124
% identity
                   52
                   (U89510) b-keto acyl reductase [Hordeum vulgare]
NCBI Description
Seq. No.
                   8408 2.R1040
Contig ID
5'-most EST
                   uxk7\overline{0}0668489.h1
                   7215
Seq. No.
Contig ID
                   8409 1.R1040
                   smw700646216.h1
5'-most EST
                   7216
Seq. No.
                   8413 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810041a04a1
                   7217
Seq. No.
                   8413 2.R1040
Contig ID
5'-most EST
                   LIB3039-018-Q1-E1-H4
                  7218
Seq. No.
Contig ID
                   8417 1.R1040
                   LIB3074-029-Q1-K1-A6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1173456
BLAST score
                   328
E value
                   3.0e - 30
Match length
                   97
                   58
% identity
                   SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN
NCBI Description
                   D3) (SM-D3) >gi 600750 (U15009) Sm D3 [Homo sapiens]
Seq. No.
                   7219
                   8417 2.R1040
Contig ID
                   LIB3170-062-Q1-J1-A1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2708715
BLAST score
                   142
E value
                   1.0e-08
Match length
                   46
% identity
                   (AF038598) small nuclear ribonucleoprotein Sm D3
NCBI Description
                   [Drosophila melanogaster]
                   7220
Seq. No.
                   8422 1.R1040
Contig ID
5'-most EST
                   trc700562809.h1
Method
                  BLASTX
NCBI GI
                   g1877026
BLAST score
                   202
E value
                   1.0e-20
Match length
                  86
% identity
                   55
NCBI Description (D78336) ribosomal protein S19 [Oryza sativa]
```

Contig ID

```
7221
Seq. No.
Contig ID
                   8427 1.R1040
5'-most EST
                   LIB3094-078-Q1-K1-A11
                   BLASTX
Method
                   g4508069
NCBI GI
BLAST score
                   230
E value
                   7.0e-19
Match length
                   161
% identity
                   35
NCBI Description
                   (AC005882) 12246 [Arabidopsis thaliana]
                   7222
Seq. No.
                   8429 1.R1040
Contig ID
5'-most EST
                   leu701145719.hl
Method
                   BLASTX
                   g730456
NCBI GI
BLAST score
                   615
E value
                   7.0e-64
Match length
                   140
% identity
                   80
                   40S RIBOSOMAL PROTEIN S19
NCBI Description
                   7223
Seq. No.
Contig ID
                   8438 1.R1040
5'-most EST
                   wvk700681268.hl
Method
                   BLASTX
NCBI GI
                   g2493694
BLAST score
                   299
E value
                   6.0e-27
Match length
                   119
% identity
                   53
                   PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII
NCBI Description
                   6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II
                   protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein
                   of photosystem II [Spinacia oleracea]
Seq. No.
                   7224
                   8438 2.R1040
Contig ID
5'-most EST
                   leu701147974.h1
                   7225
Seq. No.
                   8438 3.R1040
Contig ID
5'-most EST
                   LIB3073-017-Q1-K1-G7
Method
                   BLASTX
NCBI GI
                   q2493694
BLAST score
                   214
E value
                   4.0e-17
Match length
                   116
% identity
NCBI Description
                   PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII
                   6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein
                   of photosystem II [Spinacia oleracea]
                   7226
Seq. No.
```

8441 1.R1040

5'-most EST

Method

```
5'-most EST
                  vwf700675988.hl
Seq. No.
                  7227
Contig ID
                  8446 1.R1040
5'-most EST
                  fC-gmro700866877d3
Method
                  BLASTX
NCBI GI
                  q1169533
BLAST score
                  155
E value
                   3.0e-10
Match length
                  37
% identity >
                  86
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
                  >gi_515827_emb_CAA56645_ (X80474) enolase [Neocallimastix
                  frontalis]
                  7228
Seq. No.
Contig ID
                  8464 1.R1040
                  LIB3049-034-Q1-E1-E11
5'-most EST
Method
                  BLASTN
                  q3927915
NCBI GI
BLAST score
                  135
E value
                  1.0e-69
Match length ,
                  311
% identity
                  86
NCBI Description
                  Fagus sylvatica mRNA for glycine-rich protein
                  7229
Seq. No.
                  8464 2.R1040
Contig ID
5'-most EST
                  uaw700663386.h1
Method
                  BLASTX
                  g1076626
NCBI GI
BLAST score
                  498
                  2.0e-50
E value
Match length
                  92
% identity
NCBI Description
                  glycine rich protein - common tobacco
                  >gi_790473_emb_CAA58702_ (X83731) soluble, glycine rich
                  protein [Nicotiana tabacum]
                  7230
Seq. No.
Contig ID
                  8464 3.R1040
5'-most EST
                  zpv700760105.hl
                  BLASTX
Method
NCBI GI
                  q1076626
BLAST score
                  166
E value
                  5.0e-16
Match length
                  46
% identity
                  glycine rich protein - common tobacco
NCBI Description
                  >gi_790473_emb_CAA58702_ (X83731) soluble, glycine rich
                  protein [Nicotiana tabacum]
Seq. No.
Contig ID
                  8464 4.R1040
```

awf700836556.hl

BLASTN

NCBI GI

BLAST score

```
q3927915
NCBI GI
BLAST score
                   61
E value
                   7.0e-26
Match length
                   133
                   86
% identity
                   Fagus sylvatica mRNA for glycine-rich protein
NCBI Description
Seq. No.
                   7232
Contig ID
                   8465 1.R1040
5'-most EST
                   LIB3039-039-Q1-E1-G9
Method
                   BLASTN
NCBI GI
                   g3819163
BLAST score
                   283
E value
                   1.0e-158
Match length
                   335
% identity
                   96
NCBI Description
                   Glycine max cctd gene
Seq. No.
                   7233
                   8465 2.R1040
Contig ID
5'-most EST
                   zhf700956825.h1
Method
                   BLASTN
NCBI GI
                   q3819163
BLAST score
                   146
E value
                   2.0e-76
Match length
                   319
% identity
                   93
NCBI Description
                   Glycine max cctd gene
Seq. No.
Contig ID
                   8468 1.R1040
5'-most EST
                   uC-gmropic023h03b1
Method
                   BLASTX
NCBI GI
                   q3935167
BLAST score
                   533
E value
                   3.0e-54
Match length
                   123
% identity
NCBI Description
                   (AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.
                   7235
                   8468 2.R1040
Contig ID
5'-most EST
                   wrg700787076.h2
Method
                   BLASTX
NCBI GI
                   g3935167
BLAST score
                   520
E value
                   7.0e-53
Match length
                   123
% identity
                   83
                   (AC004557) F17L21.10 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7236
                   8473 1.R1040
Contig ID
                   bth700845213.h1
5'-most EST
Method
                   BLASTX
```

g2979550

```
E value
                   6.0e-43
Match length
                   173
% identity
                   50
NCBI Description
                   (AC003680) putative 7-ethoxycoumarin O-deethylase
                   [Arabidopsis thaliana]
Seq. No.
                   7237
Contig ID
                   8475 1.R1040
5'-most EST
                   LIB3039-040-Q1-E1-A11
Method
                   BLASTX
NCBI GI
                   q3687250
BLAST score
                   361
E value
                   6.0e-34
Match length
                   241
% identity
                   38
NCBI Description
                   (AC005169) putative arginine n-methyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                   7238
                   8476 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910027d07a1
Method
                   BLASTX
NCBI GI
                   q4056503
BLAST score
                   180
E value
                   6.0e-13 ·
Match length
                   36
% identity
NCBI Description
                   (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                   8476 2.R1040
Contig ID
5'-most EST
                   LIB3049-052-Q1-E1-G5
Method
                   BLASTX
NCBI GI
                   g4056488
BLAST score
                   324
E value
                   2.0e-46
Match length
                   199
% identity
NCBI Description
                   (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                   7240
                   8476 3.R1040
Contig ID
5'-most EST
                   LIB3106-031-Q1-K1-A11
Seq. No.
                   7241
Contig ID
                   8476 4.R1040
5'-most EST
                   eep700865621.hl
Method
                   BLASTX
NCBI GI
                   q730826
BLAST score
                   218
E value
                   1.0e-17
Match length
                   97
                   31
% identity
NCBI Description
                  SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING
```

[Homo sapiens]

FACTOR SRP75) >gi_1082713_pir__A48133 pre-mRNA splicing SRp75 - human >gi_307438 (L14076) pre-mRNA splicing factor

E value

5.0e-34

```
7242
Seq. No.
                   8476 5.R1040
Contig ID
5'-most EST
                   uaw700666680.hl
Method
                   BLASTX
                   g4056503
NCBI GI
BLAST score
                   180
                   3.0e-13
E value
Match length
                   36
                   92
% identity
NCBI Description
                   (AC005896) unknown protein [Arabidopsis thaliana]
                   7243
Seq. No.
                   8476 8.R1040
Contig ID
5'-most EST
                   gsv701054710.hl
                   7244
Seq. No.
                   8476 11.R1040
Contig ID
                   hyd700727629.h1
5'-most EST
Method
                   BLASTX
                   g4056488
NCBI GI
BLAST score
                   187
E value
                   1.0e-28
Match length
                   96
% identity
                   65
NCBI Description
                   (AC005896) unknown protein [Arabidopsis thaliana]
                   7245
Seq. No.
                   8483 1.R1040
Contig ID
5'-most EST
                   LIB3051-051-Q1-K1-F9
Seq. No.
Contig ID
                   8483 2.R1040
5'-most EST
                   awf700842960.hl
Seq. No.
                   7247
Contig ID
                   8483 3.R1040
5'-most EST
                   uC-gmrominsoy204g02b1
                   7248
Seq. No.
Contig ID
                   8487 1.R1040
5'-most EST
                   LIB3039-039-Q1-E1-G5
Method
                   BLASTX
NCBI GI
                   g2809246
BLAST score
                   246
E value
                   5.0e-21
Match length
                   78
% identity
NCBI Description
                   (AC002560) F2401.15 [Arabidopsis thaliana]
                   7249
Seq. No.
Contig ID
                   8490 1.R1040
                   LIB3039-039-Q1-E1-F2
5'-most EST
Method
                   BLASTX
                   g1065515
NCBI GI
BLAST score
                   359
```

5'-most EST

```
154
 Match length
                     47
 % identity
                     (U40420) weak similarity to procollagen alpha chain 1(V)
 NCBI Description
                     chain [Caenorhabditis elegans]
                     7250
 Seq. No.
                     8492 1.R1040
 Contig ID
 5'-most EST
                     leu7\overline{0}1144444.h1
 Method
                     BLASTX
 NCBI GI
                     g2351374
 BLAST score
                     533
                     2.0e-54
 E value
 Match length
                     111
                     92
 % identity
 NCBI Description
                     (U54560) putative 26S proteasome subunit athMOV34
                     [Arabidopsis thaliana]
 Seq. No.
                     7251
                     8493 1.R1040
 Contig ID
 5'-most EST
                     leu7\overline{0}1149723.h1
 Method
                     BLASTX
                     g3810594
 NCBI GI
 BLAST score
                     456
                     2.0e-45
 E value
 Match length
                     123
 % identity
                     (ACO05398) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                     7252
 Seq. No.
                     8494 1.R1040
 Contig ID
 5'-most EST
                     LIB3039-039-Q1-E1-E4
 Method
                     BLASTX
 NCBI GI
                     g2702274
 BLAST score
                     362
 E value
                     2.0e-34
 Match length
                     103
 % identity
 NCBI Description
                     (AC003033) unknown protein [Arabidopsis thaliana]
                     7253
 Seq. No.
 Contig ID
                     8497 1.R1040
 5'-most EST
                    LIB3039-039-Q1-E1-F1
 Method
                    BLASTX
 NCBI GI
                     g2894596
BLAST score
                     639
 E value
                     1.0e-66
 Match length
                     187.
 % identity
                     67
 NCBI Description
                     (AL021889) putative protein [Arabidopsis thaliana]
                     7254
 Seq. No.
                     8497 2.R1040
 Contig ID
 5'-most EST
                    trc700562114.h1
                    7255
 Seq. No.
                    8500 1.R1040
 Contig ID
```

 $LIB3\overline{0}51-018-Q1-E1-H7$

Seq. No.

```
7256
Seq. No.
                  8500 2.R1040
Contig ID
5'-most EST
                  hrw701063012.hl
                  7257
Seq. No.
                  8506 1.R1040
Contig ID
                  pcp700993831.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4220474
                  240
BLAST score
                  4.0e-20
E value
Match length
                  84
% identity
                   (AC006069) putative myosin heavy chain [Arabidopsis
NCBI Description
                  thaliana]
                  7258
Seq. No.
Contig ID
                  8511 1.R1040
5'-most EST
                  LIB3039-039-Q1-E1-B11
                  BLASTX
Method
NCBI GI
                  g3913794
BLAST score
                  665
E value
                  1.0e-69
Match length
                  166
                  73
% identity
NCBI Description
                  GLUTATHIONE PEROXIDASE 1 >gi 2326453 emb CAA74775 (Y14429)
                  glutathione peroxidase [Helianthus annuus]
                  7259
Seq. No.
                  8511 2.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy045c07b1
Method
                  BLASTX
NCBI GI
                  g2760606
BLAST score
                  162
E value
                  6.0e-28
Match length
                  93
% identity
                  80
NCBI Description
                  (AB001568) phospholipid hydroperoxide glutathione
                  peroxidase-like protein [Arabidopsis thaliana] >gi 3004869
                  (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis
                  thaliana] >gi 4539451 emb CAB39931.1 (AL049500)
                  phospholipid hydroperoxide glutathione peroxidase
                  [Arabidopsis thaliana]
Seq. No.
                  7260
Contig ID
                  8517 1.R1040
5'-most EST
                  seb700651955.hl
Method
                  BLASTX
NCBI GI
                  g2431771
BLAST score
                  228
                  2.0e-18
E value
Match length
                  113
% identity
NCBI Description
                  (U62753) acidic ribosomal protein P2b [Zea mays]
```

Contig ID

```
8518 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy187d07b1
                   7262
Seq. No.
                   8520 1.R1040
Contig ID
                   leu7\overline{0}1154316.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1172977
BLAST score
                   766
E value
                   2.0e-81
Match length
                   171
                   86
% identity
                   60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                   ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                   8520 2.R1040
Contig ID
                   LIB3170-018-Q1-J1-A1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1172977
BLAST score
                   556
E value
                   4.0e-57
Match length
                   122
% identity
                   84
                   60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                   ribosomal protein L18 [Arabidopsis thaliana]
                   7264
Seq. No.
                   8521 1.R1040
Contig ID
5'-most EST
                   pxt700943611.hl
                   BLASTX
Method
NCBI GI
                   g2737973
BLAST score
                   590
E value
                   4.0e-61
Match length
                   156
% identity
                   (U83625) protein kinase ZmMEK1 [Zea mays]
NCBI Description
                   7265
Seq. No.
                   8524 1.R1040
Contig ID
                   LIB3040-058-Q1-E1-E4
5'-most EST
Method
                   BLASTX
                   g549732
NCBI GI
BLAST score
                   211
E value
                   1.0e-16
Match length
                   79
% identity
                   HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION
NCBI Description
                   >qi 481110 pir S37791 hypothetical protein YKL160w - yeast
                   (Saccharomyces cerevisiae) >gi 407488 emb CAA81494
                   (Z26877) unknown [Saccharomyces cerevisiae]
                   >gi_486279_emb_CAA82002_ (Z28160) ORF YKL160w
                   [Saccharomyces cerevisiae] >gi_1582545_prf__2118404F ORF
                   [Saccharomyces cerevisiae]
Seq. No.
                   7266
```

8546 1.R1040

NCBI GI

```
5'-most EST
                   LIB3074-024-Q1-E1-C12
Seq. No.
                   7267
                   8552 1.R1040
Contig ID
5'-most EST
                   LIB3039-038-Q1-E1-D7
                   7268
Seq. No.
Contig ID
                   8558 1.R1040
5'-most EST
                   LIB3039-038-Q1-E1-C7
                   7269
Seq. No.
Contig ID
                   8562 1.R1040
5'-most EST
                   LIB3094-046-Q1-K1-H11
Method
                   BLASTN
NCBI GI
                   a499066
BLAST score
                   488
E value
                   0.0e + 00
Match length
                   678
                   99
% identity
NCBI Description
                   G.max gmr1 gene
Seq. No.
                   7270
Contig ID
                   8565_1.R1040
5'-most EST
                   jC-gmro02910006c04a1
Seq. No.
Contig ID
                   8565 2.R1040
5'-most EST
                   gsv7\overline{0}1048378.h1
Seq. No.
Contig ID
                   8570 1.R1040
5'-most EST
                   taw700655350.hl
                   7273
Seq. No.
Contig ID
                   8579_1.R1040
5'-most EST
                   jC-gmst02400075g11d1
Method
                   BLASTX
NCBI GI
                   q2367418
BLAST score
                   489
E value
                   3.0e-49
Match length
                   140
% identity
NCBI Description
                   (AF000392) peptide transporter [Lotus japonicus]
                   7274
Seq. No.
Contig ID
                   8581 1.R1040
5'-most EST
                   LIB3039-037-Q1-E1-G7
                   7275
Seq. No.
                   8584 1.R1040
Contig ID
5'-most EST
                   qsv701050179.hl
                   7276
Seq. No.
                   8591 1.R1040
Contig ID
                   V4L-01-Q1-B1-C3
5'-most EST
Method
                   BLASTX
```

g3451075

% identity

```
BLAST score
                   1683
E value
                   0.0e+00
Match length
                   432
% identity
                   70
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                   7277
Contig ID
                   8594 1.R1040
5'-most EST
                   LIB3039-012-Q1-E1-D9
Method
                   BLASTX
NCBI GI
                   q2851506
BLAST score
                   323
E value
                   5.0e-30
Match length
                   82
% identity
                   70
NCBI Description
                   DYSKERIN (NUCLEOLAR PROTEIN NAP57)
                   >gi_2739325_emb_CAA84402_ (Z34922) NAP57 [Rattus
                   norvegicus]
Seq. No.
                   7278
                   8594 2.R1040
Contig ID
5'-most EST
                   LIB3051-034-Q1-K1-G7
Method
                   BLASTX
                   q2851506
NCBI GI
BLAST score
                   340
E value
                   5.0e-34
Match length
                   98
                   71
% identity
                   DYSKERIN (NUCLEOLAR PROTEIN NAP57)
NCBI Description
                   >gi_2739325_emb_CAA84402_ (Z34922) NAP57 [Rattus
                   norvegicus] ·
Seq. No.
                   7279
Contig ID
                   8617 1.R1040
5'-most EST
                   kl1701208274.h1
Seq. No.
                  .7280
Contig ID
                   8618 1.R1040
5'-most EST
                   LIB3049-024-01-E1-D10
Method
                   BLASTX
NCBI GI
                   q3176874
BLAST score
                   2036
E value
                   0.0e + 00
Match length
                   733
% identity
NCBI Description
                   (AF065639) cucumisin-like serine protease [Arabidopsis
                   thaliana]
                   7281
Seq. No.
                   8618 5.R1040
Contig ID
5'-most EST
                   ncj700978984.h1
Method
                   BLASTX
NCBI GI
                   q3176874
BLAST score
                   225
E value
                   1.0e-18
Match length
                   62
```

Seq. No.

```
(AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    7282
                    8620 1.R1040
Contig ID
5'-most EST
                    fC-gmse700752057a2
                    BLASTX
Method
NCBI GI
                    g1174470
BLAST score
                    820
                    9.0e-88
E value
Match length
                    264
% identity
                    58
                   OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
NCBI Description
                    (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A
                    integral membrane protein [Mus musculus]
Seq. No.
                    8620 2.R1040
Contig ID
5'-most EST
                    smc7\overline{0}0745470.h1
Seq. No.
                    7284
Contig ID
                    8630 1.R1040
5'-most EST
                    LIB3039-036-Q1-E1-F10
Method
                    BLASTX
NCBI GI
                    q2464915
BLAST score
                    473
                    1.0e-47
E value
                    111
Match length
% identity
NCBI Description
                    (Z99708) transcription initiation factor like protein
                    [Arabidopsis thaliana]
Seq. No.
                    8632 1.R1040
Contig ID
5'-most EST
                    LIB3040-010-Q1-E1-B9
                    7286
Seq. No.
                    8632 3.R1040
Contig ID
5'-most EST
                    LIB3106-074-Q1-K1-B10
Seq. No.
                    7287
                    8634 1.R1040
Contig ID
5'-most EST
                    leu701150274.h1
Method
                    BLASTX
NCBI GI
                    g445613
BLAST score
                    967
E value
                    1.0e-105
Match length
                    237
% identity
                    78
                    ribosomal protein L7 [Solanum tuberosum]
NCBI Description
                    7288
Seq. No.
                    8639 1.R1040
Contig ID
                    crh700851304.hl
5'-most EST
```

BLAST score

```
Contig ID
                   8645 1.R1040
5'-most EST
                   LIB3040-043-Q1-E1-E12
Method
                   BLASTN
NCBI GI
                   g166739
BLAST score
                   126
E value
                   2.0e-64
Match length
                   314
                   85
% identity
NCBI Description A.thaliana histone H4 gene, complete cds
Seq. No.
                   7290
                   8647 1.R1040
Contig ID
5'-most EST
                   zhf700954010.hl
Seq. No.
                   7291
                   8647 2.R1040
Contig ID
                   LIB3039-036-Q1-E1-B2
5'-most EST
                   7292
Seq. No.
Contig ID
                   8649 1.R1040
                   LIB3093-047-Q1-K1-H7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3434986
BLAST score
                   430
                   2.0e-42
E value
Match length
                   118
% identity
                   (AB016895) Pop3 [Schizosaccharomyces pombe]
NCBI Description
                   7293
Seq. No.
Contig ID
                   8650 1.R1040
5'-most EST
                   uC-gmronoir031b08b1
                   BLASTX
Method
NCBI GI
                   q4510347
BLAST score
                   232
E value
                   3.0e-19
Match length
                   72
% identity
NCBI Description
                   (AC006921) hypothetical protein [Arabidopsis thaliana]
                   7294
Seq. No.
Contig ID
                   8654 1.R1040
5'-most EST
                   uC-gmronoir058f08b1
Method
                   BLASTX
NCBI GI
                   g3953458
BLAST score
                   482
E value
                   2.0e-48
Match length
                   150
% identity
                   69
                   (AC002328) F20N2.3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7295
                   8654 2.R1040
Contig ID
                   LIB3092-041-Q1-K1-H11
5'-most EST
Method
                   BLASTX
                   g3953458
NCBI GI
```

NCBI GI

BLAST score

```
E value
                   3.0e-34
Match length
                   116
                   67
% identity
NCBI Description
                   (AC002328) F20N2.3 [Arabidopsis thaliana]
                   7296
Seq. No.
Contig ID
                   8655 1.R1040
5'-most EST
                   g5678154
Seq. No.
                   7297
Contig ID
                   8681_1.R1040
5'-most EST
                   uC-gmrominsoy250g03b1
Method
                   BLASTX
NCBI GI
                   g2244799
BLAST score
                   398
E value
                   1.0e-38
                   136
Match length
% identity
                   57
NCBI Description
                   (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
Seq. No.
                   7298
                   8682_1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1157256.h1
Method
                   BLASTX
                   g3152606
NCBI GI
BLAST score
                   601
E value
                   5.0e-62
Match length
                   170
% identity
                   64
NCBI Description
                   (AC004482) putative ring zinc finger protein [Arabidopsis
                   thaliana]
                   7299
Seq. No.
                   8682 4.R1040
Contig ID
5'-most EST
                   kl1701207818.h1
Seq. No.
                   7300
                   8684 1.R1040
Contig ID
5'-most EST
                   LIB3039-035-Q1-E1-F12
Seq. No.
                   7301
Contig ID
                   8685 1.R1040
5'-most EST
                   jC-gmf102220103e03a1
Method
                   BLASTX
NCBI GI
                   q4567283
BLAST score
                   1561
E value
                   0.0e + 00
Match length
                   523
% identity
NCBI Description
                   (AC006841) unknown protein [Arabidopsis thaliana]
Seq. No.
                   8685 2.R1040
Contig ID
5'-most EST
                   uC-gmropic026b05b1
Method
                   BLASTX
```

g4567283

```
E value
                   7.0e-83
Match length
                   285
                   58
% identity
NCBI Description
                   (AC006841) unknown protein [Arabidopsis thaliana]
                   7303
Seq. No.
                   8685 3.R1040
Contig ID
5'-most EST
                   LIB3051-013-Q1-E1-F6
Seq. No.
                   7304
                   8691 1.R1040
Contig ID
                   LIB3072-014-Q1-E1-D8
5'-most EST
                   7305
Seq. No.
Contig ID
                   8699 1.R1040
                   LIB3039-035-Q1-E1-E2
5'-most EST
Method
                   BLASTX
                   g2827086
NCBI GI
BLAST score
                   322
E value
                   6.0e-30
                   100
Match length
                   58
% identity
                   (AF022778) DNA recombination and repair protein [Homo
NCBI Description
                   sapiens] >gi_3328152 (AF073362) endo/exonuclease Mre11
                   [Homo sapiens]
Seq. No.
                   7306
Contig ID
                   8701 1.R1040
5'-most EST
                   LIB3039-005-Q1-E1-B3
                   7307
Seq. No.
Contig ID
                   8702 1.R1040
5'-most EST
                   LIB3039-035-Q1-E1-E5
Method
                   BLASTX
NCBI GI
                   g4335759
BLAST score
                   165
E value
                   2.0e-11
Match length
                   98
                   47
% identity
NCBI Description
                   (AC006284) unknown protein [Arabidopsis thaliana]
                   7308
Seq. No.
                   8706 1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1155875.h1
                   7309
Seq. No.
Contig ID
                   8707 1.R1040
5'-most EST
                   LIB3039-035-Q1-E1-C12
Method
                   BLASTX
NCBI GI
                   q2832629
BLAST score
                   153
                   7.0e-10
E value
Match length
                   116
% identity
                   (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis
NCBI Description
```

thaliana]

5'-most EST

```
Seq. No.
                   7310
                   8709 1.R1040
Contig ID
5'-most EST
                   qsv701047702.hl
Seq. No.
                   7311
                   8714 1.R1040
Contig ID
5'-most EST
                   k117\overline{0}1211410.h1
Method
                   BLASTX
NCBI GI
                   g1076427
BLAST score
                   570
E value
                   6.0e-59
Match length
                   115
% identity
                   89
NCBI Description
                   ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis
                   thaliana
Seq. No.
                   7312
                   8716 1.R1040
Contig ID
5'-most EST
                   LIB3049-055-Q1-E1-H4
Method
                   BLASTN
NCBI GI
                   q3860314
BLAST score
                   207
E value
                   1.0e-112
Match length
                   345
                   92
% identity
NCBI Description Cicer arietinum mRNA for 40S ribosomal protein S19, partial
Seq. No.
                   7313
Contig ID
                   8716 2.R1040
5'-most EST
                   LIB3051-032-Q1-K1-G5
Method
                   BLASTN
NCBI GI
                   q3860314
BLAST score
                   123
E value
                   1.0e-62
Match length
                   275
% identity
                  Cicer arietinum mRNA for 40S ribosomal protein S19, partial
NCBI Description
Seq. No.
                   7314
Contig ID
                   8717 1.R1040
5'-most EST
                   LIB3106-019-Q1-K1-C1
Seq. No.
                   7315
Contig ID
                   8720 1.R1040
5'-most EST
                   LIB3039-035-Q1-E1-A9
Method
                   BLASTX
NCBI GI
                   g2281092
BLAST score
                   233
E value
                   3.0e-19
Match length
                   68
% identity
                   72
NCBI Description
                   (AC002333) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   8721 1.R1040
Contig ID
```

4- 0

 $zhf7\overline{0}0958240.h1$

```
Seq. No. 7317
Contig ID 8721_2.R1040
5'-most EST sat701009738.h1
Seq. No. 7318
```

Contig ID 8723_1.R1040

5'-most EST LIB3039-035-Q1-E1-A11

Method BLASTN
NCBI GI g4220422
BLAST score 106
E value 2.0e-52
Match length 226
% identity 87

NCBI Description Fragaria x ananassa putative cellulase mRNA, complete cds

Seq. No. 7319

Contig ID 8727_1.R1040

5'-most EST LIB3170-043-Q1-K1-D6

Method BLASTX
NCBI GI 9730030
BLAST score 157
E value 1.0e-09
Match length 279
% identity 12

NCBI Description MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS:

LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]

>qi 161804 (M87306) micronuclear linker histone polyprotein

[Tetrahymena thermophila]

 Seq. No.
 7320

 Contig ID
 8727_2.R1040

 5'-most EST
 g4284398

 Method
 BLASTX

 NCBI GI
 g1066104

 BLAST score
 147

 E value
 6.0e-09

E value 6.0e-09 Match length 236 % identity 12

NCBI Description (U39735) high molecular weight basic nuclear protein

[Pleuronectes americanus]

Seq. No. 7321

Contig ID 8740_1.R1040 5'-most EST epx701105109.h1

Method BLASTX
NCBI GI 94455172
BLAST score 836
E value 2.0e-89
Match length 228
% identity 70

NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 7322

Contig ID 8742 1.R1040

5'-most EST uC-gmrominsoy086a04b1

Method BLASTX NCBI GI g4337210

NCBI GI

```
BLAST score
                   371
E value
                   3.0e-35
Match length
                   135
% identity
NCBI Description
                   (AC006403) hypothetical protein [Arabidopsis thaliana]
                   7323
Seq. No.
                   8742 2.R1040
Contig ID
5'-most EST
                   jC-gmf102220097b01d1
Seq. No.
                   7324
                   8742 3.R1040
Contig ID
5'-most EST
                   wvk700680217.h2
Seq. No.
                   7325
                   8743 1.R1040
Contig ID
5'-most EST
                   hyd7\overline{0}0726342.h1
                   7326
Seq. No.
Contig ID
                   8743 2.R1040
5'-most EST
                   LIB3138-029-Q1-N1-F10
Seq. No.
                   7327
Contig ID
                   8744 1.R1040
5'-most EST
                   LIB3106-106-Q1-K1-F9
                   7328
Seq. No.
                   8748 1.R1040
Contig ID
                   ncj700985843.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4567251
BLAST score
                   682
E value
                   2.0e-71
Match length
                   303
% identity
                   67
NCBI Description
                   (AC007070) unknown protein [Arabidopsis thaliana]
                   7329
Seq. No.
Contig ID
                   8748 2.R1040
5'-most EST
                   a534\overline{2}502
Method
                   BLASTX
NCBI GI
                   g4567251
BLAST score
                   538
E value
                   1.0e-54
Match length
                   154
% identity
NCBI Description
                   (AC007070) unknown protein [Arabidopsis thaliana]
                   7330
Seq. No.
                   8748 5.R1040
Contig ID
5'-most EST
                   gsv701051285.hl
                   7331
Seq. No.
                   8748 6.R1040
Contig ID
5'-most EST
                   ncj700985348.h1
Method
                   BLASTX
```

g4567251



```
BLAST score
                   243
                   9.0e-21
E value
Match length
                   77
                   58
% identity
                   (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7332
                   8754 1.R1040
Contig ID
                   LIB3039-034-Q1-E1-E7
5'-most EST
                   7333
Seq. No.
                   8759 1.R1040
Contig ID
                   leu701153853.h1
5'-most EST
                   7334
Seq. No.
                   8764 1.R1040
Contig ID
5'-most EST
                   LIB3039-016-Q1-E1-C8
Method
                   BLASTN
                   g3281847
NCBI GI
BLAST score
                   42
E value
                   2.0e-14
Match length
                   86
                   87
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20
NCBI Description
                   (ESSAII project)
                   7335
Seq. No.
                   8764 2.R1040
Contig ID
                   fua701040759.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3281847
BLAST score
                   42
E value
                   2.0e-14
Match length
                   86
% identity
                   87
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20
NCBI Description
                   (ESSAII project)
                   7336
Seq. No.
                   8765 1.R1040
Contig ID
                   leu7\overline{0}1149120.h1
5'-most EST
Method
                   BLASTX
                   g2739279
NCBI GI
BLAST score
                   535
E value
                   2.0e-54
Match length
                   208
% identity
                   53
                   (AJ223177) short chain alcohol dehydrogenase [Nicotiana
NCBI Description
                   tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain
                   alcohol dehydrogenase [Nicotiana tabacum]
                   7337
Seq. No.
                   8767 1.R1040
```

5'-most EST zsg701124165.hl Seq. No. 7338 8777_1.R1040 Contig ID

Contig ID

```
5'-most EST
                   LIB3039-034-Q1-E1-B2
Method
                   BLASTX
NCBI GI
                   q3845099
BLAST score
                   169
E value
                   1.0e-11
Match length
                   124
% identity
                   3
NCBI Description
                   (AE001373) predicted secreted protein [Plasmodium
                   falciparum]
Seq. No.
                   7339
                   8777 2.R1040
Contig ID
5'-most EST
                   LIB3049-022-Q1-E1-D4
Seq. No.
                   7340
Contig ID
                   8777 4.R1040
5'-most EST
                   LIB3073-004-Q1-K1-A6
Seq. No.
                   7341
Contig ID
                   8780 1.R1040
5'-most EST
                   LIB3051-082-Q1-K1-D2
Method
                   BLASTN
NCBI GI
                   q2696018
BLAST score
                   108
E value
                   1.0e-53
Match length
                   332
% identity
                   83
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   7342
Contig ID
                   8783 1.R1040
5'-most EST
                   epx701106758.h1
Seq. No.
                   7343
                   8784 1.R1040
Contig ID
                   zhf700961867.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3023956
BLAST score
                   191
E value
                   3.0e-14
Match length
                   168
% identity
                   4
                   VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 >gi 607003
NCBI Description
                   (L28125) beta transducin-like protein [Podospora anserina]
Seq. No.
                   7344
                   8792 1.R1040
Contig ID
                   LIB3039-033-Q1-E1-G5
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1181589
BLAST score
                   284
E value
                   2.0e-25
Match length
                   120
% identity
                   54
NCBI Description
                   (D83070) high mobility group protein [Canavalia gladiata]
```

>gi_1483173 dbj BAA13133 (D86594) high mobility group

5'-most EST

protein [Canavalia gladiata]

7345 Seq. No. 8802 1.R1040 Contig ID 5'-most EST $q430\overline{1}037$ 7346 Seq. No. 8802 3.R1040 Contig ID $LIB3\overline{0}39-013-Q1-E1-F5$ 5'-most EST 7347 Seq. No. 8806 1.R1040 Contig ID 5'-most EST LIB3049-008-Q1-E1-E4 Method BLASTX NCBI GI g2407800 BLAST score 509 2.0e-51 E value Match length 110 % identity 93 (Y12575) histone H2A.F/Z [Arabidopsis thaliana] NCBI Description Seq. No. 8806 2.R1040 Contig ID 5'-most EST LIB3049-056-Q1-E1-B10 Method BLASTX NCBI GI q2407800 BLAST score 373 7.0e-36 E value Match length 83 % identity 92 (Y12575) histone H2A.F/Z [Arabidopsis thaliana] NCBI Description Seq. No. 7349 Contig ID 8815 1.R1040 5'-most EST epx701107574.h1 Method BLASTN NCBI GI g432488 BLAST score 138 E value 3.0e-71282 Match length % identity 87 NCBI Description Wheat initiation factor 1A (eIF-1A) mRNA Seq. No. 7350 8815 2.R1040 Contig ID 5'-most EST $fua7\overline{0}1041538.h1$ Method BLASTN NCBI GI g432488 BLAST score 170 E value 2.0e-90 Match length 282 % identity 90 NCBI Description Wheat initiation factor 1A (eIF-1A) mRNA Seq. No. 7351 Contig ID 8815 3.R1040

LIB3049-017-Q1-E1-H7





```
Method
                    BLASTN
 NCBI GI
                    q432488
 BLAST score
                    135
 E value
                    2.0e-69
 Match length
                    282
 % identity
                    87
 NCBI Description
                    Wheat initiation factor 1A (eIF-1A) mRNA
 Seq. No.
                    7352
                    8815 4.R1040
 Contig ID
 5'-most EST
                    LIB3051-053-Q1-K2-H1
 Method
                    BLASTN
 NCBI GI
                    q432488
 BLAST score
                    137
 E value
                    5.0e-71
 Match length
                    217
                    91
 % identity
 NCBI Description
                    Wheat initiation factor 1A (eIF-1A) mRNA
 Seq. No.
                    7353
                    8815 6.R1040
 Contig ID
 5'-most EST
                    zsg7\overline{0}1118418.h1
 Method
                    BLASTN
 NCBI GI
                    g432488
 BLAST score
                    50
 E value
                    3.0e-19
 Match length
                    74
                    92
 % identity
 NCBI Description
                    Wheat initiation factor 1A (eIF-1A) mRNA
 Seq. No.
                    7354
                    8821 1.R1040
 Contig ID
 5'-most EST
                    LIB3039-033-Q1-E1-B7
 Method
                    BLASTX
 NCBI GI
                    q4539005
 BLAST score
                    295

    E value

                    1.0e-26
 Match length
                    132
 % identity
                    46
 NCBI Description
                    (ALO49481) putative oxidoreductase [Arabidopsis thaliana]
 Seq. No.
                    8825 1.R1040
 Contig ID
                    fua701040082.hl
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g1345933
 BLAST score
                    1398
 E value
                    1.0e-155
                    296
 Match length
 % identity
                    89
                    CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS)
 NCBI Description
                    >gi_1084323_pir__S53007 citrate synthase - cucurbit
                    >gi_975633_dbj_BAA07328_ (D38132) glyoxysomal citrate
                    synthase [Cucurbita sp.]
```

7356

8828 1.R1040

Seq. No. Contig ID

```
5'-most EST
                   LIB3039-039-Q1-E1-D2
Method
                   BLASTX
NCBI GI
                   a2500378
BLAST score
                   409
                   7.0e-40
E value
Match length
                   83
                   89
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L37
                   7357
Seq. No.
Contig ID
                   8828 2.R1040
5'-most EST
                   LIB3074-039-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   a2500378
BLAST score
                   437
E value
                   5.0e-43
Match length
                   95
                   83
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L37
                   7358
Seq. No.
                   8835 1.R1040
Contig ID
5'-most EST
                   fua701042366.h1
Method
                   BLASTX
NCBI GI
                   q1304227
BLAST score
                   633
E value
                   6.0e-66
Match length
                   149
% identity
                   78
NCBI Description
                   (D63781) Epoxide hydrolase [Glycine max]
                   >gi 2764804 emb CAA55293 (X78547) epoxide hydrolase
                   [Glycine max]
Seq. No.
                   7359
Contig ID
                   8840 1.R1040
5'-most EST
                   LIB3109-047-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   q4519539
BLAST score
                   1526
E value
                   1.0e-170
Match length
                   364
                   79
% identity
NCBI Description
                   (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
                   domestica]
Seq. No.
                   7360
Contig ID
                   8840 2.R1040
                   asn701134864.h2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4519539
BLAST score
                   230
E value
                   1.0e-36
                   104
Match length
                   76
% identity
                   (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
NCBI Description
                   domestica]
```

Match length

```
Seq. No.
                   7361
                   8842 1.R1040
Contig ID
                   LIB3049-012-Q1-E1-H3
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4432837
BLAST score
                   268
E value
                   3.0e-23
Match length
                   148
% identity
                   47
NCBI Description
                   (AC006283) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   8856 1.R1040
Contig ID
5'-most EST
                   hyd700726103.h1
Method
                   BLASTX
NCBI GI
                   q3928150
BLAST score
                   491
E value
                   2.0e-49
Match length
                   113
% identity
                   (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
Seq. No.
                   7363
Contig ID
                   8866 1.R1040
5'-most EST
                   LIB3039-032-Q1-E1-D9
Method
                   BLASTX
                   g478318
NCBI GI
BLAST score
                   174
E value
                   3.0e-12
Match length
                   100
% identity
                   36
NCBI Description
                   immunophilin p59 - mouse >gi_410499_emb_CAA50231_ (X70887)
                   p59 immunophilin [Mus musculus]
Seq. No.
                   7364
Contig ID
                   8871 1.R1040
5'-most EST
                   LIB3039-032-Q1-E1-E7
                   7365
Seq. No.
                   8873 1.R1040
Contig ID
5'-most EST
                   leu701148713.hl
Method
                   BLASTX
NCBI GI
                   g2842486
BLAST score
                   390
E value
                   1.0e-37
Match length
                   120
% identity
                   (AL021749) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7366
                   8873 2.R1040
Contig ID
                   LIB3039-032-Q1-E1-F1
5'-most EST
Method
                   BLASTX
                   g4204306
NCBI GI
BLAST score
                   296
E value
                   6.0e-27
```

% identity NCBI Description (AC003027) 1cl prt seq No definition line found [Arabidopsis thaliana] 7367 Seq. No. 8875 1.R1040 Contig ID 5'-most EST LIB3039-032-Q1-E1-C2 BLASTX Method NCBI GI q2921209 BLAST score 499 E value 2.0e-50 Match length 143 % identity 73 NCBI Description (AF026148) beta-ketoacyl-ACP synthase I [Perilla frutescensl 7368 Seq. No. 8883 1.R1040 Contig ID 5'-most EST LIB3109-001-Q1-K1-G11 Method BLASTX NCBI GI q2827536 BLAST score 338 E value 5.0e-31 Match length 176 % identity 41 NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana] Seq. No. Contig ID 8883 3.R1040 5'-most EST LIB3107-006-Q1-K1-A7 Seq. No. Contig ID 8883 4.R1040 5'-most EST LIB3052-016-Q1-N1-E3 Seq. No. 8891 1.R1040 Contig ID leu701157334.h1 5'-most EST 7372 Seq. No. Contig ID 8892 1.R1040 $gsv7\overline{0}1052888.h1$ 5'-most EST BLASTX Method NCBI GI g3881780 BLAST score 176 E value 3.0e-12 116 Match length 37 % identity (Z48638) similar to lipid transfer protein [Caenorhabditis NCBI Description

755 . .

Seq. No. 7373

Contig ID 8901_1.R1040

5'-most EST LIB3039-004-Q1-E1-G1

elegans]

Method BLASTX NCBI GI g1183961 BLAST score 477

NCBI Description

```
2.0e-57
E value
Match length
                   205
                   57
% identity
NCBI Description
                   (Z69382) RNA elicase [Saccharomyces cerevisiae]
                   7374
Seq. No.
Contig ID
                   8914 1.R1040
                   LIB3053-001-Q1-B1-H12
5'-most EST
Seq. No.
                   7375
Contig ID
                   8922 1.R1040
5'-most EST
                   LIB3106-041-Q1-K1-E3
Method
                   BLASTX
                   g3426039
NCBI GI
BLAST score
                   315
E value
                   5.0e-29
Match length
                   91
                   65
% identity
NCBI Description
                   (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   7376
                   8923 1.R1040
Contig ID
5'-most EST
                   LIB3138-104-Q1-N1-G7
Method
                   BLASTX
                   g266936
NCBI GI
BLAST score
                   527
E value
                   2.0e-53
Match length
                   143
% identity
                   72
                   50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27)
NCBI Description
                   >gi 282960 pir A42840 ribosomal protein L27 - common
                   tobacco >gi_170306 (M98473) ribosomal protein L27
                   [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein
                   L27 [Nicotiana tabacum]
Seq. No.
                   7377
Contig ID
                   8924 1.R1040
5'-most EST
                   LIB3050-013-Q1-E1-G4
Method
                   BLASTX
NCBI GI
                   q2979565
BLAST score
                   475
E value
                   2.0e-47
Match length
                   120
% identity
NCBI Description
                   (AC003680) putative sin3 associated polypeptide (SAP18)
                   [Arabidopsis thaliana]
Seq. No.
                   7378
                   8931 1.R1040
Contig ID
                   jex7\overline{0}0905931.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3650030
BLAST score
                   291
E value
                   5.0e-26
Match length
                   114
% identity
                   58
```

(AC005396) unknown protein [Arabidopsis thaliana]

5'-most EST

```
7379
Seq. No.
Contig ID
                    8931 2.R1040
5'-most EST
                   LIB3039-031-Q1-E1-D3
Method
                   BLASTX
                   g3650030
NCBI GI
BLAST score
                   317
E value
                    3.0e-29
Match length
                   133
% identity
                    55
                    (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
                    7380
Seq. No.
                    8941 1.R1040
Contig ID
5'-most EST
                   LIB3170-005-Q1-K1-E2
                    7381
Seq. No.
                   8941 2.R1040
Contig ID
5'-most EST
                   LIB3039-031-Q1-E1-B12
Method
                   BLASTX
NCBI GI
                   g3859570
BLAST score
                   150
E value
                    3.0e-13
                   87
Match length
% identity
                   53
NCBI Description
                   (AF098753) unknown [Oryza sativa]
Seq. No.
                    7382
                   8953 1.R1040
Contig ID
5'-most EST
                   ncj7\overline{0}0982909.h1
Method
                   BLASTX
NCBI GI
                   q1170543
BLAST score
                   679
E value
                   3.0e-71
Match length
                   244
                   57
% identity
                   DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD) (2,3-DIHYDROXY
NCBI Description
                   ACID HYDROLYASE) >gi_1077091_pir__S55205 dihydroxy-acid dehydratase (EC 4.2.1.9) - yeast (Saccharomyces cerevisiae)
                   >gi_854590_emb_CAA60939_ (X87611) dihydroxyacid dehydratase
                    [Saccharomyces cerevisiae] >gi_1015650_emb_CAA89540_
                    (Z49516) ORF YJR016c [Saccharomyces cerevisiae]
                   7383
Seq. No.
Contig ID
                   8957 1.R1040
5'-most EST
                   LIB3072-055-Q1-K1-E12
Method
                   BLASTX
NCBI GI
                   g2827655
BLAST score
                   185
E value
                   1.0e-13
                   128
Match length
                    41
% identity
NCBI Description
                    (AL021637) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   7384
Contig ID
                   8957 2.R1040
```

LIB3094-080-Q1-K1-A9

```
Method .
                   BLASTX
NCBI GI
                   q2827655
BLAST score
                   175
E value
                   5.0e-12
Match length
                   208
                   33
% identity
NCBI Description
                   (AL021637) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   7385
                   8958 1.R1040
Contig ID
5'-most EST
                   epx701109691.h1
                   BLASTX
Method
NCBI GI
                   q3204129
BLAST score
                   502
E value
                   1.0e-50
Match length
                   133
                   77
% identity
NCBI Description
                   (AJ006768) histone H2A [Cicer arietinum]
Seq. No.
                   7386
                   8958 2.R1040
Contig ID
                   LIB3074-040-Q1-K1-B2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3776566
BLAST score
                   398
E value
                   1.0e-38
                   106
Match length
% identity
                   (AC005388) Strong similarity to histone H2A gb AJ006768
NCBI Description
                   from Cicer arietinum. [Arabidopsis thaliana]
Seq. No.
                   7387
                   8978 1.R1040
Contig ID
                   LIB3039-030-Q1-E1-E7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g140474
BLAST score
                   251
                   7.0e-21
E value
Match length
                   203
% identity
                   HYPOTHETICAL 69.2 KD PROTEIN IN HSP30-PMP1 INTERGENIC
NCBI Description
                   REGION >gi_83212_pir__S19434 probable transport protein
                   YCR023c - yeast (Saccharomyces cerevisiae)
                   >gi_1907167_emb_CAA42315_ (X59720) YCR023c, len:611
                   [Saccharomyces cerevisiae]
Seq. No.
                   7388
Contig ID
                   8978 2.R1040
5'-most EST
                   leu701153306.hl
Method
                   BLASTX
NCBI GI
                   q140474
BLAST score
                   159
E value
                   1.0e-10
Match length
                   67
                   45
% identity
                  HYPOTHETICAL 69.2 KD PROTEIN IN HSP30-PMP1 INTERGENIC
NCBI Description
                   REGION >gi_83212_pir__S19434 probable transport protein
```

```
[Saccharomyces cerevisiae]
                   7389
Seq. No.
                   8978 3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy172a11b1
Seq. No.
                   7390
Contig ID
                   8978 4.R1040
5'-most EST
                   g5753013
Seq. No.
                   7391
Contig ID
                   8978 5.R1040
5'-most EST
                   fua701041256.hl
Method
                   BLASTX
NCBI GI
                   g140474
BLAST score
                   178
E value
                   7.0e-13
Match length
                   76
% identity
                   43
NCBI Description
                   HYPOTHETICAL 69.2 KD PROTEIN IN HSP30-PMP1 INTERGENIC
                   REGION >gi_83212_pir__S19434 probable transport protein
YCR023c - yeast (Saccharomyces cerevisiae)
                   >gi 1907167 emb CAA42315 (X59720) YCR023c, len:611
                   [Saccharomyces cerevisiae]
                   7392
Seq. No.
Contig ID
                   8979 1.R1040
5'-most EST
                   LIB3109-037-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   g1903364
BLAST score
                   392
E value
                   9.0e-38
Match length
                   154
% identity
                   58
NCBI Description
                    (AC000104) EST gb T45093 comes from this gene. [Arabidopsis
                   thaliana]
                   7393
Seq. No.
Contig ID
                   8983 1.R1040
5'-most EST
                   LIB3039-030-Q1-E1-F2
Method
                   BLASTX
NCBI GI
                   g3395436
BLAST score
                   387
E value
                   3.0e-37
Match length
                   133
% identity
                   (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7394
                   8999 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400056c01a1
Method
                   BLASTX
                   g3560264
NCBI GI
BLAST score
                   170
E value
                   6.0e-12
```

YCR023c - yeast (Saccharomyces cerevisiae)

>qi 1907167 emb CAA42315 (X59720) YCR023c, len:611

Contig ID 5'-most EST

```
110
Match length
                   39
% identity
                   (AL031535) soll family protein [Schizosaccharomyces pombe]
NCBI Description
                   7395
Seq. No.
                   8999 3.R1040
Contig ID
                   jC-gmf102220144f04a1
5'-most EST
                   7396
Seq. No.
                   9002 1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1147244.h1
                   7397
Seq. No.
                   9004 1.R1040
Contig ID
                   uC-gmrominsoy276f10b1
5'-most EST
                   BLASTN
Method
                   g517257
NCBI GI
                   74
BLAST score
                   2.0e-33
E value
Match length
                   130
% identity
                   89
NCBI Description
                   Z.mays MNBla mRNA for DNA-binding protein
                   7398
Seq. No.
                   9010 1.R1040
Contig ID
5'-most EST
                   vzy700751182.h1
Seq. No.
                   7399
                   9013_1.R1040
Contig ID
5'-most EST
                   LIB3039-030-Q1-E1-A12
                   7400
Seq. No.
Contig ID
                   9024 1.R1040
                   LIB3039-037-Q1-E1-F12
5'-most EST
                   BLASTN
Method
                   g1806145
NCBI GI
BLAST score
                   196
E value
                   1.0e-106
                   532
Match length
                   84
% identity
                   M.sativa mRNA for cdc2 kinase homologue, cdc2MsF
NCBI Description
                   7401
Seq. No.
                   9024 2.R1040
Contig ID
5'-most EST
                   LIB3170-034-Q1-K1-F1
                   BLASTX
Method
NCBI GI
                   g1806146
BLAST score
                   624
E value
                   3.0e-65
Match length
                   135
                   93
% identity
NCBI Description
                   (X97317) cdc2MsF [Medicago sativa]
Seq. No.
                   7402
                   9025 1.R1040
```

 $LIB3\overline{0}51-030-Q1-K1-E12$

```
Seq. No.
                   7403
                   9025 2.R1040
Contig ID
5'-most EST
                   uaw700664486.h1
                   7404
Seq. No.
Contig ID
                   9034 1.R1040
5'-most EST
                   zzp700832030.hl
Method
                   BLASTX
NCBI GI
                   q4406814
BLAST score
                   495
E value
                   1.0e-49
Match length
                   113
% identity
                   82
NCBI Description
                   (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
                   thalianal
Seq. No.
                   7405
                   9034 2.R1040
Contig ID
5'-most EST
                   seb7\overline{0}0653725.h1
Method
                   BLASTN
NCBI GI
                   q531828
BLAST score
                   41
E value
                   1.0e-13
Match length
                   81
                   88
% identity
NCBI Description
                   Cloning vector pSport1, complete cds
Seq. No.
Contig ID
                   9040 1.R1040
5'-most EST
                   LIB3039-029-Q1-E1-D10
                   7407
Seq. No.
Contig ID
                   9042 1.R1040
5'-most EST
                   fC-gmf1700905086i1
Seq. No.
                   9042 2.R1040
Contig ID
5'-most EST
                   LIB3039-029-Q1-E1-D12
Seq. No.
                   7409
Contig ID
                   9043 1.R1040
5'-most EST
                   LIB3039-029-Q1-E1-D2
Method
                   BLASTX
NCBI GI
                   q4539470
BLAST score
                   358
E value
                   1.0e-33
Match length
                   123
% identity
NCBI Description
                   (AL049500) hypothetical protein [Arabidopsis thaliana]
                   7410
Seq. No.
Contig ID
                   9049 1.R1040
5'-most EST
                   qsv701051392.h1
                   BLASTX
Method
NCBI GI
                   g4544399
BLAST score
                   274
```

6.0e-24

E value

Method

BLASTN

```
102
Match length
                   54
% identity
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   7411
Seq. No.
                   9050 1.R1040
Contig ID
                   yuv700862829.h1
5'-most EST
Method
                   BLASTN
                   g536891
NCBI GI
BLAST score
                   107
                   9.0e-53
E value
                   264
Match length
                   88
% identity
NCBI Description Wheat mRNA for protein H2A, complete cds, clone wcH2A-4
                   7412
Seq. No.
                   9050 2.R1040
Contig ID
                   leu701144726.hl
5'-most EST
Method
                  BLASTN
NCBI GI
                   g536891
BLAST score
                   94
E value
                   4.0e-45
Match length
                  274
% identity
                  86
                  Wheat mRNA for protein H2A, complete cds, clone wcH2A-4
NCBI Description
                   7413
Seq. No.
Contig ID
                   9050 3.R1040
                  LIB3040-021-Q1-E1-C2
5'-most EST
Method
                  BLASTN
                   g536891
NCBI GI
                   99
BLAST score
E value
                   4.0e-48
                   285
Match length
% identity
                   86
NCBI Description
                  Wheat mRNA for protein H2A, complete cds, clone wcH2A-4
                   7414
Seq. No.
                   9050 4.R1040
Contig ID
                   jC-gmle01810087g06a1
5'-most EST
Method
                  BLASTX
                  g3269284
NCBI GI
BLAST score
                   281
E value
                   7.0e-25
Match length
                  56
% identity
                   100
NCBI Description
                   (AL030978) histone H2A- like protein [Arabidopsis thaliana]
                   7415
Seq. No.
Contig ID
                   9053 1.R1040
5'-most EST
                  LIB3039-029-Q1-E1-B5
                   7416
Seq. No.
                   9065 1.R1040
Contig ID
5'-most EST
                  uC-gmropic040f08b1
```

BLAST score

```
q556421
NCBI GI
BLAST score
                   56
E value
                   2.0e-22
Match length
                   120
                   96
% identity
                  Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1)
NCBI Description
                  mRNA, complete cds
Seq. No.
                   7417
                   9065 2.R1040
Contig ID
5'-most EST
                   qsv701051084.hl
                   BLASTN
Method
NCBI GI
                   q556421
BLAST score
                   52
E value
                   3.0e-20
Match length
                   109
                   94
% identity
                   Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1)
NCBI Description
                   mRNA, complete cds
                   7418
Seq. No.
                   9071 1.R1040
Contig ID
5'-most EST
                   pmv700894565.hl
                   7419
Seq. No.
Contig ID
                   9076 1.R1040
                   LIB3106-011-Q1-K1-B5
5'-most EST
                   BLASTX
Method
                   g3738329
NCBI GI
BLAST score
                   322
E value
                   1.0e-29
                   88
Match length
% identity
NCBI Description
                   (AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   9076 2.R1040
5'-most EST
                   ssr700557608.hl
                   7421
Seq. No.
Contiq ID
                   9079 1.R1040
5'-most EST
                   LIB3039-028-Q1-E1-H10
Method.
                   BLASTX
NCBI GI
                   q4006872
BLAST score
                   231
E value
                   4.0e-19
Match length
                   60
% identity
                   (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   7422
Seq. No.
                   9080 1.R1040
Contig ID
                   bth700845178.h1
5'-most EST
                   BLASTX
Method
                   g2708750
NCBI GI
```

Method

NCBI GI

BLASTN

g1150931

```
2.0e-34
E value
                   134
Match length
                   58
% identity
NCBI Description
                   (AC003952) putative physical impedence protein [Arabidopsis
                   thaliana]
                   7423
Seq. No.
                   9084 1.R1040
Contig ID
5'-most EST
                   LIB3039-039-Q1-E1-G8
Seq. No.
                   7424
Contig ID
                   9084 2.R1040
5'-most EST
                  LIB3170-088-Q1-K1-G1
                   7425
Seq. No.
                   9089 1.R1040
Contig ID
                  LIB3073-019-Q1-K1-F10
5'-most EST
Method
                   BLASTX
                   g629858
NCBI GI
BLAST score
                   546
                   9.0e-56
E value
Match length
                  128
% identity
                   82
NCBI Description
                  protein kinase C inhibitor - maize
                   7426
Seq. No.
Contig ID
                   9096 1.R1040
                  LIB3039-028-Q1-E1-F8
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3925703
BLAST score
                  1007
                   1.0e-109
E value
                  242
Match length
% identity
                  (X95905) 14-3-3 protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   7427
                   9096 2.R1040
Contiq ID
5'-most EST
                  LIB3049-047-Q1-E1-C7
Method
                  BLASTX
NCBI GI
                   q3023186
BLAST score
                   360
E value
                   2.0e-34
Match length
                  91
                   77
% identity
                  14-3-3-LIKE PROTEIN 9 >gi_1771180_emb_CAA67373.1_ (X98865)
NCBI Description
                   14-3-3 protein [Lycopersicon esculentum]
Seq. No.
                   7428
                  9103 1.R1040
Contig ID
5'-most EST
                  LIB3039-028-Q1-E1-D4
                   7429
Seq. No.
Contig ID
                   9104 1.R1040
5'-most EST
                  sat701013255.hl
```

```
BLAST score
                   44
E value
                   2.0e-15
Match length
                   56
% identity
                   95
NCBI Description
                   M.sativa mRNA for cyclin protein
                   7430
Seq. No.
Contig ID
                   9104 2.R1040
5'-most EST
                   LIB3040-057-Q1-E1-C8
Method
                   BLASTN
NCBI GI
                   g1150931
BLAST score
                   36
E value
                   1.0e-10
Match length
                   52
% identity
                   92
NCBI Description
                   M.sativa mRNA for cyclin protein
Seq. No.
                   7431
                   9114 1.R1040
Contig ID
5'-most EST
                   zzp7\overline{0}0833874.h1
Method
                   BLASTX
NCBI GI
                   q3033397
BLAST score
                   1699
E value
                   0.0e + 00
Match length
                   403
% identity
                   79
NCBI Description
                  (AC004238) unknown protein [Arabidopsis thaliana]
Seq. No.
                   7432
                   9123 1.R1040
Contig ID
5'-most EST
                   bth700845623.h1
Seq. No.
                   7433
Contig ID
                   9125 1.R1040
5'-most EST
                   LIB3170-011-Q1-K1-B2
Method
                   BLASTN
NCBI GI
                   g336391
BLAST score
                   79
E value
                   3.0e-36
Match length
                   159
% identity
                   87
NCBI Description
                   A.thaliana chloroplast ribosomal protein S17 (rps17) mRNA,
                   3' end
Seq. No.
                   7434
Contig ID
                   9125 2.R1040
5'-most EST
                   LIB3049-024-Q1-E1-D12
Method
                   BLASTX
NCBI GI
                   g336392
BLAST score
                   148
E value
                   2.0e-09
                   53
Match length
                   58
% identity
NCBI Description
                   (J05215) ribosomal protein S17 [Arabidopsis thaliana]
                   7435
Seq. No.
```

9128 1.R1040

Contig ID

```
uC-qmropic044e06b1
5'-most EST
                   7436
Seq. No.
Contig ID
                   9132 1.R1040
                   seb7\overline{0}0653953.h1
5'-most EST
Method
                   BLASTX
                   g3327868
NCBI GI
BLAST score
                   140
E value
                   1.0e-08
                   89
Match length
% identity
                   35
                   (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   7437
                   9139 1.R1040
Contig ID
                   LIB3039-007-Q1-E1-G9
5'-most EST
Method
                   BLASTN
NCBI GI
                   g168492
BLAST score
                   229
E value
                   1.0e-125
Match length
                   385
% identity
                   90
NCBI Description
                  Corn histone H3 (H3C3) gene, complete cds
                   7438
Seq. No.
                   9139 2.R1040
Contig ID
5'-most EST
                   LIB3073-014-Q1-K1-D11
Method
                   BLASTN
NCBI GI
                   g20252
BLAST score
                   179
                   6.0e-96
E value
Match length
                   371
                   87
% identity
NCBI Description Oryza sativa H3 histone H3R-21 clone RH3-2
Seq. No.
                   7439
                   9139 3.R1040
Contig ID
5'-most EST
                   LIB3049-049-Q1-E1-B3
Method
                   BLASTN
NCBI GI
                   g168492
BLAST score
                   173
E value
                   2.0e-92
Match length
                   297
% identity
                   90
NCBI Description
                  Corn histone H3 (H3C3) gene, complete cds
Seq. No.
                   7440
Contig ID
                   9141 1.R1040
5'-most EST
                   LIB3051-048-Q1-K1-D3
Method
                   BLASTX
NCBI GI
                   q2598575
BLAST score
                   219
E value
                   2.0e-17
Match length
                   219
% identity
NCBI Description
                   (Y15293) MtN21 [Medicago truncatula]
```

NCBI GI

BLAST score

```
7441
Seq. No.
Contig ID
                   9148 1.R1040
5'-most EST
                   LIB3039-027-Q1-E1-H3
Method
                   BLASTX
NCBI GI
                   q2583134
BLAST score
                   143
E value
                   6.0e-09
Match length
                   94
% identity
NCBI Description
                   (AC002387) putative proline-rich protein [Arabidopsis
                   thaliana]
Seq. No.
                   7442
                   9154 1.R1040
Contig ID
5'-most EST
                   LIB3040-035-Q1-E1-D7
                   7443
Seq. No.
Contig ID
                   9154 2.R1040
5'-most EST
                   LIB3107-050-Q1-K1-C1
Method
                   BLASTN
NCBI GI
                   q940287
BLAST score
                   35
E value
                   4.0e-10
Match length
                   75
% identity
                   87
NCBI Description Pisum sativum L. (clone na-481-5) mRNA, complete cds
Seq. No.
                   7444
Contig ID
                   9155 1.R1040
5'-most EST
                   LIB3039-027-Q1-E1-F6
Method
                   BLASTX
                   g3021598
NCBI GI
BLAST score
                   171
E value
                   2.0e-11
Match length
                   346
% identity
                   25 -
NCBI Description
                  (Y10389) nuclear protein [Xenopus laevis]
Seq. No.
                   9155 2.R1040
Contig ID
5'-most EST
                   leu701151007.hl
                   7446
Seq. No.
                   9159 1.R1040
Contig ID
5'-most EST
                   LIB3087-007-Q1-K1-D5
                   7447
Seq. No.
                   9169 1.R1040
Contig ID
                   LIB3039-027-Q1-E1-E11
5'-most EST
Seq. No.
                   7448
                   9171_1.R1040
Contig ID
                   LIB3039-027-Q1-E1-E5
5'-most EST
Method
                   BLASTX
                   g3763934
```

```
E value
                   1.0e-18
Match length
                  124
                   50
% identity
NCBI Description
                   (AC004450) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   9176 1.R1040
Contig ID
5'-most EST
                  LIB3053-001-Q1-B1-A8
Method
                  BLASTX
NCBI GI
                   q2384956
BLAST score
                   327
E value
                   3.0e-30
Match length
                   159
                   43
% identity
NCBI Description
                   (AF022985) No definition line found [Caenorhabditis
                   elegans]
                   7450
Seq. No.
                   9178_1.R1040
Contig ID
5'-most EST
                   fC-gmse7000762491d1
Seq. No.
Contig ID
                   9179 1.R1040
5'-most EST
                  uC-gmropic029d10b1
Seq. No.
                   9179 2.R1040
Contia ID
5'-most EST
                  LIB3049-023-Q1-E1-D11
Seq. No.
Contig ID
                   9186 1.R1040
5'-most EST
                   jex700909242.h1
Method
                  BLASTX
NCBI GI
                  q585565
BLAST score
                   634
E value
                  8.0e-66
Match length
                  155
% identity
                  82
                  RIBOSOME RECYCLING FACTOR HOMOLOG (NUCLEAR LOCATED PROTEIN
NCBI Description
                  D2) >gi_629661_pir__S32716 nuclear protein - carrot
                   >gi 297891 emb CAA51077 (X72384) nuclear located protein
                   [Daucus carota]
                   7454
Seq. No.
                   9186 3.R1040
Contig ID
5'-most EST
                  epx701109783.hl
                  7455
Seq. No.
                   9194 1.R1040
Contig ID
5'-most EST
                  LIB3039-027-Q1-E1-A11
                  7456
Seq. No.
                   9203 1.R1040
Contig ID
5'-most EST
                  LIB3039-026-Q1-E1-H4
Seq. No.
                   7457
```

9212 1.R1040

Contig ID

```
5'-most EST
                   q5688377
                   BLASTX
Method
NCBI GI
                   q3879734
BLAST score
                   258
E value
                   8.0e-22
Match length
                   228
% identity
                   33
NCBI Description
                   (Z93388) predicted using Genefinder; cDNA EST EMBL:D70912
                   comes from this gene; cDNA EST EMBL: D73452 comes from this
                   gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST
                   EMBL: D74229 comes from this gene; cDNA EST EMBL: D727
Seq. No.
                   7458
Contig ID
                   9213 1.R1040
5'-most EST
                   q5606317
Method
                   BLASTX
NCBI GI
                   q4220482
BLAST score
                   423
E value
                   2.0e-41
Match length
                   135
% identity
                   37
NCBI Description
                   (AC006069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   9213 2.R1040
5'-most EST
                   LIB3039-026-Q1-E1-A1
Method
                   BLASTX
NCBI GI
                   q4220482
BLAST score
                   226
E value
                   1.0e-18
Match length
                   74
% identity
NCBI Description
                   (AC006069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   7460
Contig ID
                   9214 1.R1040
5'-most EST
                   LIB3039-026-Q1-E1-F5
Method
                   BLASTX
NCBI GI
                   q498040
BLAST score
                   555
E value
                   8.0e-57
                   191
Match length
                   60
% identity
NCBI Description
                   (L33793) ORF [Senecio odorus]
Seq. No.
                   7461
                   9214 2.R1040
Contig ID
5'-most EST
                   uC-gmropic102f04b1
Method
                   BLASTX
                   g498040
NCBI GI
BLAST score
                   254
E value
                   6.0e-22
                   70
Match length
% identity
                   73
                   (L33793) ORF [Senecio odorus]
NCBI Description
```

7462

Seq. No.

E value

2.0e-61

```
Contig ID
                   9219 1.R1040
5'-most EST
                   jC-qmst02400027f12a1
Method
                   BLASTX
NCBI GI
                   g2511574
BLAST score
                   1117
                   1.0e-122
E value
                   235
Match length
% identity
NCBI Description
                   (Y13176) multicatalytic endopeptidase [Arabidopsis
                   thaliana] >gi 3421075 (AF043520) 20S proteasome subunit
                   PAB1 [Arabidopsis thaliana]
                   7463
Seq. No.
                   9219 2.R1040
Contig ID
                   LIB3049-052-Q1-E1-G3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2511574
BLAST score
                   480
E value
                   2.0e-48
                  106
Match length
                   92
% identity
NCBI Description
                   (Y13176) multicatalytic endopeptidase [Arabidopsis
                   thaliana] >gi 3421075 (AF043520) 20S proteasome subunit
                   PAB1 [Arabidopsis thaliana]
                   7464
Seq. No.
                   9222 1.R1040
Contig ID
                   vwf700676570.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2981475
BLAST score
                   315
E value
                   5.0e-29
                   107
Match length
% identity
                   60
NCBI Description
                   (AF053084) putative cinnamyl alcohol dehydrogenase [Malus
                   domestical
                   7465
Seq. No.
                   9226 1.R1040
Contig ID
                   seb7\overline{0}0654110.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3219969
BLAST score
                  158
                   3.0e-10
E value
Match length
                  56
% identity
                  HYPOTHETICAL 22.4 KD PROTEIN C6G10.10C IN CHROMOSOME I
NCBI Description
                   >gi 2330874 emb CAB11296 (Z98603) hypothetical protein
                   [Schizosaccharomyces pombe]
Seq. No.
                   7466
                   9227 1.R1040
Contig ID
5'-most EST
                  LIB3039-025-Q1-E1-F10
Method
                  BLASTX
                  g1743354
NCBI GI
                  593
BLAST score
```

```
179
Match length
                   60
% identity
NCBI Description
                   (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
                   7467
Seq. No.
Contig ID
                   9228 1.R1040
5'-most EST
                   LIB3039-026-Q1-E1-E5
Method
                   BLASTN
NCBI GI
                   g1778373
BLAST score
                   135
E value
                   1.0e-69
Match length
                   359
% identity
                   84
NCBI Description
                   Pisum sativum glycine-rich RNA-binding protein PsGRBP mRNA,
                   complete cds
Seq. No.
                   7468
Contig ID
                   9239 1.R1040
5'-most EST
                   LIB3039-026-Q1-E1-C7
Method
                   BLASTX
NCBI GI
                   q2500345
BLAST score
                   440
E value
                   3.0e-43
Match length
                   128
                   70
% identity
NCBI Description
                   NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY
                   GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)
                   >gi 2618578 dbj BAA23363 (D50420) OTK27 [Homo sapiens]
                   >gi_3859990 (AF091076) OTK27 [Homo sapiens]
                   >gi 1589072 prf 2210268A nuclear protein-NHP2-like protein
                   [Homo sapiens]
Seq. No.
                   7469
Contig ID
                   9250 1.R1040
5'-most EST
                   leu701150345.hl
Method
                   BLASTX
NCBI GI
                   q1477565
BLAST score
                   166
E value
                   2.0e-13
Match length
                   120
% identity
                   (U50078) p532 [Homo sapiens]
NCBI Description
                   >gi_4557026_ref_NP_003913.1_pHERC1_ hect (homologous to the
                   E6-AP (UBE3A) carboxyl terminus) domain and RCC1
                   (CHC1)-like domain (RLD)
                   7470
Seq. No.
                   9251 1.R1040
Contig ID
                   smw7\overline{0}0646267.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2739168
BLAST score
                   1118
E value
                   1.0e-122
Match length
                   365
                   57
% identity
NCBI Description
                   (AF032386) aldose-1-epimerase-like protein [Nicotiana
```

tabacum]

Method

BLASTX

```
7471
Seq. No.
                   9251 3.R1040
Contig ID
5'-most EST
                   jC-gmle01810047g07d1
Seq. No.
                   9292 1.R1040
Contig ID
                   LIB3039-024-Q1-E1-H5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2829208
BLAST score
                   178
                   1.0e-12
E value
Match length
                   203
% identity
NCBI Description
                   (AF044076) candidate tumor suppressor p33ING1 [Homo
                   sapiens]
                   7473
Seq. No.
                   9295_1.R1040
Contig ID
5'-most EST
                   LIB3087-006-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   g2252866
                   230
BLAST score
E value
                   1.0e-18
Match length
                   69
% identity
                   65
                   (AF013294) contains region of similarity to SYT
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   7474
Contig ID
                   9295 2.R1040
                   fC-gmst700653716f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2252866
BLAST score
                   177
E value
                   1.0e-12
Match length
                   48
% identity
                   69
                   (AF013294) contains region of similarity to SYT
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   7475
Contig ID
                   9295 3.R1040
5'-most EST
                   LIB3049-010-Q1-E1-B5
Method
                   BLASTX
NCBI GI
                   q2252866
BLAST score
                   194
E value
                   9.0e-15
Match length
                   49
% identity
NCBI Description
                   (AF013294) contains region of similarity to SYT
                   [Arabidopsis thaliana]
Seq. No.
                   7476
Contig ID
                   9295 4.R1040
                   gsv7\overline{0}1047345.h1
5'-most EST
```

```
NCBI GI
                   g2252866
BLAST score
                   190
                   3.0e-14
E value
Match length
                   52
                   69
% identity
NCBI Description
                   (AF013294) contains region of similarity to SYT
                   [Arabidopsis thaliana]
Seq. No.
                   7477
                   9295 5.R1040
Contig ID
5'-most EST
                   crh700852275.h1
                   BLASTX
Method
NCBI GI
                   g2252866
BLAST score
                   216
E value
                   4.0e-17
Match length
                   73
                   60
% identity
NCBI Description
                   (AF013294) contains region of similarity to SYT
                   [Arabidopsis thaliana]
                   7478
Seq. No.
                   9295 6.R1040
Contig ID
5'-most EST
                   fua701043038.hl
                   7479
Seq. No.
Contig ID
                   9310 1.R1040
5'-most EST
                   k117\overline{0}1204787.h1
                   7480
Seq. No.
                   9327 1.R1040
Contig ID
5'-most EST
                   LIB3039-023-Q1-E1-H11
                   7481
Seq. No.
                   9327 2.R1040
Contig ID
5'-most EST
                   LIB3040-048-Q1-E1-E11
Seq. No.
                   7482
Contig ID
                   9329 1.R1040
5'-most EST
                   LIB3087-006-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3924823
BLAST score
                   255
E value
                   1.0e-21
Match length
                   135
% identity
                   38
NCBI Description
                   (Z83113) cDNA EST yk491a11.5 comes from this gene; cDNA EST
                   yk491a11.3 comes from this gene [Caenorhabditis elegans]
                   7483
Seq. No.
                   9329 2.R1040
Contig ID
                   LIB3167-004-P1-K1-E7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3924823
BLAST score
                   203
E value
                   8.0e-16
Match length
                   71
```

51

% identity

Seq. No.

```
(Z83113) cDNA EST yk491a11.5 comes from this gene; cDNA EST
NCBI Description
                   yk491a11.3 comes from this gene [Caenorhabditis elegans]
                   7484
Seq. No.
Contig ID
                   9345 1.R1040
                   LIB3039-023-Q1-E1-C7
5'-most EST
Method
                   BLASTN
                   g3021347
NCBI GI
BLAST score
                   191
                   1.0e-103
E value
Match length
                   554
% identity
                   84
NCBI Description Cicer arietinum mRNA for cytoplasmic ribosomal protein L18
                   7485
Seq. No.
                   9345_3.R1040
Contig ID
5'-most EST
                   g4284518
Method
                   BLASTX
                   g1172977
NCBI GI
BLAST score
                   270
E value
                   1.0e-23
Match length
                   59
                   85
% identity
                   60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
NCBI Description
                   ribosomal protein L18 [Arabidopsis thaliana]
                   7486
Seq. No.
                   9347 1.R1040
Contig ID
                   hrw701060933.hl
5'-most EST
                   7487
Seq. No.
Contig ID
                   9355 1.R1040
                   uaw7\overline{0}0666059.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3775995
BLAST score
                   738
E value
                   2.0e-78
Match length
                   182
                   74
% identity
                   (AJ010461) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7488
Contig ID
                   9368 1.R1040
5'-most EST
                   LIB3039-023-Q1-E1-A7
Method
                   BLASTX
NCBI GI
                   g2459438
BLAST score
                   276
E value
                   3.0e-24
                   74
Match length
% identity
                   (AC002332) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   7489
Seq. No.
                   9370 1.R1040
Contig ID
5'-most EST
                   LIB3039-022-Q1-E1-G8
```

Method

BLASTX

```
9382 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy310f07b1
Seq. No.
                  9382 2.R1040
Contig ID
5'-most EST
                  LIB3072-037-Q1-E1-H3
Seq. No.
Contig ID
                  9385 1.R1040
5'-most EST
                  q5607125
Method
                  BLASTX
NCBI GI
                  q1723176
BLAST score
                  363
E value
                  5.0e-34
Match length
                  209
                  40
% identity
NCBI Description
                  HYPOTHETICAL 22.4 KD PROTEIN SLL0615
                  >gi_1001617_dbj_BAA10348_ (D64002) transmembrane protein
                  FT27 [Synechocystis sp.] >gi_1256592 (U38892) similar to
                  Mus musculus transmembrane protein (clone pFT27); Method:
                  conceptual translation supplied by author; ORF206
                  [Synechocystis sp.]
Seq. No.
                  7493
                  9385 2.R1040
Contig ID
5'-most EST
                  LIB3106-110-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  a4539323
BLAST score
                  405
E value
                  6.0e-39
Match length
                  159
% identity
NCBI Description
                  (AL035679) putative protein [Arabidopsis thaliana]
Seq. No.
                  7494
Contig ID
                  9398 1.R1040
5'-most EST
                  LIB3039-022-Q1-E1-F3
                  7495
Seq. No.
Contig ID
                  9409 1.R1040
5'-most EST
                  LIB3073-026-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3281868
BLAST score
                  197
                  7.0e-15
E value
                  73
Match length
% identity
NCBI Description
                  (AL031004) putative protein [Arabidopsis thaliana]
                  7496
Seq. No.
Contig ID
                  9409 2.R1040
5'-most EST
                  LIB3039-021-Q1-E1-H3
                  7497
Seq. No.
                  9411 1.R1040
Contig ID
5'-most EST
                  LIB3073-011-Q1-K1-C10
```

% identity

```
NCBI GI
                    q132825
BLAST score
                    215
E value
                    4.0e-17
Match length
                    80
% identity
                    62
                    50S RIBOSOMAL PROTEIN CL25, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_71308_pir__R5PM25 ribosomal protein PsCL25 precursor,
                   chloroplast - garden pea >gi_20877_emb_CAA32187_ (X14022)
PsCL25 ribosomal preprotein (AA -30 to 74) [Pisum sativum]
                    7498
Seq. No.
                    9411 2.R1040
Contig ID
5'-most EST
                   pcp700988732.hl
Method
                   BLASTN
NCBI GI
                    q18729
BLAST score
                    73
E value
                    3.0e-33
Match length
                    93
                    95
% identity
NCBI Description
                   Soybean (Glycine max) 18S ribosomal RNA
                    7499
Seq. No.
Contig ID
                9418 1.R1040
5'-most EST
                   LIB3050-002-Q1-E1-G10
Method
                   BLASTX
NCBI GI
                   q2827554
BLAST score
                   167
E value
                    2.0e-11
Match length
                    53
% identity
NCBI Description
                    (AL021635) putative DNA binding protein [Arabidopsis
                    thaliana]
Seq. No.
                    7500
Contig ID
                    9426 1.R1040
5'-most EST
                    leu701157796.hl
Method
                   BLASTX
NCBI GI
                    q2997686
BLAST score
                   290
E value
                   1.0e-25
Match length
                   165
% identity
NCBI Description
                    (AF053303) putative transcriptional co-activator
                    [Arabidopsis thaliana] >gi_3513735 (AF080118) contains
                   similarity to RNA polymerase II transcription cofactor pl5
                    [Arabidopsis thaliana] >gi_4539366_emb_CAB40060.1
                    (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.
                   7501
                   9430 1.R1040
Contig ID
                   kl1701213576.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3482924
BLAST score
                   250
E value
                   3.0e-21
Match length
                   92
```

(AC003970) Highly similar to cinnamyl alcohol NCBI Description dehydrogenase, gi 1143445 [Arabidopsis thaliana] Seq. No. 9430 2.R1040 Contig ID 5'-most EST LIB3039-021-Q1-E1-F8 Method BLASTX NCBI GI q3482926 BLAST score 323 7.0e-30 E value Match length 118 % identity NCBI Description (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi 1143445 [Arabidopsis thaliana] Seq. No. 9433 1.R1040 Contig ID 5'-most EST LIB3049-021-Q1-E1-H2 Method BLASTX NCBI GI q1173027 BLAST score 446 5.0e-44 E value Match length 120 % identity 60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal NCBI Description protein L31 [Nicotiana glutinosa] Seq. No. 9435 1.R1040 Contig ID 5'-most EST LIB3039-021-Q1-E1-F1 Method BLASTX NCBI GI q3132470 BLAST score 255 E value 6.0e-22 Match length 113 % identity NCBI Description (AC003096) unknown protein [Arabidopsis thaliana] Seq. No. 7505 Contig ID 9439 1.R1040 5'-most EST qsv701048747.h1 Seq. No. 7506 Contig ID 9446 1.R1040 5'-most EST zzp700835432.h1 Method BLASTX NCBI GI g2147966 BLAST score 369 E value 5.0e-46 115 Match length 79 % identity

NCBI Description

probable 1-acyl-sn-glycerol-3-phosphate acyltransferase - Limnanthes douglasii >gi_1067138_emb_CAA88620_ (Z48730) 1-acyl-sn-glycerol-3-phosphate acyltransferase (putative)

[Limnanthes douglasii]

Seq. No. 7507

```
9451 1.R1040
Contig ID
5'-most EST
                   pxt700943324.h1
                   BLASTX
Method
NCBI GI
                   g3152583
BLAST score
                   204
                   1.0e-15
E value
Match length
                   209
                   34
% identity
                   (AC002986) Contains similarity to inhibitor of apoptosis
NCBI Description
                   protein gb_U45881 from D. melanogaster. [Arabidopsis.
                   thaliana]
Seq. No.
                   7508
                   9471 1.R1040
Contig ID
                  LIB3106-050-Q1-K1-G2
5'-most EST
Method
                  BLASTX
                   g4514716
NCBI GI
BLAST score
                   192
                   2.0e-14
E value
                   119
Match length
                   36
% identity
                   (AB017533) EPc [Nicotiana tabacum]
NCBI Description
                   7509
Seq. No.
                   9478 1.R1040
Contig ID
5'-most EST
                  LIB3170-083-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                   g3152565
BLAST score
                   412
E value
                   7.0e-40
                   251
Match length
% identity
                   (AC002986) EST gb N65759 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  7510
Seq. No.
Contig ID ·
                   9482 1.R1040
5'-most EST
                  uC-gmrominsoy232d05b1
                  7511
Seq. No.
                   9482 2.R1040
Contig ID
5'-most EST
                  asn701141173.hl
                  7512
Seq. No.
Contig ID
                  9482 3.R1040
5'-most EST
                  LIB3107-074-Q1-K1-F11
Seq. No.
                  7513
                  9483 1.R1040
Contig ID
5'-most EST
                  LIB3039-020-Q1-E1-H3
Method
                  BLASTX
                  g2497226
NCBI GI
BLAST score
                  188
                  9.0e-14
E value
                  214
Match length
                  32
% identity
                  HYPOTHETICAL 38.2 KD PROTEIN IN PRE5-FET4 INTERGENIC REGION
NCBI Description
```

Method

NCBI GI

BLASTX

g4314356

```
(Z54141) unknown [Saccharomyces cerevisiae]
Seq. No.
                   7514
                   9483 2.R1040
Contig ID
5'-most EST
                   uC-gmropic067b04b1
                   7515
Seq. No.
                   9487 1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1145178.h1
Method
                   BLASTX
                   g4115949
NCBI GI
BLAST score
                   248
E value
                   3.0e-21
Match length
                   104
                   55
% identity
NCBI Description
                   (AF118223) contains similarity to adenosine deaminases
                   [Arabidopsis thaliana]
Seq. No.
                   7516
                   9494 1.R1040
Contig ID
5'-most EST
                   uxk7\overline{0}0672041.h1
Method
                   BLASTX
NCBI GI
                   g1170504
BLAST score
                   1801
                   0.0e + 00
E value
Match length
                   606
                   61
% identity
NCBI Description
                   EUKARYOTIC INITIATION FACTOR (ISO) 4F SUBUNIT P82
                   (IEIF-(ISO)4F P82) >gi 452440 (M95747) initiation factor
                   (iso)4f p82 subunit [Triticum aestivum]
                   7517
Seq. No.
                   9495 1.R1040
Contig ID
5'-most EST
                   pcp7\overline{0}0991891.h1
Seq. No.
                   7518
Contig ID
                   9511 1.R1040
5'-most EST
                   LIB3074-004-Q1-K1-F12
Method
                   BLASTX
NCBI GI
                   q3724328
BLAST score
                   145
E value
                   1.0e-08
Match length
                   151
% identity
                   (AB013095) heme-binding protein [Mus musculus]
NCBI Description
Seq. No.
                   7519
                   9511 2.R1040
Contig ID
5'-most EST
                   LIB3109-003-Q1-K1-A6
Seq. No.
                   7520
Contig ID
                   9522 1.R1040
5'-most EST
                   pcp700993234.h1
```

>gi_1363796_pir__S59308 probable membrane protein YMR315w yeast (Saccharomyces cerevisiae) >gi_984688_emb_CAA90833_

```
BLAST score
                   605
E value
                   2.0e-62
Match length
                   347
                   37
% identity
                   (AC006340) putative anthocyanidin-3-glucoside
NCBI Description
                   rhamnosyltransferase [Arabidopsis thaliana]
                   7521
Seq. No.
                   9525 1.R1040
Contig ID
                   rlr700902209.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3913633
BLAST score
                   347
E value
                   2.0e-32
Match length
                   160
% identity
                   47
NCBI Description
                   HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown
                   protein [Arabidopsis thaliana]
                   7522
Seq. No.
Contig ID
                   9529 1.R1040
5'-most EST
                   gsv7\overline{0}1055536.h1
                   7523
Seq. No.
Contig ID
                   9532 1.R1040
5'-most EST
                   LIB3109-031-Q1-K1-H7
Method
                   BLASTX
NCBI GI
                   q3894197
BLAST score
                   152
                   7.0e-10
E value
Match length
                   82
% identity
                   (AC005662) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   7524
Seq. No.
Contig ID
                   9541 1.R1040
5'-most EST
                   LIB3107-071-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   g2276463
BLAST score
                   762
                   9.0e-81
E value
Match length
                   475
% identity
                   (AF002020) Niemann-Pick C disease protein [Homo sapiens]
NCBI Description
                   >gi_4557803_ref_NP_000262.1_pNPC1_ Niemann-Pick disease,
                   type C1
Seq. No.
                   7525
                   9547 1.R1040
Contig ID
5'-most EST
                   LIB3106-089-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   q2982432
BLAST score
                   325
E value
                   5.0e-30
                   73
Match length
% identity
NCBI Description
                   (AL022224) putative protein [Arabidopsis thaliana]
```

BLAST score

```
7526
Seq. No.
Contig ID
                   9547 2.R1040
                   LIB3106-067-P1-K1-F7
5'-most EST
Method
                   BLASTX
                   g2982432
NCBI GI
BLAST score
                   325
                   4.0e-30
E value
Match length
                   73
% identity
                   81
NCBI Description
                   (AL022224) putative protein [Arabidopsis thaliana]
                   7527
Seq. No.
                   9548 1.R1040
Contig ID
5'-most EST
                   leu7\overline{0}1154367.h1
Method
                   BLASTX
                   g4544436
NCBI GI
BLAST score
                   293
E value
                   2.0e-26
Match length
                   102
% identity
                   60
                    (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase,
NCBI Description
                   3' partial [Arabidopsis thaliana]
Seq. No.
                   7528
                   9552 1.R1040
Contig ID
                   kmv7\overline{0}0740207.h1
5'-most EST
                   BLASTX
Method
                   g2632106
NCBI GI
BLAST score
                   711
E value
                   3.0e-75
Match length
                   212
% identity
                   61
                   (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                   7529
Seq. No.
                   9558 1.R1040
Contig ID
5'-most EST
                   LIB3039-019-Q1-E1-G11
                   7530
Seq. No.
                   9558 2.R1040
Contig ID
5'-most EST
                   jC-gmf102220075f08a1
Seq. No.
                   7531
                   9560 1.R1040
Contig ID
5'-most EST
                   vzy7\overline{0}0754495.h1
Seq. No.
                   7532
Contig ID
                   9562 1.R1040
5'-most EST
                   leu7\overline{0}1157074.h1
                   7533
Seq. No.
Contig ID
                   9565 1.R1040
5'-most EST
                   LIB3170-026-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   g3876465
```

Match length

```
2.0e-30
E value
Match length
                   83
                   76
% identity
NCBI Description
                   (Z81071) predicted using Genefinder; Similarity to Human
                   small nuclear ribonucleoprotein E (SW:P08578); cDNA EST
                   yk375g7.3 comes from this gene; cDNA EST yk375g7.5 comes
                   from this gene; cDNA EST yk435f5.3 comes from this gene;
                   7534
Seq. No.
                   9568 1.R1040
Contig ID
5'-most EST
                   wvk700686485.hl
Method
                   BLASTX
                   q3668074
NCBI GI
BLAST score
                   526
E value
                   2.0e-53
Match length
                   159
                   62
% identity
NCBI Description
                   (AC004667) hypothetical protein [Arabidopsis thaliana]
                   7535
Seq. No.
Contig ID
                   9585 1.R1040
5'-most EST
                   txt700734422.h1
Method
                   BLASTX
                   g3482973
NCBI GI
BLAST score
                   293
E value
                   3.0e-26
Match length
                   168
% identity
                   44
                   (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   7536
Seq. No.
Contig ID
                   9585 2.R1040
5'-most EST
                   LIB3039-019-Q1-E1-D7
Method
                   BLASTX
                   g3482973
NCBI GI
BLAST score
                   144
E value
                   8.0e-09
Match length
                   98
% identity
                   41
                   (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7537
                   9593 1.R1040
Contig ID
5'-most EST
                   ncj700982214.hl
Seq. No.
                   7538
Contig ID
                   9593 2.R1040
5'-most EST
                   kl1701204547.h2
Seq. No.
                   7539
                   9597 1.R1040
Contig ID
5'-most EST
                   LIB3039-012-Q1-E1-A5
Method
                   BLASTX
NCBI GI
                   q3738309
BLAST score
                   303
E value
                  .2.0e-27
```

E value

1.0e-17

```
% identity
                  59
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
                  7540
Seq. No.
                  9600 1.R1040
Contig ID
                  leu701150153.h1
5'-most EST
                  BLASTX
Method
                  g549577
NCBI GI
BLAST score
                  227
                  1.0e-18
E value
Match length
                  66
                  65
% identity
                  HYPOTHETICAL 17.1 KD PROTEIN IN MECB-GLTX INTERGENIC REGION
NCBI Description
                  >gi 2127059_pir__S66120 hypothetical protein - Bacillus
                  subtilis >gi 289281 (L14580) unknown [Bacillus subtilis]
                  >gi 467479 dbj BAA05325 (D26185) unknown [Bacillus
                  subtilis] >gi 2632358 emb CAB11867 (Z99104) similar to
                  hypothetical proteins [Bacillus subtilis]
                  7541
Seq. No.
                  9601 1.R1040
Contig ID
5'-most EST
                  epx701107762.h1
                  7542
Seq. No.
                  9603 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810089e12d1
Seq. No.
                  7543
                  9606 1.R1040
Contig ID
5'-most EST
                  leu7\overline{0}1152657.h1
                  BLASTX
Method
NCBI GI
                  q4455202
BLAST score
                  405
                  2.0e-39
E value
                  114
Match length
% identity
                  (AL035440) putative APG protein [Arabidopsis thaliana]
NCBI Description
                  7544
Seq. No.
                  9610 1.R1040
Contig ID
                  rlr700901982.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4559310
BLAST score
                  154
                  1.0e-09
E value
                  119
Match length
                  31
% identity
NCBI Description
                  (AF129131) putative Zic3 binding protein; CBP3 protein
                  homolog [Xenopus laevis]
                  7545
Seq. No.
                  9626 1.R1040
Contig ID
5'-most EST
                  gsv701051404.h1
Method
                  BLASTX
NCBI GI
                  g2194122
                  221
BLAST score
```

Match length 151 % identity 40

NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]

Seq. No. 7546

Contig ID 9626_2.R1040

5'-most EST LIB3051-020-Q1-E1-G3

Method BLASTX
NCBI GI g3123176
BLAST score 287
E value 4.0e-25
Match length 249
% identity 22

NCBI Description HYPOTHETICAL 43.1 KD TRP-ASP REPEATS CONTAINING PROTEIN

K04G11.4 IN CHROMOSOME X >gi_3878300_emb_CAB01760_ (Z78544) predicted using Genefinder; Similarity to C.elegans Guanine nucleotide binding protein (WP:C14B1.4) [Caenorhabditis

elegans]

Seq. No. 7547

Contig ID 9626 3.R1040

5'-most EST LIB3039-018-Q1-E1-E3

Method BLASTX
NCBI GI g3451472
BLAST score 155
E value 1.0e-09

Match length 112 % identity 9

NCBI Description (AL031349) transcription initiation factor TFIID subunit

[Schizosaccharomyces pombe]

Seq. No. 7548

Contig ID 9626_6.R1040

5'-most EST jC-gmle01810035d06d1

Seq. No. 7549

Contig ID 9630_1.R1040

5'-most EST jC-gmf102220114c12a1

Method BLASTX
NCBI GI g3367537
BLAST score 372
E value 4.0e-35
Match length 137
% identity 54

NCBI Description (AC004392) Contains similarity to ANK repeat region of

Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from Caenorhabditis elegans cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375.

[Arabid

Seq. No. 7550

Contig ID 9638 1.R1040

5'-most EST LIB3039-018-Q1-E1-D1

Seq. No. 7551

Contig ID 9644 1.R1040

5'-most EST jC-gmf102220053a07a1

```
7552
Seq. No.
                  9646_1.R1040
Contig ID
                  LIB3039-018-Q1-E1-C2
5'-most EST
                  BLASTX
Method
                  g3451067
NCBI GI
                  189
BLAST score
                  2.0e-14
E value
                  44
Match length
                  84
% identity
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  7553
                  9665 1.R1040
Contig ID
                  LIB3039-017-Q1-E1-H4
5'-most EST
                  7554
Seq. No.
                  9666 1.R1040
Contig ID
                  LIB3039-017-Q1-E1-H5
5'-most EST
                  7555
Seq. No.
Contig ID
                  9672 1.R1040
                  LIB3039-018-Q1-E1-A12
5'-most EST
                  BLASTX
Method
NCBI GI
                  g632220
BLAST score
                  315
                  6.0e-29
E value
                  112
Match length
                  61
% identity
                  ribosomal protein L2 - evening primrose mitochondrion
NCBI Description
                  >gi_516394_emb_CAA56451_ (X80170) 70s mitochondrial
                  ribosomal protein L2 [Oenothera berteriana]
                  7556
Seq. No.
                  9673_1.R1040
Contig ID
5'-most EST
                  LIB3039-018-Q1-E1-A3
Method
                  BLASTX
NCBI GI
                  g2253579
BLAST score
                  141
E value
                  9.0e-09
Match length
                  83
% identity
NCBI Description
                   (U78721) hypothetical protein [Arabidopsis thaliana]
                  7557
Seq. No.
                  9676_1.R1040
Contig ID
5'-most EST
                  LIB3039-017-Q1-E1-E3
Method
                  BLASTX
NCBI GI
                  g109219
BLAST score
                  272
E value
                  1.0e-23
                  230
Match length
% identity
                  dimethylaniline monooxygenase (N-oxide-forming) (EC
NCBI Description
                  1.14.13.8), hepatic 1 - rabbit
```

7558

Seq. No.

NCBI Description

```
9677 1.R1040
Contig ID
5'-most EST
                   g5677150
                   7559
Seq. No.
                   9680 1.R1040
Contig ID
5'-most EST
                   bth700846387.h1
                   7560
Seq. No.
Contig ID
                   9690_1.R1040
5'-most EST
                   jC-gmle01810086e11a1
                   7561
Seq. No.
                   9702 1.R1040
Contig ID
5'-most EST
                   LIB3039-017-Q1-E1-C11
Method
                   BLASTX
                   g2262165
NCBI GI
BLAST score
                   255
                   4.0e-22
E value
Match length
                   101
% identity
                   51
                   (AC002329) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   7562
Seq. No.
                   9717 1.R1040
Contig ID
                                                            1.
5'-most EST
                   LIB3039-016-Q1-E1-G5
Method
                   BLASTX
                   q3097321
NCBI GI
BLAST score
                   550
                   3.0e-58
E value
Match length
                   283
% identity
                   45
                   (AB013289) Bd 30K [Glycine max]
NCBI Description
                   7563
Seq. No.
Contig ID
                   9722 1.R1040
5'-most EST
                   LIB3039-016-Q1-E1-H11
Method
                   BLASTX
NCBI GI
                   q1699370
BLAST score
                   296
E value
                   1.0e-26
Match length
                   149
% identity
                   46
NCBI Description
                   (S82620) prolidase=peptidase D/imidopeptidase {EC 3.4.13.9}
                   [mice, liver, Peptide, 493 aa] [Mus sp.]
Seq. No.
                   7564
                   9727 1.R1040
Contig ID
                   epx701107982.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3415134
BLAST score
                   165
E value
                   2.0e-11
Match length
                   40
                   75
% identity
```

(AF082024) Phyb1 [Pimpinella brachycarpa]

E value

1.0e-22

```
7565
Seq. No.
                   9727 2.R1040
Contig ID
5'-most EST
                   LIB3139-041-P1-N1-H5
                   BLASTX
Method
                   g3415134
NCBI GI
                   279
BLAST score
                   6.0e-25
E value
                   76
Match length
                   71
% identity
                   (AF082024) Phyb1 [Pimpinella brachycarpa]
NCBI Description
                   7566
Seq. No.
Contig ID
                   9728 1.R1040
                   ncj700981368.hl
5'-most EST
Seq. No.
                   7567
                   9728 2.R1040
Contig ID
5'-most EST
                   wrg7\overline{0}0790469.h2
                   7568
Seq. No.
Contig ID
                   9732_1.R1040
5'-most EST
                   LIB3049-054-Q1-E1-H2
                   BLASTX
Method
NCBI GI
                   g4056506
BLAST score
                   201
E value
                   2.0e-15
Match length
                   137
% identity
                   32
                   (AC005896) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   7569
Seq. No.
                   9732 2.R1040
Contig ID
5'-most EST
                  LIB3092-058-Q1-K1-E1
                   7570
Seq. No.
Contig ID
                   9732_3.R1040
5'-most EST
                   zhf700960794.h1
Method
                   BLASTX
                   g2623304
NCBI GI
BLAST score
                   204
E value
                   7.0e-16
Match length
                   132
% identity
                   32
                   (AC002409) similar to Medicago nodulin N21 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   7571
Contig ID
                   9733 1.R1040
5'-most EST
                   LIB3040-056-Q1-E1-D10
                   7572
Seq. No.
Contig ID
                   9736 1.R1040
5'-most EST
                  LIB3039-016-Q1-E1-F6
Method
                  BLASTX
NCBI GI
                   q3413703
BLAST score
                   263
```

Match length

143

```
184
Match length
% identity
                   45
                   (AC004747) unknown protein [Arabidopsis thaliana]
NCBI Description
                   7573
Seq. No.
                   9739 1.R1040
Contig ID
5'-most EST
                   pcp700990081.hl
Seq. No.
                   7574
                   9744 2.R1040
Contig ID
5'-most EST
                   gsv701056547.hl
                   7575
Seq. No.
                   9744 3.R1040
Contig ID
5'-most EST
                   crh700856518.hl
                   7576
Seq. No.
                   9751 1.R1040
Contig ID
5'-most EST
                   pmv7\overline{0}0895050.h1
                   7577
Seq. No.
                   9755 1.R1040
Contig ID
5'-most EST
                   hrw701061761.hl
Method
                   BLASTX
NCBI GI
                   q4454051
BLAST score
                   267
E value
                   8.0e-35
Match length
                   147
% identity
                   (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                   thaliana]
                   7578
Seq. No.
                   9757 1.R1040
Contig ID
5'-most EST
                   LIB3039-016-Q1-E1-C4
Seq. No.
                   7579
                   9769 1.R1040
Contig ID
5'-most EST
                   fde700875709.hl
Method
                   BLASTX
NCBI GI
                   q3600032
BLAST score
                   240
E value
                   4.0e-20
Match length
                   128
                   48
% identity
NCBI Description
                   (AF080119) contains similarity to tropomyosin (Pfam:
                   Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam:
                   ATP-synt B.hmm, score: 10.89) [Arabidopsis thaliana]
Seq. No.
                   7580
Contig ID
                   9770 1.R1040
5'-most EST
                   LIB3040-003-Q1-E1-H1
Method
                   BLASTX
NCBI GI
                   g3687251
BLAST score
                   546
                   9.0e-56
E value
```

```
% identity
                  73
NCBI Description
                   (AC005169) unknown protein [Arabidopsis thaliana]
                  7581
Seq. No.
                  9784 1.R1040
Contig ID
                  LIB3107-003-Q1-K1-B10
5'-most EST
                  7582
Seq. No.
                  9785 1.R1040
Contig ID
5'-most EST
                  xpa700795562.h1
                  7583
Seq. No.
                  9788 1.R1040
Contig ID
5'-most EST
                  g5606786
Method
                  BLASTX
                  g4539390
NCBI GI
BLAST score
                  1815
                  0.0e + 00
E value
                  380
Match length
% identity
                  88
                   (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)
NCBI Description
                   [Arabidopsis thaliana]
                  7584
Seq. No.
Contig ID
                  9788 2.R1040
                  jC-gmst02400055c01a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4056456
BLAST score
                   686
                  3.0e-72
E value
Match length
                  204
                  69
% identity
NCBI Description
                   (AC005990) Strong similarity to gb U20808 auxin-induced
                  protein from Vigna radiata and a member of the zinc-binding
                  dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006
                  and gb_AA395179 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  7585
                  9788 3.R1040
Contig ID
5'-most EST
                  crh700851255.h1
                  BLASTX
Method
NCBI GI
                  q4539390
BLAST score
                  626
E value
                  4.0e-65
Match length
                  135
% identity
                   (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)
NCBI Description
                   [Arabidopsis thaliana]
                  7586
Seq. No.
                  9788_4.R1040
Contig ID
5'-most EST
                  LIB3049-020-Q1-E1-B6
Method
                  BLASTX
                  g2182029
NCBI GI
                  579
BLAST score
E value
                  1.0e-61
```

148

Match length

Method

NCBI GI

BLASTX

g1877397

```
% identity
                   84
NCBI Description
                   (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]
Seq. No.
                   7587
Contig ID
                   9788 5.R1040
5'-most EST
                  xpa700792520.h1
Method
                  BLASTX
NCBI GI
                   q2129738
BLAST score
                   560
E value
                   1.0e-57
Match length
                   141
% identity
                   74
NCBI Description
                   shaggy-like kinase dzeta - Arabidopsis thaliana
                  >gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta
                   [Arabidopsis thaliana] >gi_1669653 emb_CAA70483 (Y09300)
                  serine/threonine kinase [Arabidopsis thaliana]
Seq. No.
Contig ID
                  9788 6.R1040
5'-most EST
                  uC-gmflminsoy079c09b1
Seq. No.
Contig ID
                  9788 9.R1040
5'-most EST
                  LIB3170-024-Q1-J1-A12
Seq. No.
Contig ID
                  9788 11.R1040
5'-most EST
                  LIB3049-002-01-E1-G7
Method
                  BLASTX
NCBI GI
                  g1532168
BLAST score
                  194
E value
                  7.0e-15
Match length
                  66
% identity
NCBI Description
                   (U63815) localized according to blastn similarity to EST
                  sequences; therefore, the coding span corresponds only to
                  an area of similarity since the initation codon and stop
                  codon could not be precisely determined [Arabidopsis
                  thaliana]
Seq. No.
                  7591
                  9788 12.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy069b05b1
Method
                  BLASTX
NCBI GI
                  q4539390
BLAST score
                  413
E value
                  2.0e-52
Match length
                  119
% identity
                  81
NCBI Description
                  (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)
                  [Arabidopsis thaliana]
                  7592
Seq. No.
                  9788 13.R1040
Contig ID
5'-most EST
                  LIB3049-020-Q1-E1-B4
```

Method

BLASTX

```
207
BLAST score
E value
                   4.0e-16
Match length
                   48
% identity
                   81
NCBI Description
                   (Y11591) shaggy-like kinase [Ricinus communis]
                   7593
Seq. No.
                   9792 1.R1040
Contig ID
5'-most EST
                   LIB3039-015-Q1-E1-G10
Method
                   BLASTX
NCBI GI
                   q4335754
                   191
BLAST score
                   2.0e-23
E value
                   76
Match length
                   71
% identity
NCBI Description
                   (AC006284) putative acid phophatase (contains
                   metallo-phosphoesterase motif, prosite: QDOC50185)
                   [Arabidopsis thaliana]
                   7594
Seq. No.
Contig ID
                   9799 1.R1040
5'-most EST
                   zsg7\overline{0}1123467.h1
Method
                   BLASTX
NCBI GI
                   g3702332
BLAST score
                   480
                   8.0e-48
E valuè
Match length
                   222
                   42
% identity
NCBI Description
                   (AC005397) unknown protein [Arabidopsis thaliana]
                   7595
Seq. No.
Contig ID
                   9799 2.R1040
                   LIB3106-085-Q1-K1-E12
5'-most EST
Method
                   BLASTX
                   g3702332
NCBI GI
BLAST score
                   243
                   1.0e-20
E value
Match length
                   82
% identity
                   54
                   (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7596
Contig ID
                   9800 1.R1040
5'-most EST
                   LIB3039-015-Q1-E1-D9
Seq. No.
Contig ID
                   9800 2.R1040
5'-most EST
                   zsg701129547.hl
                   7598
Seq. No.
Contig ID
                   9804 1.R1040
5'-most EST
                   LIB3056-013-Q1-N1-B12
Seq. No.
                   7599
Contig ID
                   9807 1.R1040
                   vzy7\overline{0}0750953.h1
5'-most EST
```

```
NCBI GI
                   g2854153
BLAST score
                   296
                   1.0e-35
E value
                   166
Match length
                   51
% identity
                   (AF045640) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
                   7600
Seq. No.
                   9807 2.R1040
Contig ID
                   LIB3093-039-Q1-K1-A3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2854153
BLAST score
                   149
                   2.0e-09
E value
                   55
Match length
% identity
                   56
                   (AF045640) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
                   7601
Seq. No.
Contig ID
                   9811 1.R1040
                   leu701154049.hl
5'-most EST
                   7602
Seq. No.
                   9813_1.R1040
Contig ID
5'-most EST
                   LIB3039-015-Q1-E1-D8
                   7603
Seq. No.
                   9815 1.R1040
Contig ID
5'-most EST
                   trc7\overline{0}0562769.h1
                   BLASTX
Method
NCBI GI
                   g3063710
BLAST score
                   188
E value
                   2.0e-13
Match length
                   116
% identity
                   34
NCBI Description
                   (AL022537) putative protein [Arabidopsis thaliana]
                   7604
Seq. No.
Contig ID
                   9815 4.R1040
5'-most EST
                   jC-gmro02910019e01a1
Seq. No.
                   7605
Contig ID
                   9818 1.R1040
                   LIB3039-015-Q1-E1-C7
5'-most EST
Method
                   BLASTX
                   g3892050
NCBI GI
BLAST score
                   550
                   1.0e-81
E value
Match length
                   281
% identity
NCBI Description
                   (AC002330) hypothetical protein [Arabidopsis thaliana]
                   7606
Seq. No.
Contig ID
                   9830 1.R1040
```

LIB3039-015-Q1-E1-B10

NCBI Description

```
7607
Seq. No.
                   9830 2.R1040
Contig ID
5'-most EST
                   LIB3106-095-Q1-K1-D6
                   7608
Seq. No.
                   9830_3.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy017c12b1
Seq. No.
Contig ID
                   9841 1.R1040
5'-most EST
                   hrw701062003.h1
                   7610
Seq. No.
Contig ID
                   9858 1.R1040
5'-most EST
                   xpa700795673.h1
Method
                   BLASTX
NCBI GI
                   g1532175
BLAST score
                   408
E value
                   1.0e-39
                   104
Match length
% identity
                   68
NCBI Description
                   (U63815) similar to protein disulfide isomerase
                   [Arabidopsis thaliana]
Seq. No.
                   7611
                   9859 1.R1040
Contig ID
5'-most EST
                   LIB3039-001-Q1-E1-H4
Method
                   BLASTX
NCBI GI
                   g3128177
BLAST score
                   508
                   3.0e-51
E value
Match length
                   136
% identity
                   74
                   (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7612
                   9859 2.R1040
Contig ID
5'-most EST
                   pcp700991855.h1
Method
                   BLASTX
NCBI GI
                   q3128177
BLAST score
                   294
E value
                   1.0e-26
Match length
                   79
% identity
                   73
NCBI Description
                   (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                   7613
Contig ID
                   9862 1.R1040
5'-most EST
                   qsv701048517.hl
Method
                   BLASTX
NCBI GI
                   q3236245
BLAST score
                   635
E value
                   7.0e-72
                   241
Match length
% identity
```

(AC004684) myb-related protein [Arabidopsis thaliana]

13:00

```
7614
Seq. No.
                   9862 2.R1040
Contig ID
5'-most EST
                   6HA - \overline{0}2 - Q1 - B1 - B10
Method
                   BLASTX
                   g3236245
NCBI GI
BLAST score
                   333
                   5.0e-31
E value
Match length
                   73
% identity
                   85
NCBI Description
                   (AC004684) myb-related protein [Arabidopsis thaliana]
                   7615
Seq. No.
                   9865 1.R1040
Contig ID
5'-most EST
                   hrw701061053.h1
Method
                   BLASTX
                   q1171870
NCBI GI
BLAST score
                   163
E value
                   7.0e-11
Match length
                   93
% identity
                   33
                   NADH-UBIQUINONE OXIDOREDUCTASE 19 KD SUBUNIT (COMPLEX
NCBI Description
                   I-19KD) (CI-19KD) (COMPLEX I-PGIV) (CI-PGIV)
                   >gi 89670 pir S16208 NADH dehydrogenase (ubiquinone) (EC
                   1.6.5.3) 19K chain - bovine >gi_599681_emb_CAA42218
                   (X59697) 19 kDa subunit of NADH:ubiquinone oxidoreductase
                   complex (complex I) [Bos taurus]
                   7616
Seq. No.
                   9867 1.R1040
Contig ID
5'-most EST
                   LIB3039-014-Q1-E1-E6
                   BLASTX
Method
NCBI GI
                   g1351018
BLAST score
                   391
E value
                   1.0e-37
Match length
                   99
% identity
                   67
NCBI Description
                   RSI-1 PROTEIN PRECURSOR (TR132) >gi_1076597_pir__S43909
                   RSI-1 protein - tomato >gi_405585 (L22188) RSI-1 protein
                   [Lycopersicon esculentum] >gi_405587 (L22189) RSI-1 protein
                   [Lycopersicon esculentum]
Seq. No.
                   7617
Contig ID
                   9872 1.R1040
                   LIB3072-018-Q1-E1-G1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1172995
BLAST score
                   251
E value
                   3.0e-21
                   99
Match length
                   57
% identity
                   60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal
NCBI Description
                   protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus]
                   >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus
```

norvegicus]

Seq. No.

Contig ID

7623

9908 2.R1040

```
7618
Seq. No.
                   9883 1.R1040
Contig ID
                  LIB3039-014-Q1-E1-D1
5'-most EST
Method
                   BLASTX
                   q1076531
NCBI GI
BLAST score
                   728
                   3.0e-77
E value
                   152
Match length
% identity
                  hypothetical protein, pollen allergen homolog - garden pea
NCBI Description
                  >gi_2129891_pir__S65056 pollen allergen homolog precursor
                   (clone PPA1) - garden pea >gi_732905_emb_CAA59470_ (X85187)
                  homology with pollen allergens [Pisum sativum]
Seq. No.
                   7619
                   9886 1.R1040
Contig ID
                   LIB3039-014-Q1-E1-A12
5'-most EST
Method
                   BLASTX
                   q4249414
NCBI GI
BLAST score
                   245
E value
                   1.0e-20
Match length
                   113
% identity
                   47
NCBI Description
                   (AC006072) unknown protein [Arabidopsis thaliana]
                   7620
Seq. No.
                   9886 3.R1040
Contig ID
5'-most EST
                   nci7\overline{0}0979452.h1
Method
                   BLASTN
                   g4249393
NCBI GI
BLAST score
                   41
                   7.0e-14
E value
                   81
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T9J23 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   9890 1.R1040
Contig ID
5'-most EST
                   LIB3073-005-01-K1-F1
Seq. No.
                   7622
Contig ID
                   9908 1.R1040
5'-most EST
                   fua701041841.h1
Method
                  BLASTX
NCBI GI
                   q3915186
BLAST score
                   344
E value
                   5.0e-32
Match length
                   147
% identity
                   47
                  UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >gi 3128447
                   (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4
                   [Pichia angusta]
```

```
uC-gmflminsoy037b04b1
5'-most EST
Method
                   BLASTX
                   q3273562
NCBI GI
BLAST score
                   255
                   8.0e-22
E value
                   104
Match length
% identity
                   45
                   (AF036707) RAD6 [Candida albicans]
NCBI Description
Seq. No.
                   7624
Contig ID
                   9915 1.R1040
5'-most EST
                   LIB3039-013-Q1-E1-F6
Method
                   BLASTX
NCBI GI
                   q285741
BLAST score
                   152
                   6.0e-10
E value
                   79
Match length
                   39
% identity
NCBI Description
                   (D14550) EDGP precursor [Daucus carota]
Seq. No.
                   7625
Contig ID
                   9927_1.R1040
5'-most EST
                   LIB3107-040-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   q3024629
BLAST score
                   201
                   2.0e-15
E value
Match length
                   137
% identity
                   33
                   GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-GAMMA)
NCBI Description
                   >gi_423252_pir__S32369 gamma-SNAP protein - bovine
>gi_298669_bbs_127528 gamma soluble NSF attachment protein,
                   gamma SNAP=N-ethyl-maleimide-sensitive fusion protein
                   attachment protein [cattle, brain, Peptide, 328 aa]
                   >gi_445846_prf__1910317C NSF attachment protein
                   (SNAP):ISOTYPE=gamma [Bos taurus]
                   7626
Seq. No.
                   9930 1.R1040
Contig ID
5'-most EST
                   LIB3139-107-P1-N1-B3
Method
                   BLASTX
NCBI GI
                   q2494113
BLAST score
                   1038
E value
                   1.0e-113
Match length
                   226
% identity
NCBI Description
                   (AC002376) Strong similarity to Musa pectate lyase
                   (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come
                   from this gene. [Arabidopsis thaliana]
                   7627
Seq. No.
                   9933 1.R1040
Contig ID
5'-most EST
                   LIB3052-012-Q1-N1-B3
                   7628
Seq. No.
                   9938 1.R1040
Contig ID
5'-most EST
                   sat701015315.h1
```

1401

% identity

89

```
Method
                  BLASTX
NCBI GI
                   g4538965
BLAST score
                  250
                  2.0e-21
E value
                  105
Match length
                   47
% identity
                   (AL049488) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  7629
Seq. No.
                   9942_1.R1040
Contig ID
                  LIB3170-055-Q1-K1-G2
5'-most EST
Method
                  BLASTX
                   g2494162
NCBI GI
BLAST score
                   776
E value
                   2.0e-82
Match length
                   335
                   49 -
% identity
                  HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II
NCBI Description
                   PRECURSOR >gi 3879803 emb CAA87414 (Z47356) similar to
                  DNAJ [Caenorhabditis elegans]
Seq. No.
                  7630
                   9942 4.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy128f10b1
Method
                  BLASTX
                            ----
NCBI GI
                   g144832
BLAST score
                   152
E value
                   6.0e-10
                   41
Match length
                   63
% identity
                   (M74569) dnaJ [Clostridium acetobutylicum]
NCBI Description
                  7631
Seq. No.
                   9944 1.R1040
Contig ID
5'-most EST
                  LIB3039-013-Q1-E1-B3
Seq. No.
                  7632
Contig ID
                   9944 2.R1040 ·
5'-most EST
                  uC-gmflminsoy056e05b1
                  7633
Seq. No.
                   9948 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy271a10b1
                  7634
Seq. No.
                   9948 2.R1040
Contig ID
5'-most EST
                  LIB3109-014-Q1-K1-B8
Seq. No.
                  7635
                   9949 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800041h12a1
Method
                  BLASTX
NCBI GI
                  q2760362
BLAST score
                   647
E value
                  1.0e-67
Match length
                  138
```

```
(AF016511) 15.9 kDa subunit of RNA polymerase II
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   7636
                   9949 2.R1040
Contig ID
5'-most EST
                   xpa700797793.hl
                   BLASTX
Method
                   q2760362
NCBI GI
BLAST score
                   633
                   6.0e-66
E value
Match length
                   138
                   88
% identity
                   (AF016511) 15.9 kDa subunit of RNA polymerase II
NCBI Description
                   [Arabidopsis thaliana]
                   7637
Seq. No.
                   9949 4.R1040
Contig ID
5'-most EST
                   rca700999513.h1
                   BLASTN
Method
NCBI GI
                   q2760361
BLAST score
                   120
                   7.0e-61
E value
Match length
                   240
% identity
                   Arabidopsis thaliana 15.9 kDa subunit of RNA polymerase II
NCBI Description
                   (RPB15.9) mRNA, complete cds
                   7638
Seq. No.
                   9955 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810008e01a1
Method
                   BLASTX
NCBI GI
                   g3928543
BLAST score
                   1499
E value
                   1.0e-167
Match length
                   475
% identity
NCBI Description
                   (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
                   thaliana]
                   7639
Seq. No.
Contig ID
                   9956 1.R1040
5'-most EST
                   jC-gmro02910018a04a1 .
Seq. No.
                   7640
                   9956 2.R1040
Contig ID
5'-most EST
                   LIB3039-012-Q1-E1-H8
Method
                   BLASTX
NCBI GI
                   q4309884
BLAST score
                   284
E value
                   2.0e-25
                   79
Match length
% identity
                   (AC006389) similar to Schizosaccharomyces pombe splicing
NCBI Description
                   factor; similar to PID:3395591 [Homo sapiens]
Seq. No.
                   7641
```

9956 3.R1040

Contig ID

```
5'-most EST
                    LIB3074-026-Q1-E1-C4
 Method
                    BLASTX
                    q4309884
 NCBI GI
 BLAST score
                    116
                    2.0e-09
 E value
 Match length
                    68
 % identity
                    53
                    (AC006389) similar to Schizosaccharomyces pombe splicing
 NCBI Description
                    factor; similar to PID:3395591 [Homo sapiens]
 Seq. No.
                    7642
                    9958 1.R1040
 Contig ID
                    seb7\overline{0}0649775.h1
 5'-most EST
 Method
                    BLASTN
                    q410285
 NCBI GI
 BLAST score
                    367
                    0.0e + 00
 E value
                    804
· Match length
                    90
 % identity
 NCBI Description
                    Pisum sativum rho (ras-related) GTP-binding protein mRNA,
                    complete cds
                    7643
 Seq. No.
                    9958 3.R1040
 Contig ID
 5'-most EST
                    jC-qmst02400031h06a1
                                                                 BLASTN
 Method
                    q410285
 NCBI GI
                    90
 BLAST score
 E value
                    7.0e-43
 Match length
                    186
                    87
 % identity
                    Pisum sativum rho (ras-related) GTP-binding protein mRNA,
 NCBI Description
                    complete cds
 Seq. No.
                    7644
 Contig ID
                    9958 7.R1040
 5'-most EST
                    eep7\overline{0}0869546.h1
 Method
                    BLASTN
                    q410285
 NCBI GI
 BLAST score
                    42
                    2.0e-14
 E value
 Match length
                    62
                    92
 % identity
                    Pisum sativum rho (ras-related) GTP-binding protein mRNA,
 NCBI Description
                    complete cds
 Seq. No.
                    7645
 Contig ID
                    9966 1.R1040
 5'-most EST
                    asn701141112.h1
                    7646
 Seq. No.
                    9966 2.R1040
 Contig ID
 5'-most EST
                    LIB3039-012-01-E1-G10
                    7647
 Seq. No.
 Contig ID
                    9967 1.R1040
```

LIB3039-012-Q1-E1-G12

```
Method
                   BLASTX
NCBI GI
                   q1330343
BLAST score
                   312
E value
                   8.0e-29
                   99
Match length
% identity
                   60
                   (U58755) C34D4.12 gene product [Caenorhabditis elegans]
NCBI Description
Seq. No.
                   7648
                   9979 1.R1040
Contig ID
                   LIB3092-018-Q1-K1-D12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3212852
BLAST score
                   387
E value
                   2.0e-46
Match length
                   176
% identity
NCBI Description
                   (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                   9988 1.R1040
Contig ID
5'-most EST
                   LIB3139-088-P1-N1-A7
Method
                   BLASTX
NCBI GI
                   q4240116
BLAST score
                   844
E value
                   9.0e-91
Match length
                   189
% identity
                   (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
NCBI Description
                   thaliana] >gi 4240118 dbj BAA74838 (AB007800)
                   NADH-cytochrome b5 reductase [Arabidopsis thaliana]
                   7650
Seq. No.
                   9988 2.R1040
Contig ID
                   LIB3039-012-Q1-E1-C10
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4336205
BLAST score
                   362
E value
                   2.0e-34
Match length
                   104
% identity
                   64
NCBI Description
                   (AF077372) cytochrome b5 reductase [Zea mays]
Seq. No.
                   7651
                   9989 2.R1040
Contig ID
5'-most EST
                   zsq7\overline{0}1128847.h1
Method
                   BLASTX
NCBI GI
                   g3894191
BLAST score
                   423
                   2.0e-41
E value
Match length
                   158
% identity
NCBI Description
                   (AC005662) unknown protein [Arabidopsis thaliana]
                   7652
Seq. No.
                   9999 1.R1040
Contig ID
```

...

LIB3039-012-Q1-E1-D1

```
Method
                   BLASTX
NCBI GI
                   g4006867
BLAST score
                   741
                   3.0e-81
E value
Match length
                   197
                   81
% identity
                   (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
                   7653
Seq. No.
                   10010 1.R1040
Contig ID
5'-most EST
                   ncj70\overline{0}979503.h2
Method
                   BLASTX
NCBI GI
                   g3860319
BLAST score
                   1682
E value
                   0.0e+00
Match length
                   442
                   77
% identity
NCBI Description
                   (AJ012686) nucleolar protein [Cicer arietinum]
                   7654
Seq. No.
                   10010 2.R1040
Contig ID
5'-most EST
                   LIB3049-026-Q1-E1-F6
Method
                   BLASTX
NCBI GI
                   g4160346
BLAST score
                   337
                   2.0e-31
E value
Match length
                   142
% identity
                   50
NCBI Description
                   (AL035216) nucleolar protein involved in pre-rRNA
                   processing [Schizosaccharomyces pombe]
                   7655
Seq. No.
Contig ID
                   10010 3.R1040
5'-most EST
                   LIB3139-026-P1-N1-C1
Method
                   BLASTN
                   g3860318
NCBI GI
BLAST score
                   135
E value
                   1.0e-69
Match length
                   281 `
                   89
% identity
NCBI Description
                  Cicer arietinum mRNA for nucleolar protein, partial
                   7656
Seq. No.
Contig ID
                   10018 1.R1040
                   trc700565153.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2462822
BLAST score
                   354
E value
                   4.0e-33
Match length
                   148
% identity
                   53
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   7657
Seq. No.
                   10027 1.R1040
Contig ID
```

 $jsh70\overline{1}063965.h1$

NCBI Description

```
7658
Seq. No.
                   10027 2.R1040
Contig ID
                   ncj700979507.h2
5'-most EST
                   7659
Seq. No.
                   10030 1.R1040
Contig ID
5'-most EST
                   k11701213218.h1
Method
                   BLASTX
NCBI GI
                   g2462758
BLAST score
                   561
E value
                   3.0e-57
Match length
                   274
% identity
NCBI Description
                   (AC002292) putative RNA-binding protein [Arabidopsis
                   thaliana]
                   7660
Seq. No.
                   10040 1.R1040
Contig ID
                   fua701038228.h1
5'-most EST
Method
                   BLASTX
                   q3688172
NCBI GI
BLAST score
                   176
E value
                   2.0e-12
Match length
                   64
% identity
NCBI Description
                   (AL031804) putative protein [Arabidopsis thaliana]
                   7661
Seq. No.
                   10040 2.R1040
Contig ID
5'-most EST
                   LIB3109-052-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   q3688172
BLAST score
                   176
E value
                   1.0e-12
Match length
                   64
% identity
NCBI Description
                   (AL031804) putative protein [Arabidopsis thaliana]
                   7662
Seq. No.
                   10040 3.R1040
Contig ID
5'-most EST
                   trc700566501.hl
                   7663
Seq. No.
                   10048 1.R1040
Contig ID
                   txt700737261.h1
5'-most EST
Seq. No.
                   7664
                   10062 1.R1040
Contig ID
5'-most EST
                   LIB3040-050-Q1-E1-D1
Method
                   BLASTX
NCBI GI
                   q2842662
BLAST score
                   176
E value
                   1.0e-12
Match length
                   49
% identity
                   59
```

DNA-DIRECTED RNA POLYMERASES I, II, AND III 7.0 KD

POLYPEPTIDE (ABC10-ALPHA) (RPB7.0) (METALLOTHIONEIN-I GENE

Contig ID

TRANSCRIPTION ACTIVATOR)

```
7665
Seq. No.
Contig ID
                   10068 1.R1040
5'-most EST
                   LIB3109-038-Q1-K1-A10
                   7666
Seq. No.
                   10068 4.R1040
Contig ID
5'-most EST
                   zhf70\overline{0}964470.h1
                   BLASTX
Method
                   g3876716
NCBI GI
BLAST score
                   206
E value
                   2.0e-16
Match length
                   66
% identity
                   48
                   (Z46242) similar to Zinc finger, C3HC4 type (RING finger)
NCBI Description
                   [Caenorhabditis elegans]
                   7667
Seq. No.
Contig ID
                   10071 1.R1040
5'-most EST
                   uC-gmropic115d03b1
Seq. No.
                   7668
Contig ID
                   10071_2.R1040
                   leu70\overline{1}157872.h1
5'-most EST
                   BLASTN
Method
                   g532289
NCBI GI
BLAST score
                   49
                   2.0e-18
E value
Match length
                   61
% identity
                   95
NCBI Description
                   Soybean mRNA for late nodulin, complete cds
Seq. No.
                   10071_3.R1040
Contig ID
5'-most EST
                   uC-gmropic014c09b1
Method
                   BLASTN
                   g532289
NCBI GI
BLAST score
                   76
E value
                   2.0e-34
Match length
                   84
% identity
NCBI Description
                   Soybean mRNA for late nodulin, complete cds
Seq. No.
                   7670
Contig ID
                   10073 1.R1040
5'-most EST
                   LIB3039-011-Q1-E1-B2
Method
                   BLASTX
NCBI GI
                   q2262104
BLAST score
                   439
E value
                   1.0e-43
Match length
                   121
% identity
                   69
NCBI Description
                   (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
```

10076_1.R1040

E value

```
5'-most EST
                   LIB3039-011-Q1-E1-B5
Seq. No.
                   7672
                   10078 1.R1040
Contig ID
                   gsv70\overline{1}053747.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3021409
BLAST score
                   212
E value
                   8.0e-17
Match length
                   70
% identity
                   57
                   (Y12781) transducin (beta) like 1 protein [Homo sapiens]
NCBI Description
Seq. No.
                   10098 1.R1040
Contig ID
5'-most EST
                   LIB3051-005-Q1-E1-C6
Method
                   BLASTX
NCBI GI
                   g3193298
BLAST score
                   214
                   2.0e-35
E value
Match length
                   137
% identity
                   55
NCBI Description
                   (AF069298) T14P8.17 gene product [Arabidopsis thaliana]
Seq. No.
                   7674
                   10098 2.R1040
Contig ID
5'-most EST
                   zhf700955551.h1
Seq. No.
                   7675
Contig ID
                   10100 1.R1040
5'-most EST
                   LIB3039-010-Q1-E1-G5
Method
                   BLASTN
NCBI GI
                   q1732468
BLAST score
                   64
E value
                   2.0e-27
Match length
                   136
% identity
                   87
NCBI Description
                   Soybean mRNA for Mg chelatase subunit (46 kD), complete cds
Seq. No.
                   10105 1.R1040
Contig ID
5'-most EST
                   LIB3039-010-Q1-E1-E11
Method
                   BLASTX
NCBI GI
                   g3608154
BLAST score
                   288
E value
                   7.0e-26
Match length
                   137
% identity
                   43
                   (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
                   7677
Seq. No.
                   10107 1.R1040
Contig ID
5'-most EST
                   LIB3053-002-Q1-B1-C4
Method
                   BLASTX
NCBI GI
                   g4539422
BLAST score
                   1186
```

1.0e-130

```
306
Match length
                   74
% identity
                   (AL049171) putative protein [Arabidopsis thaliana]
NCBI Description
                   7678
Seq. No.
                   10120 1.R1040
Contig ID
                   LIB3039-010-Q1-E1-D1
5'-most EST
                   BLASTX
Method
                   g498040
NCBI GI
BLAST score
                   315
                   4.0e-29
E value
Match length
                   94
                   66
% identity
                   (L33793) ORF [Senecio odorus]
NCBI Description
                   7679
Seq. No.
                   10127 1.R1040
Contig ID
5'-most EST
                   g4302191
Method
                   BLASTX
                   g730463
NCBI GI
BLAST score
                   310
                   3.0e-28
E value
                   105
Match length
                   55
% identity
                   60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
NCBI Description
                   >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                   (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
                   protein L37 [Saccharomyces cerevisiae]
                   >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c
                   [Saccharomyces cerevisiae]
                   7680
Seq. No.
                   10130 1.R1040
Contig ID
5'-most EST
                  hrw70\overline{1}063208.h1
                   7681
Seq. No.
Contig ID
                   10130 2.R1040
5'-most EST
                   sat701012105.h1
                   7682
Seq. No.
                   10144 1.R1040
Contig ID
5'-most EST
                   LIB3109-052-Q1-K1-B5
Method
                  BLASTX
                   g135053
NCBI GI
                   705
BLAST score
E value
                   3.0e-74
Match length
                   302
% identity
                   47
NCBI Description
                   SULFITE OXIDASE >gi_86440_pir__A34180 sulfite oxidase (EC
                   1.8.3.1), hepatic - chicken
                   7683
Seq. No.
Contig ID
                   10146 1.R1040
5'-most EST
                   LIB3039-010-Q1-E1-A2
                   7684
Seq. No.
```

10158 1.R1040

Contig ID

Method

BLASTX

```
5'-most EST
                  LIB3039-009-Q1-E1-G8
Method
                  BLASTX
NCBI GI
                  g3335359
BLAST score
                   337
                   1.0e-31
E value
                   92
Match length
% identity
NCBI Description
                   (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                   10159 1.R1040
Contig ID
5'-most EST
                  uC-gmropic087d11b1
Method
                  BLASTX
NCBI GI
                  q2190187
BLAST score
                  194
E value
                   2.0e-14
Match length
                   201
% identity
                   33
NCBI Description
                   (D64087) nuclear matrix constituent protein 1 (NMCP1)
                   [Daucus carota]
Seq. No.
                   7686
                   10166 1.R1040
Contig ID
5'-most EST
                  LIB3039-009-Q1-E1-F10
                  7687
Seq. No.
                   10179 1.R1040
Contig ID
                  LIB3138-028-Q1-N1-G10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4455326
BLAST score
                   621
                  2.0e-64
E value
                  196
Match length
% identity
                   60
NCBI Description
                   (AL035525) putative protein [Arabidopsis thaliana]
                  7688
Seq. No.
                  10180 1.R1040
Contig ID
5'-most EST
                   sat701003879.hl
Method
                  BLASTX
NCBI GI
                  g421843
BLAST score
                  1396
E value
                   1.0e-155
Match length
                  315
                  84
% identity
NCBI Description
                  protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana
                  >gi 217861 dbj BAA01715 (D10909) serine/threonine protein
                  kinase [Arabidopsis thaliana]
                  7689
Seq. No.
                  10183 1.R1040
Contig ID
5'-most EST
                  fC-gmse700675307a1
                  7690
Seq. No.
                  10183 2.R1040
Contig ID
5'-most EST
                  leu701148361.hl
```

% identity

93

```
g1280434
NCBI GI
BLAST score
                   178
E value
                   5.0e-13
Match length
                   117
% identity
                   38
NCBI Description
                   (U42014) hemomucin [Drosophila melanogaster]
                   7691
Seq. No.
                   10188_1.R1040
Contig ID
                   LIB3053-008-Q1-N1-A10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3894168
BLAST score
                   503
                   9.0e-51
E value
Match length
                   190
% identity
                   52
NCBI Description
                   (AC005312) similar to phloem-specific lectin [Arabidopsis
                   thaliana]
                   7692
Seq. No.
                   10188 2.R1040
Contig ID
5'-most EST
                   LIB3049-055-Q1-E1-B2
                   BLASTX
Method
NCBI GI
                   g3894158
BLAST score
                   218
E value
                   1.0e-22
Match length
                   131
% identity
NCBI Description
                   (AC005312) similar to phloem-specific lectin [Arabidopsis
                   thaliana]
                   7693
Seq. No.
                   10206 1.R1040
Contig ID
5'-most EST
                   LIB3039-008-Q1-E1-G6
Seq. No.
                   7694
Contig ID
                   10207 1.R1040
5'-most EST
                   q4303898
Method
                   BLASTN
                   q170643
NCBI GI
BLAST score
                   301
E value
                   1.0e-168
Match length
                   440
% identity
NCBI Description
                   Vigna aconitifolia
                   5'-phosphoribosyl-4-(N-succinocarboxamide)-5-
                   aminoimidazole synthetase mRNA
Seq. No.
                   7695
                   10207 2.R1040
Contig ID
                   xpa70\overline{0}798252.h1
5'-most EST
Method
                   BLASTN
                   g170643
NCBI GI
BLAST score
                   77
E value
                   4.0e-35
Match length
                   225
```

E value

3.0e-18

```
NCBI Description
                  Vigna aconitifolia
                   5'-phosphoribosyl-4-(N-succinocarboxamide)-5-
                  aminoimidazole synthetase mRNA
Seq. No.
                  7696
                  10213 1.R1040
Contig ID
                   awf700838202.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2213614
BLAST score
                  268
E value
                   2.0e-23
Match length
                  116
% identity
                   46
NCBI Description
                   (AC000103) F21J9.8 [Arabidopsis thaliana]
Seq. No.
Contig ID
                  10221 1.R1040
5'-most EST
                  LIB3167-010-P1-K1-G8
Seq. No.
                  7698
                  10221 2.R1040
Contig ID
5'-most EST
                  wvk700681917.h1
                  7699
Seq. No.
Contig ID
                  10224 1.R1040
5'-most EST
                  leu701151970.hl
Method
                  BLASTX
NCBI GI
                  q2462834
BLAST score
                  206
E value
                   3.0e-16
Match length
                  121
% identity
                   40
NCBI Description
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  7700
Contig ID
                  10225 1.R1040
5'-most EST
                  LIB3040-008-Q1-E1-A3
                  7701
Seq. No.
                  10228 1.R1040
Contig ID
5'-most EST
                  LIB3039-008-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                  g541950
BLAST score
                  160
E value
                  7.0e-11
Match length
                  80
% identity
                  46
                  SPCP1 protein - soybean >gi 310576 (L12257) nodulin-26
NCBI Description
                   [Glycine max]
Seq. No.
                  7702
                  10235 1.R1040
Contig ID
5'-most EST
                  jC-gmle01810065b01a1
Method
                  BLASTX
                  g4539420
NCBI GI
BLAST score
                  224
```

```
-3.
Match length
                   80
                   61
% identity
                   (AL049171) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   7703
Seq. No.
                   10249 2.R1040
Contig ID
                   uxk70\overline{0}672272.h1
5'-most EST
Seq. No.
                   7704
                   10250_1.R1040
Contig ID
                   LIB3107-005-Q1-K1-F9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3025188
BLAST score
                   366
E value
                   1.0e-34
Match length
                   107
                   61
% identity
NCBI Description
                   HYPOTHETICAL 11.9 KD PROTEIN SLR1846
                   >gi 1652154 dbj BAA17078 (D90903) hypothetical protein
                   [Synechocystis sp.]
                   7705
Seq. No.
                   10261 1.R1040
Contig ID
5'-most EST
                   ncj700978977.hl
Method .
                   BLASTX
NCBI GI
                   q1362615
BLAST score
                   810
E value
                   2.0e-86
Match length
                   404
% identity
                   44
NCBI Description
                   iswi protein - fruit fly (Drosophila melanogaster)
                   >gi_439197 (L27127) ISWI protein [Drosophila melanogaster]
                   7706
Seq. No.
Contig ID
                   10264_1.R1040
5'-most EST
                   LIB3039-008-Q1-E1-A10
Method
                   BLASTX
                   q2760326
NCBI GI
BLAST score
                   145
                   3.0e-09
E value
Match length
                   88
% identity
                   34
NCBI Description
                   (AC002130) F1N21.11 [Arabidopsis thaliana]
                   7707
Seq. No.
Contig ID
                   10269 1.R1040
5'-most EST
                   qsv70\overline{1}044623.h1
Method
                   BLASTX
NCBI GI
                   q2911799
BLAST score
                   724
E value
                   1.0e-76
Match length
                   222
% identity
NCBI Description
                   (AF008184) 4-coumarate:CoA ligase 1 [Populus balsamifera
                   subsp. trichocarpa X Populus deltoides]
```

```
Seq. No.
                   7708
                   10276 1.R1040
Contig ID
5'-most EST
                   LIB3040-060-Q1-E1-F6
                   7709
Seq. No.
Contig ID
                   10284 1.R1040
5'-most EST
                   LIB3049-001-Q1-E1-A1
Method
                   BLASTX
NCBI GI
                   g4539417
BLAST score
                   357
E value
                   2.0e-33
Match length
                   106
% identity
                   65
NCBI Description
                   (AL049171) putative protein [Arabidopsis thaliana]
Seq. No.
                   7710
                   10284 2.R1040
Contig ID
5'-most EST
                   LIB3106-041-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g4539417
BLAST score
                   511
E value
                  1.0e-51
Match length
                   121
% identity
                   76
NCBI Description
                   (AL049171) putative protein [Arabidopsis thaliana]
Seq. No.
                   7711
                   10289 1.R1040
Contig ID
                   ssr700554183.hl
5'-most EST
Seq. No.
                   7712
                   10289 2.R1040
Contig ID
5'-most EST
                   uC-qmropic029g05b1
Seq. No.
                   7713
Contig ID
                   10298 1.R1040
5'-most EST
                   LIB3039-007-Q1-E1-A9
Method
                   BLASTX
NCBI GI
                   q913227
BLAST score
                   491
E value
                   3.0e-49
Match length
                   200
                   53
% identity
                   transcription factor XlDP-1 [Xenopus laevis, embryos,
NCBI Description
                   Peptide, 409 aa]
Seq. No.
                   7714
                   10298 2.R1040
Contig ID
5'-most EST
                   vzy700755726.h1
Method
                   BLASTX
NCBI GI
                   q3122929
BLAST score
                   170
E value
                   8.0e-12
Match length
                   63
                   57
% identity
NCBI Description
                  TRANSCRIPTION FACTOR DP-2 (E2F DIMERIZATION PARTNER 2)
```

(DP-3)

% identity

70

```
7715
Seq. No.
                   10298 3.R1040
Contig ID
                   pcp70\overline{0}994367.h1
5'-most EST
                   7716
Seq. No.
                   10312 1.R1040
Contig ID
5'-most EST
                   LIB3051-080-Q1-K1-G2
Method
                   BLASTN
NCBI GI
                   g2618602
BLAST score
                   41
E value
                   2.0e-13
Match length
                   104
                   85
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   7717
Contig ID
                   10318 1.R1040
5'-most EST
                   LIB30\overline{3}9-007-Q1-E1-A2
Method
                   BLASTX
NCBI GI
                   g4455202
BLAST score
                   199
                   2.0e-15
E value
Match length
                   55
% identity
NCBI Description
                   (AL035440) putative APG protein [Arabidopsis thaliana]
                   7718
Seq. No.
                   10328 1.R1040
Contig ID
5'-most EST
                   smc70\overline{0}749713.h1
                   7719
Seq. No.
                   10341_1.R1040
Contig ID
5'-most EST
                   trc700564224.h1
                   BLASTX
Method
NCBI GI
                   g3445208
BLAST score
                   601
E value
                   2.0e-62
Match length
                   146
                   78
% identity
                   (AC004786) putative amino-acid acetyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   7720
Seq. No.
                   10342 1.R1040
Contig ID
5'-most EST
                   fC-gmle700787001a2
Seq. No.
                   7721
                   10347 1.R1040
Contig ID
                   LIB3039-006-Q1-E1-E7
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4335763
BLAST score
                   329
E value
                   9.0e-31
Match length
                   91
```

Match length

400

```
(AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
                   7722
Seq. No.
Contig ID
                   10349 1.R1040
                   LIB3039-006-Q1-E1-B11
5'-most EST
                   7723
Seq. No.
                   10358 1.R1040
Contig ID
5'-most EST
                   LIB3106-069-P1-K1-A1
Method
                   BLASTX
                   g3980254
NCBI GI
                   600
BLAST score
                   5.0e-62
E value
Match length
                   183
                   61
% identity
                   (AJ006053) peroxisomal membrane protein [Arabidopsis
NCBI Description
                   thaliana]
                   7724
Seq. No.
                   10358 5.R1040
Contig ID
5'-most EST
                   g5753066
                   7725
Seq. No.
Contig ID
                   10360_1.R1040
5'-most EST
                   epx701107133.h1
                   BLASTX
Method
NCBI GI
                   q4538929
BLAST score
                   356
E value
                   9.0e-34
Match length
                   90
                   74
% identity
                   (AL049483) putative nucleic acid binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   7726
Seq. No.
Contig ID
                   10364_1.R1040
5'-most EST
                   LIB3039-005-Q1-E1-H11
Method
                   BLASTX
                   g3702323
NCBI GI
BLAST score
                   185
                   1.0e-13
E value
Match length
                   83
% identity
                   48
                   (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                   7727
Seq. No.
Contig ID
                   10375 1.R1040
5'-most EST
                   leu701153565.h1
                   7728
Seq. No.
                   10389 1.R1040
Contig ID
5'-most EST
                   LIB3040-008-Q1-E1-H1
Method
                   BLASTX
NCBI GI
                   q1653767
BLAST score
                   1176
E value
                   1.0e-129
```

```
% identity
                   56
NCBI Description
                   (D90916) oligopeptidase A [Synechocystis sp.]
                   7729
Seq. No.
                   10391 1.R1040
Contig ID
5'-most EST
                   pxt70\overline{0}944410.h1
Method
                   BLASTN
NCBI GI
                   g166409
                   235
BLAST score
                   1.0e-129
E value
Match length
                   423
                   89
% identity
                   Alfalfa nucleic acid binding protein (alfin-1) mRNA,
NCBI Description
                   partial cds
                   7730
Seq. No.
Contig ID
                   10391 2.R1040
5'-most EST
                   sat701005773.hl
Method
                   BLASTN
NCBI GI
                   q166409
BLAST score
                   135
                   5.0e-70
E value
Match length
                   203
                   92
% identity
                   Alfalfa nucleic acid binding protein (alfin-1) mRNA,
NCBI Description
                   partial cds
Seq. No.
                   7731
Contig ID
                   10391 3.R1040
5'-most EST
                   zsq701130201.h1
Method
                   BLASTN
NCBI GI
                   q166409
BLAST score
                   65
                   4.0e-28
E value
                   153
Match length
% identity
                   Alfalfa nucleic acid binding protein (alfin-1) mRNA,
NCBI Description
                   partial cds
Seq. No.
                   7732
                   10394 1.R1040
Contig ID
5'-most EST
                   LIB3039-005-Q1-E1-D9
                   BLASTX
Method
NCBI GI
                   g728868
BLAST score
                   239
                   4.0e-20
E value
                   79
Match length
                   58
% identity
                   ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
NCBI Description
                   >gi_99824_pir__S16748 proline-rich protein - rape
(fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich
                   protein [Brassica napus]
Seq. No.
                   7733
                   10394 2.R1040
Contig ID
```

 $zhf70\overline{0}954572.h1$

BLASTX

5'-most EST Method.

```
g728868
NCBI GI
BLAST score
                    140
E value
                    1.0e-08
Match length
                    44
% identity
                    61
                    ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
NCBI Description
                    >gi_99824_pir__S16748 proline-rich protein - rape
(fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich
                    protein [Brassica napus]
                    7734
Seq. No.
                    10395 1.R1040
Contig ID
                    LIB30\overline{4}9-016-Q1-E1-H10
5'-most EST
Method
                    BLASTX
NCBI GI
                    q2618702
BLAST score
                    461
E value
                    5.0e-46
Match length
                    143
                    68
% identity
NCBI Description
                    (AC002510) unknown protein [Arabidopsis thaliana]
                    7735
Seq. No.
                    10396_1.R1040
Contig ID
5'-most EST
                    LIB30\overline{5}1-062-Q1-K1-E12
Method
                    BLASTX
NCBI GI
                    g4090257
BLAST score
                    467
E value
                    8.0e-47
Match length
                    91
% identity
NCBI Description
                    (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
                    7736
Seq. No.
                    10396 2.R1040
Contig ID
                    LIB3039-005-Q1-E1-E11
5'-most EST
Method
                    BLASTX
NCBI GI
                    q4090257
BLAST score
                    452
                    7.0e-45
E value
                    91
Match length
                    96
% identity
NCBI Description
                    (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
Seq. No.
                    7737
                    10410 1.R1040
Contig ID
5'-most EST
                    q5606468
Method
                    BLASTX
NCBI GI
                    g3121825
BLAST score
                    994
E value
                    1.0e-108
Match length
                    260
                    77
% identity
NCBI Description
                    2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
                    ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)
                   bas1 protein [Spinacia oleracea]
```

Seq. No. 7738

Method

BLASTX

```
Contig ID
                  10410 2.R1040
                  LIB3039-005-Q1-E1-D11
5'-most EST
Method
                  BLASTX
                  q3121825
NCBI GI
                  619
BLAST score
                  2.0e-64
E value
                  182
Match length
                  70
% identity
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
NCBI Description
                  ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)
                  bas1 protein [Spinacia oleracea]
                  7739
Seq. No.
                  10418 1.R1040
Contig ID
5'-most EST
                  LIB3039-005-Q1-E1-B10
Method
                  BLASTN
                  q1495767
NCBI GI
BLAST score
                  238
                  1.0e-131
E value
                  611
Match length
                  84
% identity
                  P.sativum mRNA for 110 kD chloroplast inner envelope
NCBI Description
                  protein IEP110
                  7740
Seq. No.
                  10425 1.R1040
Contig ID
                  leu701157388.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2897942
BLAST score
                  317
                  7.0e-29
E value
Match length
                  165
                  42
% identity
                   (AF003938) thioredoxin-like protein [Homo sapiens]
NCBI Description
                  >gi_2961254 (AF051896) thioredoxin homolog [Homo sapiens]
                  >gi 2970689 (AF052659) thioredoxin-related protein [Homo
                  sapiens]
Seq. No.
                  7741
Contig ID
                  10428 1.R1040
                  LIB3049-026-Q1-E1-G3
5'-most EST
                  BLASTX
Method
                  g4538959
NCBI GI
BLAST score
                  460
E value
                  7.0e-46
Match length
                  105
                  80
% identity
NCBI Description
                  (AL049488) putative protein [Arabidopsis thaliana]
                  7742
Seq. No.
                  10430 1.R1040
Contig ID
5'-most EST
                  LIB3039-004-Q1-E1-H1
                  7743
Seq. No.
                  10432 1.R1040
Contig ID
                  rlr700902245.hl
5'-most EST
```

```
NCBI GI
                   q2618688
BLAST score
                   681
                   1.0e-71
E value
Match length
                   157
                   82
% identity
                   (AC002510) putative esterase D [Arabidopsis thaliana]
NCBI Description
                   7744
Seq. No.
                   10435 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-116-Q1-K1-A2
                   7745
Seq. No.
                   10439 1.R1040
Contig ID
                   leu701144983.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4191782
                   2171
BLAST score
                   0.0e+00
E value
                   503
Match length
                   82
% identity
                   (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
NCBI Description
                   7746
Seq. No.
                   10449 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{3}9-004-Q1-E1-D9
                   BLASTX
Method
                   g4263517
NCBI GI
                   199
BLAST score
                   2.0e-31
E value
Match length
                   112
                   64
% identity
NCBI Description
                   (AC004044) similar to PHZF, catalyzing the hydroxylation of
                   phenazine-1-carboxylic acid to
                   2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis
                   thaliana]
Seq. No.
                   7747
Contig ID
                   10453 1.R1040
                   LIB3040-043-Q1-E1-H7
5'-most EST
                   BLASTX
Method
                   q4406774
NCBI GI
BLAST score
                  920
E value
                   2.0e-99
Match length
                   264
                   64
% identity
NCBI Description
                   (AC006836) putative nonsense-mediated mRNA decay protein,
                   5' partial [Arabidopsis thaliana]
Seq. No.
                   7748
                   10458 1.R1040
Contig ID
                   seb70\overline{0}652912.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   a3138972
BLAST score
                   258
                   3.0e-22
E value
Match length
                   67
```

73

% identity

```
(AF038505) dihydrolipoylacyltransferase subunit of the
NCBI Description
                   branched-chain alpha-keto acid dehydrogenase complex
                   [Arabidopsis thaliana]
                   7749
Seq. No.
                   10462 1.R1040
Contig ID
5'-most EST
                   LIB3092-010-Q1-K1-C3
                   7750
Seq. No.
Contig ID
                   10470 1.R1040
5'-most EST
                   LIB30\overline{5}0-022-Q1-K1-A3
Method
                   BLASTX
                   q2131767
NCBI GI
BLAST score
                   165
                   3.0e-11
E value
Match length
                   96
                   40
% identity
NCBI Description
                   hypothetical protein YLR074c - yeast (Saccharomyces
                   cerevisiae) >gi 1360432 emb CAA97631 (Z73246) ORF YLR074c
                   [Saccharomyces cerevisiae]
Seq. No.
                   7751
Contig ID
                   10476 1.R1040
5'-most EST
                   LIB3109-020-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   q2832680
BLAST score
                   476
                   8.0e-48
E value
                   107
Match length
                   40
% identity
NCBI Description
                   (AL021712) putative protein [Arabidopsis thaliana]
                   7752
Seq. No.
                   10490 1.R1040
Contig ID
5'-most EST
                   pcp700993962.h1
Seq. No.
                   7753
                   10491_1.R1040
Contig ID
5'-most EST
                   LIB3039-003-Q1-E1-F7
                   BLASTX
Method
NCBI GI
                   q4415906
BLAST score
                   302
E value
                   2.0e-27
Match length
                   96
% identity
                   62
NCBI Description
                   (AC006282) putative DNA binding protein with homeobox
                   domain [Arabidopsis thaliana]
Seq. No.
                   7754
                   10492 1.R1040
Contig ID
                   LIB3039-003-Q1-E1-F8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1709543
BLAST score
                   229
                   1.0e-18
E value
Match length
                   95
```

48

% identity

```
NCBI Description RED CELL ACID PHOSPHATASE 1, ISOZYME F (ACP1) (LOW
                  MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE)
                  (ADIPOCYTE ACID PHOSPHATASE, ISOZYME ALPHA)
                  >gi_284353_pir__A38148 protein-tyrosine-phosphatase (EC
                  3.1.3.48), low molecular weight, splice form f - human
                  >qi 179636 (M83653) cytoplasmic phosphotyrosyl protein
                  phosphatase [Homo sapiens] >gi_1147812 (U25849) red
                  cell-type low molecular weight acid phosphatase [Homo
                  sapiens]
                  7755
Seq. No.
                  10493 1.R1040
Contig ID
                  dpv701100495.h1
5'-most EST
                  BLASTX
Method
                  q1731990
NCBI GI
                  283
BLAST score
                  1.0e-47
E value
                  247
Match length
                  43
% identity
                  (Y09602) serine carboxypeptidase II, CP-MII [Hordeum
NCBI Description
                  vulgare]
                  7756
Seq. No.
                  10495 1.R1040
Contig ID
                  LIB3039-003-Q1-E1-G12
5'-most EST
                  BLASTX
Method.
                  g4049341
NCBI GI
BLAST score
                  402
E value
                  5.0e-40
                  176
Match length
                  49
% identity
                   (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  7757
                  10496 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220148c06a1
                  BLASTX
Method
NCBI GI
                  g3342556
BLAST score
                  1960
                  0.0e+00
E value
                  480
Match length
                  80
% identity
                   (AF077528) importin alpha [Arabidopsis thaliana]
NCBI Description
                  7758
Seq. No.
                  10496_2.R1040
Contig ID
                  jC-gmro02910067a11a1
5'-most EST
                  BLASTX
Method
                  g3273243
NCBI GI
BLAST score
                  552
E value
                  1.0e-56
Match length
                  167
                  39
% identity
                  (AB004660) NLS receptor [Oryza sativa]
NCBI Description
```

sativa]

>gi 3273245 dbj_BAA31166 (AB004814) NLS receptor [Oryza

NCBI GI

```
Seq. No.
                   7759
Contig ID
                   10496 3.R1040
                   uC-gmropic073g11b1
5'-most EST
Method
                   BLASTX
                   g2950210
NCBI GI
BLAST score
                   375
                   6.0e-36
E value
                   102
Match length
                   81
% identity
NCBI Description
                   (Y14615) Importin alpha-like protein [Arabidopsis thaliana]
                   7760
Seq. No.
                   10496 7.R1040
Contig ID
                   gsv701054894.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2950210
BLAST score
                   237
                   6.0e-20
E value
                   68
Match length
                   75
% identity
                   (Y14615) Importin alpha-like protein [Arabidopsis thaliana]
NCBI Description
                   7761
Seq. No.
                   10500 1.R1040
Contig ID
5'-most EST
                   crh700856228.h1
Seq. No.
                   7762
Contig ID
                   10502 1.R1040
                   LIB3039-001-Q1-E1-H9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3341443
BLAST score
                   307
                   4.0e-28
E value
                   99
Match length
                   61
% identity
                   (AJ223074) acid phosphatase [Glycine max]
NCBI Description
Seq. No.
                   7763
                   10503 1.R1040
Contig ID
5'-most EST
                   LIB3107-009-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   g4454466
BLAST score
                   203
E value
                   1.0e-15
Match length
                   73
% identity
NCBI Description
                   (AC006234) unknown protein [Arabidopsis thaliana]
                   7764
Seq. No.
                   10504 1.R1040
Contig ID
5'-most EST
                   LIB3039-003-Q1-E1-E12
Seq. No.
                   7765
                   10517 1.R1040
Contig ID
                   LIB3109-056-Q1-K1-E5
5'-most EST
Method
                  BLASTX
```

g3107903

```
BLAST score
                  279
E value
                  1.0e-24
Match length
                  104
                  51
% identity
NCBI Description (D83719) polycomb-like protein [Daucus carota]
                  7766
Seq. No.
                  10520 1.R1040
Contig ID
5'-most EST
                  rlr700897049.h1
Method
                  BLASTX
NCBI GI
                  g470373
BLAST score
                  306
E value
                  2.0e-27
Match length
                  165
                  39
% identity
NCBI Description
                  (U00047) ZK418.5 gene product [Caenorhabditis elegans]
                  7767
Seq. No.
                  10520 2.R1040
Contig ID
5'-most EST
                  LIB3170-079-Q1-K1-F2
                  BLASTX
Method
NCBI GI
                  g470373
BLAST score
                  201
                  2.0e-15
E value
Match length
                  117
% identity
                  38
NCBI Description (U00047) ZK418.5 gene product [Caenorhabditis elegans]
                  7768
Seq. No.
                  10530 1.R1040
Contig ID
5'-most EST
                  LIB3049-007-Q1-E1-F1
                  7769
Seq. No.
                  10540 1.R1040
Contig ID
5'-most EST
                  LIB3072-017-Q1-E1-A6
Method
                  BLASTX
NCBI GI
                  g4039152
BLAST score
                  175
E value
                  2.0e-12
Match length
                  36
                  81
% identity
NCBI Description
                  (AF104221) low temperature and salt responsive protein
                  LTI6B [Arabidopsis thaliana] >gi 4325219 gb AAD17303
                  (AF122006) hydrophobic protein [Arabidopsis thaliana]
                  7770
Seq. No.
Contig ID
                  10541 1.R1040
5'-most EST
                  LIB3055-002-Q1-B1-G7
Method
                  BLASTN
NCBI GI
                  q3885510
BLAST score
                  157
                  1.0e-82
E value
Match length
                  332
% identity
                  Medicago sativa clone MS28 unknown mRNA
NCBI Description
```

7771

Seq. No.

BLAST score

580

```
Contig ID
                   10541 3.R1040
5'-most EST
                   LIB3039-003-Q1-E1-A12
Method
                   BLASTN
NCBI GI
                   q3885510
BLAST score
                   94
                   4.0e-45
E value
                   228
Match length
                   87
% identity
NCBI Description
                   Medicago sativa clone MS28 unknown mRNA
Seq. No.
                   7772
                   10546 1.R1040
Contig ID
5'-most EST
                   LIB3039-002-Q1-E1-H12
Method
                   BLASTX
NCBI GI
                   a3548810
BLAST score
                   277
E value
                   2.0e-36
Match length
                   279
                   37
% identity
                   (AC005313) putative chloroplast nucleoid DNA binding
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   7773
                   10560_1.R1040
Contig ID
                   cf1700863674.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   a3776560
BLAST score
                   484
                   9.0e-49
E value
Match length
                   145
% identity
                   69
                   (AC005388) Similar to gb_U51990 hPrp18 (splicing factor)
NCBI Description
                   gene from Homo sapiens. [Arabidopsis thaliana]
                   7774
Seq. No.
Contig ID
                   10561 1.R1040
5'-most EST
                   LIB3106-070-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   a548702
BLAST score
                   391
E value
                   9.0e-38
Match length
                   111
% identity
                   58
NCBI Description
                   DNA-DIRECTED RNA POLYMERASE II 14.5 KD POLYPEPTIDE (RPB9)
                   (RPB14.5) >gi_543001_pir_S41621 DNA-directed RNA polymerase (EC 2.7.7.6) II 14.5K chain - human
                   >gi_397150_emb_CAA80649_ (Z23102) RNA Polymerase II subunit
                   14.5 kD [Homo sapiens] >gi_1905901 (AD001527) HUMAN
                   DNA-DIRECTED RNA POLYMERASE II 14.5 KD SUBUNIT [Homo
                   sapiens]
Seq. No.
                   7775
                   10571 1.R1040
Contig ID
                   sat701006018.h2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3582339
```

```
E value
                   1.0e-59
Match length
                   141
                   74
% identity
NCBI Description
                   (AC005496) unknown protein [Arabidopsis thaliana]
                   7776
Seq. No.
                   10585_1.R1040
Contig ID
                   jC-gm\overline{l}e01810089e09a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3785983
                   312
BLAST score
E value
                   1.0e-28
                   108
Match length
                   56
% identity
NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]
                   7777
Seq. No.
Contig ID
                   10589 1.R1040
                   LIB3039-002-Q1-E1-D5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4539345
BLAST score
                   355
E value
                   7.0e-34
Match length
                   94
                   71
% identity
NCBI Description (AL035539) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   7778
                   10591 1.R1040
Contig ID
                   LIB3039-002-Q1-E1-A2
5'-most EST
Seq. No.
                   7779
                   10591 2.R1040
Contig ID
5'-most EST
                   uC-gmropic045a04b1
                   7780
Seq. No.
Contig ID
                   10596 1.R1040
                   LIB3092-055-Q1-K1-E4
5'-most EST
                   BLASTX
Method
NCBI GI
                   a2894612
BLAST score
                   2489
E value
                   0.0e+00
Match length
                   613
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                   7781
                   10596 2.R1040
Contig ID
5'-most EST
                   ncj700986073.hl
                   BLASTX
Method
NCBI GI
                   q4262174
BLAST score
                   513
E value
                   4.0e-52
Match length
                   129
% identity
                   74
```

NCBI Description (AC005508) 9058 [Arabidopsis thaliana]

Match length

92

```
7782
Seq. No.
                   10596 3.R1040
Contig ID
5'-most EST
                   LIB3092-055-Q1-K1-E6
Method
                   BLASTX
NCBI GI
                   g4262174
BLAST score
                   197
E value
                   4.0e-15
Match length
                   69
                   48
% identity .
                   (AC005508) 9058 [Arabidopsis thaliana]
NCBI Description
                   7783
Seq. No.
                   10596 5.R1040
Contig ID
                   k1170\overline{1}203144.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2894612
BLAST score
                   170
E value
                   2.0e-12
Match length
                   57
                   58
% identity
NCBI Description
                   (AL021889) putative protein [Arabidopsis thaliana]
                   7784
Seq. No.
                   10611 1.R1040
Contig ID
5'-most EST
                   LIB3039-001-Q1-E1-H1
Seq. No.
                   7785
                   10621 1.R1040
Contig ID
5'-most EST
                   LIB3039-001-Q1-E1-F10
                   BLASTX
Method
NCBI GI
                   g2769566
BLAST score
                   204
E value
                   6.0e-16
Match length
                   90
                   51
% identity
                   (Y10477) chloroplast thylakoidal processing peptidase
NCBI Description
                   [Arabidopsis thaliana]
                   7786
Seq. No.
                   10623 1.R1040
Contig ID
5'-most EST
                   bth700843521.h1
Method
                   BLASTX
                   g4090257
NCBI GI
BLAST score
                   291
E value
                   5.0e-26
                   91
Match length
% identity
                   63
                   (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
Seq. No.
                   7787
                   10623 2.R1040
Contig ID
5'-most EST
                   LIB3040-043-Q1-E1-A8
Method
                   BLASTX
NCBI GI
                   q4090257
BLAST score
                   473
                   2.0e-47
E value
```

NCBI GI

```
% identity
                   98
                   (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
                   7788
Seq. No.
                   10623 3.R1040
Contig ID
                  LIB3087-012-Q1-K1-H12
5'-most EST
                  BLASTX
Method
                   g4090257
NCBI GI
                   214
BLAST score
E value
                   3.0e-17
                   42
Match length
                   98
% identity
                  (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
                   7789
Seq. No.
                   10626 1.R1040
Contig ID
5'-most EST
                   q4283326
Method
                   BLASTX
NCBI GI
                   g3024516
BLAST score
                   619
E value
                   1.0e-97
Match length
                   217
                   88
% identity
                  RAS-RELATED PROTEIN RABIIC >gi 2160157 (AC000132) Strong
NCBI Description
                   similarity to A. thaliana ara-\overline{2} (gb_ATHARA2). ESTs
                   gb_ATTS2483,gb_ATTS2484,gb_AA042159 come from this gene.
                   [Arabidopsis thaliana] >gi_2231303 (U74669) ras-related
                   small GTPase [Arabidopsis thaliana]
                   7790
Seq. No.
                   10626 2.R1040
Contig ID
5'-most EST
                   pcp700991695.hl
                   BLASTX
Method
NCBI GI
                   g1405561
BLAST score
                   506
                   2.0e-51
E value
Match length
                   101
                                                                        % identity
                   98
                  (X98540) FSGTP1 [Fagus sylvatica]
NCBI Description
                   7791
Seq. No.
                   10638 1.R1040
Contig ID
5'-most EST
                   uC-qmflminsoy072h01b1
                   BLASTX
Method
NCBI GI
                   g2459445
BLAST score
                   815
E value
                   8.0e-87
Match length
                   323
                   51
% identity
                   (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   7792
                   10638 2.R1040
Contig ID
                   ncj70\overline{0}977531.h1
5'-most EST
                   BLASTX
Method
```

g2244786

Method

BLASTN

```
3.2.
                   196
BLAST score
E value
                   3.0e-15
Match length
                   51
% identity
                   37
                   (Z97335) ribonucleoprotein homolog [Arabidopsis thaliana]
NCBI Description
                   7793
Seq. No.
                   10644 1.R1040
Contig ID
5'-most EST
                   95607\overline{1}71
Method
                   BLASTX
                   g1707008
NCBI GI
BLAST score
                   547
E value
                   1.0e-77
Match length
                   193
% identity
                   78
                   (U78721) 30S ribosomal protein S5 isolog [Arabidopsis
NCBI Description
                   thaliana]
                   7794
Seq. No.
Contig ID
                   10644 2.R1040
                   fjg700968348.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1707008
BLAST score
                   296
E value
                   1.0e-26
Match length
                   109
% identity
                   54
                   (U78721) 30S ribosomal protein S5 isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   7795
                   10644 4.R1040
Contig ID
                   6HC-02-Q1-B1-A7
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1707008
BLAST score
                   209
E value
                   1.0e-16
Match length
                   83
                   51
% identity
NCBI Description
                   (U78721) 30S ribosomal protein S5 isolog [Arabidopsis
                   thaliana]
Seq. No.
                   7796
                   10646 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400062c06a1
Method
                   BLASTN
NCBI GI
                   q169980
BLAST score
                   407
E value
                   0.0e + 00
Match length
                   920
                   96
% identity
NCBI Description
                   Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                   10646 2.R1040
Contig ID
5'-most EST
                   LIB3094-048-Q1-K1-A5
```

Method

NCBI GI

BLASTN

g1518539

```
g1184122
NCBI GI
BLAST score
                   346
E value
                   0.0e+00
Match length
                   650
% identity
                   88
NCBI Description
                  Vigna radiata clone MII-4 auxin-induced protein mRNA,
                   partial cds
Seq. No.
                   7798
                   10646 3.R1040
Contig ID
5'-most EST
                  LIB30\overline{3}9-001-Q1-E1-E9
Method
                   BLASTN
                   g169980
NCBI GI
BLAST score
                   431
                   0.0e+00
E value
                   1070
Match length
% identity
                   93
NCBI Description
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                   7799
Seq. No.
Contig ID
                   10646_4.R1040
5'-most EST
                   zsg701126407.hl
Method
                   BLASTN
NCBI GI
                   g169980
BLAST score
                   225
E value
                   1.0e-123
                   369
Match length
                   92
% identity
NCBI Description
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                   7800
                   10646 5.R1040
Contig ID
                   rlr700900057.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g169980
BLAST score
                   188
E value
                   1.0e-101
Match length
                   509
                   88
% identity
NCBI Description
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
Contig ID
                   10646 6.R1040
5'-most EST
                  LIB3094-051-Q1-K1-A4
Method
                  BLASTN
NCBI GI
                   g169980
BLAST score
                  217
E value
                   1.0e-118
Match length
                  347
% identity
                   94
NCBI Description
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                   7802
Seq. No.
                   10648 1.R1040
Contig ID
5'-most EST
                  LIB3039-001-Q1-E1-C4
```

Contig ID

5'-most EST

```
365
BLAST score
                   0.0e+00
E value
                   765
Match length
% identity
                   87
                   Glycine max UDP-qlucose dehydrogenase mRNA, complete cds
NCBI Description
                   7803
Seq. No.
                   10665 1.R1040
Contig ID
5'-most EST
                   qsv70\overline{1}051012.h1
                   BLASTX
Method
NCBI GI
                   q2995953
BLAST score
                   379
E value
                   2.0e-36
Match length.
                   103
% identity
                   71
                   (AF053565) qlutaredoxin I [Mesembryanthemum crystallinum]
NCBI Description
                   7804
Seq. No.
                   10665 2.R1040
Contig ID
5'-most EST
                   bnu700967683.hl
Method
                   BLASTX
                   g2995953 -
NCBI GI
BLAST score
                   406
E value
                   2.0e-39
                   105
Match length
% identity
                   (AF053565) qlutaredoxin I [Mesembryanthemum crystallinum]
NCBI Description
                   7805
Seq. No.
                   10670 1.R1040
Contig ID
5'-most EST
                   leu70\overline{1}156031.h1
Method
                   BLASTX
NCBI GI
                   q481236
BLAST score
                   279
                   2.0e-24
E value
Match length
                   132
% identity
                   43
                   hypothetical protein - Madagascar periwinkle
NCBI Description
                   >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide
                   [Catharanthus roseus]
Seq. No.
                   7806
Contig ID
                   10673 1.R1040
5'-most EST
                   vzy70\overline{0}752406.h1
Method
                   BLASTX
NCBI GI
                   q2136140
BLAST score
                   793
E value
                   1.0e-84
                   272
Match length
% identity
                   serine C-palmitoyltransferase (EC 2.3.1.50) - human
NCBI Description
                   (fragment) > gi_1001945 (U15555) serine palmitoyltransferase
                   [Homo sapiens]
                   7807
Seq. No.
                   10677 2.R1040
```

leu701144384.hl

Match length

100

7808 Seq. No. 10682 1.R1040 Contig ID 5'-most EST LIB3107-052-Q1-K1-A12 Method **BLASTX** g4490292 NCBI GI BLAST score 889 E value 8.0e-96 Match length 218 % identity 78 NCBI Description (AL035678) putative protein [Arabidopsis thaliana] 7809 Seq. No. 10682 3.R1040 Contig ID 5'-most EST jsh701066564.hl Method BLASTX g4490292 NCBI GI BLAST score 214 E value 2.0e-17 Match length 57 % identity 72 NCBI Description (AL035678) putative protein [Arabidopsis thaliana] 7810 Seq. No. 10686_1.R1040 Contig ID 5'-most EST jC-gmro02910071f10a1 Method BLASTX g3236238 NCBI GI BLAST score 610 E value 2.0e-63 Match length 129 % identity NCBI Description (AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Asp1 [Arabidopsis thaliana] Seq. No. 7811 10686 2.R1040 Contig ID txt700735901.hl 5'-most EST BLASTX Method NCBI GI q3236238 BLAST score 597 E value 4.0e-85 Match length 203 77 % identity NCBI Description (AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Aspl [Arabidopsis thaliana] Seq. No. 7812 10686 3.R1040 Contig ID 5'-most EST zvj700605112.h2 Method BLASTX NCBI GI g3236238 BLAST score 468 6.0e-47 E value

Contig ID 5'-most EST

```
% identity
NCBI Description
                    (AC004684) putative ARF1 GTPase activating protein
                    [Arabidopsis thaliana] >gi 4519792_dbj_BAA75744.1_
                    (AB017876) Aspl [Arabidopsis thaliana]
Seq. No.
                    7813
Contig ID
                    10687 1.R1040
5'-most EST
                    pmv70\overline{0}892916.h1
                    BLASTX
Method
                    g141435
NCBI GI
BLAST score
                    260
E value
                    2.0e-22
                    119
Match length
                    41
% identity
                    DIHYDRONEOPTERIN ALDOLASE (DHNA) >gi 98360 pir E37854
NCBI Description
                    folate biosynthesis protein 1 (sul 3 region) - Bacillus
                    subtilis >gi 143411 (M34053) ORF1 [Bacillus subtilis]
                    >gi_467467_dbj_BAA05313_ (D26185) unknown [Bacillus
                    \widetilde{\text{subtilis}} = \overline{\text{gi}} = \overline{2}632345 = \overline{\text{mb}} = CAB11854 = (Z99104)
                    dihydroneopterin aldolase [Bacillus subtilis]
Seq. No.
                    7814
                    10688 1.R1040
Contig ID
                    LIB3039-006-Q1-E1-A1
5'-most EST
Method
                    BLASTX
                    q837
NCBI GI
BLAST score
                    359
E value
                    5.0e-34
                    99
Match length
                    70
% identity
                    (X52113) tryptophan tRNA ligase (AA 1-459) [Bos taurus]
NCBI Description
Seq. No.
                    7815
                    10688 2.R1040
Contig ID
5'-most EST
                    uC-gmropic026h04b1
Method
                    BLASTX
NCBI GI
                    q837
BLAST score
                    349
E value
                    5.0e-33
                    100
Match length
% identity
                    68
                    (X52113) tryptophan tRNA ligase (AA 1-459) [Bos taurus]
NCBI Description
Seq. No.
                    7816
                    10697 1.R1040
Contig ID
5'-most EST
                    k1170\overline{1}206518.h1
Method
                   BLASTX
NCBI GI
                    q4006893
BLAST score
                    1894
E value
                    0.0e + 00
Match length
                    517
% identity
                    68
                    (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    7817
                    10699 1.R1040
```

LIB3051-097-Q1-K1-B12

```
BLASTN
Method
                   q456713
NCBI GI
                   608
BLAST score
E value
                   0.0e+00
                   739
Match length
                   69
% identity
                   Glycine max gene for ubiquitin, complete cds
NCBI Description
                   7818
Seq. No.
                   10699 2.R1040
Contig ID
5'-most EST
                   LIB3040-024-Q1-E1-H12
                   BLASTN
Method
                   q303900
NCBI GI
                   369
BLAST score
                   0.0e+00
E value
Match length
                   586
                   61
% identity
NCBI Description
                   Soybean gene for ubiquitin, complete cds
                   7819
Seq. No.
Contig ID
                   10701 1.R1040
5'-most EST
                   LIB3039-009-Q1-E1-G5
                   BLASTX
Method
NCBI GI
                   g2129630
BLAST score
                   246
E value
                   6.0e-21
Match length
                   91
                   44
% identity
                   lamin - Arabidopsis thaliana >gi 1262754 emb CAA65750
NCBI Description
                   (X97023) lamin [Arabidopsis thaliana] >gi 3395760 (U77721)
                   unknown [Arabidopsis thaliana]
                   7820
Seq. No.
                   10701_2.R1040
Contig ID
5'-most EST
                   LIB31\overline{0}9-001-Q1-K1-H8
                   BLASTX
Method
NCBI GI
                   g2129630
BLAST score
                   150
E value
                   1.0e-09
Match length
                   51
                   49
% identity
                   lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750
NCBI Description
                   (X97023) lamin [Arabidopsis thaliana] >g\overline{1}_33\overline{9}5760 (U7\overline{7}721)
                   unknown [Arabidopsis thaliana]
                   7821
Seq. No.
                   10703_1.R1040
Contig ID
5'-most EST
                   leu701146671.hl
Method
                   BLASTX
                   g2760334
NCBI GI
                   392
BLAST score
                   1.0e-37
E value
Match length
                   90
% identity
                   (AC002130) F1N21.5 [Arabidopsis thaliana]
NCBI Description
```

7822

Seq. No.

```
Contig ID
                   10710 1.R1040
5'-most EST
                   LIB3039-014-Q1-E1-C6
Seq. No.
Contig ID
                   10718 1.R1040
5'-most EST
                   LIB3065-024-Q1-N1-B1
                   BLASTX
Method
NCBI GI
                   q3372233
BLAST score
                   827
                   1.0e-88
E value
Match length
                   205
% identity
                   77
NCBI Description
                   (AF019248) RNA polymerase I, II and III 24.3 kDa subunit
                   [Arabidopsis thaliana]
                   7824
Seq. No.
Contig ID
                   10718 3.R1040
5'-most EST
                   jsh701068423.hl
Method
                   BLASTX
NCBI GI
                   g3372233
BLAST score
                   147
                   2.0e-09
E value
                   30
Match length
% identity
                   93
                   (AF019248) RNA polymerase I, II and III 24.3 kDa subunit
NCBI Description
                   [Arabidopsis thaliana]
                   7825
Seq. No.
                   10733 2.R1040
Contig ID
                   LIB3139-057-P1-N1-B12
5'-most EST
                   7826
Seq. No.
                   10743 1.R1040
Contig ID
5'-most EST
                   LIB3087-002-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   g4406807
BLAST score
                   691
E value
                   1.0e-72
                   212
Match length
% identity
                   (AC006201) putative elongation factor beta-1 [Arabidopsis
NCBI Description
                   thaliana]
                   7827
Seq. No.
                   10746 1.R1040
Contig ID
5'-most EST
                   LIB3039-030-Q1-E1-H10
Method
                   BLASTX
NCBI GI
                   g4314355
BLAST score
                   685
E value
                   5.0e-72
                   207
Match length
% identity
NCBI Description
                   (AC006340) unknown protein [Arabidopsis thaliana]
Seq. No.
                   7828
```

10754 1.R1040

LIB3039-036-Q1-E1-A1

Contig ID 5'-most EST

5'-most EST

```
Method
                   BLASTX
                   g2586123
NCBI GI
BLAST score
                   787
E value
                   6.0e-84
Match length
                   192
% identity
                   75
NCBI Description
                   (U89511) b-keto acyl reductase [Allium porrum]
                   7829
Seq. No.
                   10762 1.R1040
Contig ID
5'-most EST .
                   LIB3039-038-Q1-E1-E5
                   BLASTX
Method
                   g1408294
NCBI GI
BLAST score
                   306
E value
                   2.0e-27
Match length
                   218
% identity
                   36
NCBI Description
                   (U61983) benzyl alcohol dehydrogenase [Acinetobacter
                   calcoaceticus]
Seq. No.
                   7830
                   10767_1.R1040
Contig ID
5'-most EST
                   LIB3040-052-Q1-E1-D3
Method
                   BLASTX
NCBI GI
                   g4335763
BLAST score
                   424
E value
                   3.0e-41
Match length
                   161
                   50
% identity
                   (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7831
                   10767 2.R1040
Contig ID
5'-most EST
                   fua701040645.hl
                   7832
Seq. No.
Contig ID
                   10768 1.R1040
5'-most EST
                   epx701106195.h1
Method
                   BLASTX
                   q4098517
NCBI GI
BLAST score
                   684
E value
                   6.0e-72 .
Match length
                   180
% identity
                   72
NCBI Description
                   (U79114) auxin-binding protein ABP19 [Prunus persica]
Seq. No.
                   7833
Contig ID
                   10771 1.R1040
5'-most EST
                   kl1701211959.hl
                   7834
Seq. No.
Contig ID
                   10771 2.R1040
5'-most EST
                   vzy700754421.h1
Seq. No.
                   7835
                   10779 1.R1040
Contig ID
```

 $epx70\overline{1}105157.h1$

NCBI Description

thaliana]

```
Method
                   BLASTX
NCBI GI
                   q119931
BLAST score
                   443
E value
                   1.0e-43
Match length
                   146
                   64
% identity
                   FERREDOXIN I PRECURSOR >gi_65740_pir__FEPM1 ferredoxin
NCBI Description
                   [2Fe-2S] I precursor - garden pea >gi_169087 (M31713)
                   ferredoxin I precursor [Pisum sativum]
Seq. No.
                   7836
                   10783 1.R1040
Contig ID
                   LIB3049-041-Q1-E1-A4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3861188
BLAST score
                   267
                   6.0e-23
E value
Match length
                   103
% identity
                   54
NCBI Description
                   (AJ235272) 50S RIBOSOMAL PROTEIN L24 (rplX) [Rickettsia
                   prowazekii]
Seq. No.
                  7837
Contig ID
                   10783 2.R1040
                   LIB3049-041-Q1-E1-G6
5'-most EST
Method
                  BLASTX
                   a3861188
NCBI GI
BLAST score
                   245
                   1.0e-20
E value
Match length
                   89
% identity
                   53
                   (AJ235272) 50S RIBOSOMAL PROTEIN L24 (rplX) [Rickettsia
NCBI Description
                  prowazekii]
                   7838
Seq. No.
Contig ID
                   10783 3.R1040
5'-most EST
                  LIB3049-039-Q1-E1-A9
Method
                  BLASTX
                   g143448
NCBI GI
BLAST score
                   181
E value
                   2.0e-13
Match length
                   75
% identity
                   51
NCBI Description
                  (M81749) ribosomal protein L24 [Bacillus subtilis]
                   7839
Seq. No.
Contig ID
                   10792 1.R1040
5'-most EST
                   jex700909892.hl
Method
                  BLASTX
NCBI GI
                  q2623298
BLAST score
                  565
E value
                   3.0e-58
Match length
                  158
% identity
```

(AC002409) putative 4-alpha-glucanotransferase [Arabidopsis

5'-most EST

```
7840
Seq. No.
                   10799 1.R1040
Contig ID
5'-most EST
                   LIB3039-052-Q1-E1-B10
Seq. No.
                   7841
                   10808 1.R1040
Contig ID
5'-most EST
                   LIB3170-018-Q1-K1-D11
                   7842
Seq. No.
Contig ID
                   10809 1.R1040
5'-most EST
                   LIB3040-043-Q1-E1-G12
Method
                   BLASTX
                   g2462834
NCBI GI
BLAST score
                   327
E value
                   6.0e-30
Match length
                   179
% identity
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7843
Contig ID
                   10814 1.R1040
5'-most EST
                   LIB3040-061-Q1-E11-H5
Method
                   BLASTX
NCBI GI
                   g2252847
BLAST score
                   162
E value ~
                   6.0e-11
Match length
                   62
% identity
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
                   7844
Seq. No.
                   10816 1.R1040
Contig ID
5'-most EST
                   LIB3138-129-Q1-N1-E8
Method
                   BLASTX
                   g2244847
NCBI GI
BLAST score
                   376
E value
                   2.0e-35
Match length
                   531 .
% identity
                   28
NCBI Description
                   (Z97337) hydroxyproline-rich glycoprotein homolog
                   [Arabidopsis thaliana]
Seq. No.
                   7845
                   10816_2.R1040
Contig ID
5'-most EST
                   uC-gmropic109c08b1
Method
                   BLASTN
NCBI GI
                   q3985934
BLAST score
                   51
E value
                   2.0e-19
Match length
                   211
                   81
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJE7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   7846
Contig ID
                   10816 4.R1040
```

...

kl1701208166.hl

```
7847
Seq. No.
                  .10816 5.R1040
Contig ID
5'-most EST
                   LIB3052-007-Q1-B1-G12
Method
                   BLASTN
                   g3985934
NCBI GI
BLAST score
                   44
                   2.0e-15
E value
Match length
                   168
% identity
                   82
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MJE7, complete sequence [Arabidopsis thaliana]
                   7848
Seq. No.
                   10817 1.R1040
Contig ID
5'-most EST
                   LIB3040-061-Q1-E11-F8
Method
                   BLASTN
NCBI GI
                   q3421345
BLAST score
                   194
E value
                   1.0e-105
Match length
                   391
                   87
% identity
                   Orobanche minor chloroplast trnS(GGA) gene, rps4 gene and
NCBI Description
                   trnT(UGU) gene
                   7849
Seq. No.
Contig ID
                   10818 1.R1040
                   ssr70\overline{0}559718.h1
5'-most EST
                   7850
Seq. No.
                   10827 1.R1040
Contig ID
5'-most EST
                   LIB3040-061-Q1-E11-E5
                   BLASTX
Method
                   g2190419
NCBI GI
BLAST score
                   327
E value
                   3.0e-32
Match length
                   103
                   69
% identity
                   (Y13632) dem [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   7851
                   10829 1.R1040
Contig ID
                   r1r70\overline{0}900449.h1
5'-most EST
Method
                   BLASTX
                   g3980383
NCBI GI
BLAST score
                   298
E value
                   4.0e-27
Match length
                   76
% identity
                   74
                   (AC004561) unknown protein [Arabidopsis thaliana]
NCBI Description
                   7852
Seq. No.
Contig ID
                   10829 2.R1040
5'-most EST
                   LIB3093-056-Q1-K1-D6
                   BLASTX
Method
```

g3980383

295

NCBI GI BLAST score

5'-most EST

```
8.0e-27
E value
Match length
                   75
                   75
% identity
                   (AC004561) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7853
                  10830 1.R1040
Contig ID
5'-most EST
                   LIB3094-017-Q1-K1-A5
                   BLASTN
Method
NCBI GI
                   g3694834
BLAST score
                   436
E value
                   0.0e+00
Match length
                   499
                   98
% identity
NCBI Description Glycine max alcohol dehydrogenase Adh-1 gene, partial cds
                   7854
Seq. No.
                   10830 2.R1040
Contig ID
                   uC-gmropic091g04b1 .
5'-most EST
Method
                   BLASTN
NCBI GI
                   g452768
BLAST score
                   319
E value
                   1.0e-179
Match length
                   451
                   93
% identity
                  P.acutifolius alcohol dehydrogenase-1F mRNA, complete CDS
NCBI Description
Seq. No.
                   7855
                   10830 3.R1040
Contig ID
5'-most EST
                  LIB3094-022-Q1-K1-C9
Method
                  BLASTN
NCBI GI
                   g3694834
                   209
BLAST score
                   1.0e-114
E value
                   423
Match length
                   97
% identity
NCBI Description
                  Glycine max alcohol dehydrogenase Adh-1 gene, partial cds
                   7856
Seq. No.
                   10830 6.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy039g09b1
Method
                   BLASTN
NCBI GI
                   q4039114
BLAST score
                   435
E value
                   0.0e + 00
Match length
                   493
                   96
% identity
NCBI Description
                  Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds
                   7857
Seq. No.
Contig ID
                   10838 1.R1040
5'-most EST
                  LIB3040-061-Q1-E11-A6
Seq. No.
                   7858
                   10838 2.R1040
Contig ID
```

jC-gmst02400027d03d1

Match length

216

```
7859
Seq. No.
                   10839 1.R1040
Contig ID
5'-most EST
                   LIB3040-061-Q1-E11-A7
Seq. No.
                   7860
Contig ID
                   10845 1.R1040
                   LIB3040-061-Q1-E11-C2
5'-most EST
                   BLASTX
Method ·
NCBI GI
                   g1709129
BLAST score
                   1988
E value
                   0.0e + 00
Match length
                   410
% identity
                   91
NCBI Description
                   GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3
                   >gi_481018_pir__S37642 protein kinase MSK-3 (EC 2.7.1.-) -
                   alfalfa >gi_313148_emb_CAA48472_ (X68409) protein kinase
                   [Medicago sativa]
Seq. No.
                   7861
Contig ID
                   10845 3.R1040
5'-most EST
                   eep70\overline{0}865347.h1
                   7862
Seq. No.
                   10845 4.R1040
Contig ID
5'-most EST
                   vwf700677426.h1
                   7863
Seq. No.
                   10849 2.R1040
Contig ID
5'-most EST
                   leu701150332.h1
Seq. No.
                   7864
                   10849 3.R1040
Contig ID
5'-most EST
                   leu70\overline{1}149558.h1
                   7865
Seq. No.
Contig ID
                   10853 1.R1040
5'-most EST
                   LIB3040-061-Q1-E1-B9
                   7866
Seq. No.
Contig ID
                   10855 1.R1040
5'-most EST
                   LIB3170-020-Q1-J1-D10
Method
                   BLASTX
NCBI GI
                   q3885941
BLAST score
                   301
E value
                   3.0e-27
Match length
                   67
% identity
NCBI Description
                   (AF095454) PII protein [Ricinus communis]
Seq. No.
                   7867
                   10857 1.R1040
Contig ID
5'-most EST
                   jC-qmst02400029c06a1
Method
                   BLASTX
NCBI GI
                   g82200
BLAST score
                   533
E value
                   3.0e-54
```

Contig ID

```
% identity
                    50
NCBI Description hypothetical protein 1244 - common tobacco chloroplast
                    7868
Seq. No.
Contig ID
                    10864 1.R1040
                    LIB3167-023-P4-K4-G3
5'-most EST
Method
                    BLASTX
                    g3600061
NCBI GI
BLAST score
                    262
E value
                    3.0e-22
Match length
                    172
% identity
                    40
NCBI Description
                    (AF080120) contains similarity to DNA binding proteins
                    [Arabidopsis thaliana]
Seq. No.
                    7869
Contig ID
                    10867 1.R1040
5'-most EST
                    LIB3107-035-Q1-K1-G5
Method
                    BLASTX
NCBI GI
                    g3915961
BLAST score
                    1582
E value
                    0.0e + 00
Match length
                    559
                    88
% identity
NCBI Description
                    HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
                   >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana
tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical
                    protein [Nicotiana tabacum]
                    7870
Seq. No.
Contig ID
                    10867 2.R1040
5'-most EST
                   LIB3170-005-Q1-K1-E11
Method
                    BLASTN
NCBI GI
                    g2924257
BLAST score
                    126
E value
                    3.0e-64
Match length
                    230
% identity
                    46
                   Tobacco chloroplast genome DNA
NCBI Description
                    7871
Seq. No.
Contig ID
                    10868 1.R1040
5'-most EST
                    uC-gmflminsoy080h03b1
                    7872
Seq. No.
Contig ID
                    10873 1.R1040
5'-most EST
                    LIB3040-018-Q1-E1-A11
Method
                    BLASTX
NCBI GI
                    q3582335
BLAST score
                    844
                    1.0e-120
E value
Match length
                    297
% identity
                    74
NCBI Description
                    (AC005496) unknown protein [Arabidopsis thaliana]
Seq. No.
```

10873_2.R1040

5'-most EST

```
5'-most EST
                   LIB3040-042-Q1-E1-A10
                   7874
Seq. No.
                   10873 3.R1040
Contig ID
5'-most EST
                   LIB3040-036-Q1-E1-D10
                   7875
Seq. No.
                   10877_1.R1040
Contig ID
5'-most EST
                   LIB3107-072-Q1-K1-E10
Method
                   BLASTN
NCBI GI
                   g343041
BLAST score
                   167
E value
                   1.0e-88
Match length
                   584
                   86
% identity
NCBI Description
                  Pisum sativum chloroplast Val-tRNA gene
                   7876
Seq. No.
                   10878 1.R1040
Contig ID
5'-most EST
                   LIB3040-060-Q1-E1-G9
Method
                   BLASTX
NCBI GI
                   g2160183
BLAST score
                   388
                   3.0e-42
E value
Match length
                   118
% identity
                   79
                   (AC000132) Identical to A. thaliana U2 SnRNP-specific A'
NCBI Description
                   protein (gb_X69137). ESTs gb_ATTS0705, gb_ATTS0339 come
                   from this gene. [Arabidopsis thaliana]
                   7877
Seq. No.
Contig ID
                   10888 1.R1040
5'-most EST
                   LIB3040-049-Q1-E1-B7
                   BLASTX
Method
NCBI GI
                   g82114
BLAST score
                   269
E value
                   2.0e-23
Match Tength
                   78
                   67
% identity
                  wound-induced protein - tomato (fragment)
NCBI Description
                   >gi 19320 emb CAA42537 (X59882) wound induced protein
                   [Lycopersicon esculentum]
                   7878
Seq. No.
Contig ID
                   10893 1.R1040
5'-most EST
                   LIB3107-030-Q1-K1-B11
Method
                   BLASTX
NCBI GI
                   g2760844
BLAST score
                   350
                   6.0e-33
E value
Match length
                   87
% identity
NCBI Description
                   (AC003105) hypothetical protein [Arabidopsis thaliana]
                   7879
Seq. No.
                   10893 3.R1040
Contig ID
```

sat701004534.hl

5'-most EST

```
7880
Seq. No.
Contig ID
                  10898 1.R1040
5'-most EST
                 LIB3040-060-Q1-E1-E9
Seq. No.
                  10902 1.R1040
Contig ID
5'-most EST
                  kl1701211184.h1
Method
                  BLASTX
NCBI GI
                  q2832623
BLAST score
                  631
                  3.0e-65
E value
                  395
Match length
                  37
% identity
                   (AL021711) protein kinase - like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  7882
Contig ID
                  10902 2.R1040
5'-most EST
                  fC-gmro700844396g1
Method
                  BLASTX
NCBI GI
                  q2832623
BLAST score
                  290
                  7.0e-26
E value
                  135
Match length
% identity
                  46
                  (AL021711) protein kinase - like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  7883
                  10903 1.R1040
Contig ID
5'-most EST
                  LIB3040-043-Q1-E1-F3
Method
                  BLASTX
NCBI GI
                  g3122724
BLAST score
                  338
E value
                  1.0e-31
Match length
                  69
% identity
                  94
NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal
                  protein L38 isolog [Arabidopsis thaliana]
Seq. No.
                  7884
                  10903 2.R1040
Contig ID
5'-most EST
                  LIB3040-048-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  q3122724
BLAST score
                  338
E value
                  1.0e-31
Match length
                  69
                  94
% identity
                  60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal
NCBI Description
                  protein L38 isolog [Arabidopsis thaliana]
Seq. No.
                  7885
Contig ID
                  10904 1.R1040
```

LIB3170-083-Q1-J1-C4

```
7886
Seq. No.
                   10907 1.R1040
Contig ID
                   LIB3170-019-Q1-J1-D3
5'-most EST
                   7887
Seq. No.
                   10912 1.R1040
Contig ID
                   LIB3170-011-Q1-K1-E9
5'-most EST
                   7888
Seq. No.
                   10915 1.R1040
Contig ID
5'-most EST
                   zhf700964946.hl
Method
                   BLASTX
NCBI GI
                   g2961378
BLAST score
                   1482
E value
                   1.0e-165
Match length
                   473
% identity
NCBI Description
                   (AL022141) putative protein [Arabidopsis thaliana]
                   7889
Seq. No.
                   10915 2.R1040
Contig ID
                   uaw700664257.hl
5'-most EST
Method
                   BLASTX
                   g2961378
NCBI GI
BLAST score
                   271
E value
                   9.0e-24
                                                                        والمراجع والمجيث
Match length
                   69
% identity
                   35
                   (AL022141) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7890
                   10917 1.R1040
Contig ID
                   uC-gmropic040d12b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1397319
BLAST score
                   209
                   3.0e-16
E value
Match length
                   118
                   38
% identity
NCBI Description
                   (U61953) No definition line found [Caenorhabditis elegans]
Seq. No.
                   7891
                   10917 2.R1040
Contig ID
5'-most EST
                  LIB3040-060-Q1-E1-C8
                   7892
Seq. No.
Contig ID
                   10920 1.R1040
5'-most EST
                   LIB3040-060-Q1-E1-D2
Method
                   BLASTX
NCBI GI
                   q3193303
BLAST score
                   234
E value
                   2.0e-19
                   90
Match length
% identity
NCBI Description
                   (AF069298) similar to several proteins containing a tandem
                   repeat region such as Plasmodium falciparum GGM tandem
```

repeat protein (GB:U27807); partial CDS [Arabidopsis

Method

NCBI GI

BLASTX

q3582335

```
7893
Seq. No.
Contig ID
                   10923 1.R1040
5'-most EST
                  LIB3051-085-Q1-K1-G4
                  BLASTX
Method
                  g2347194
NCBI GI
BLAST score
                   210
E value
                   4.0e-18
                                             ٨.
Match length
                  182
                   36
% identity
NCBI Description
                   (AC002338) hypothetical protein [Arabidopsis thaliana]
                   7894
Seq. No.
                  10929 1.R1040
Contig ID
5'-most EST
                  LIB3040-052-Q1-E1-H11
Method
                  BLASTX
                  g3810855
NCBI GI
BLAST score
                  216
E value
                   5.0e-17
Match length
                  142
                   39
% identity
                  (AL032684) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   7895
Seq. No.
                   10931 1.R1040
Contig ID
5'-most EST
                  LIB3170-019-Q1-J1-C10
                   7896
Seq. No.
                  10935 1.R1040
Contig ID
5'-most EST
                   zpv700762884.hl
Method
                  BLASTX
                  g1076316
NCBI GI
BLAST score
                  296
E value
                  1.0e-26
Match length
                  121
% identity
                   45
NCBI Description
                  drought-induced protein Di19 - Arabidopsis thaliana
                  >gi 469110 emb CAA55321 (X78584) Di19 [Arabidopsis
                  thaliana]
                   7897
Seq. No.
Contig ID
                  10936 1.R1040
5'-most EST
                  LIB3092-056-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3582335
BLAST score
                  1852
E value
                  0.0e + 00
Match length
                  375
% identity
NCBI Description
                   (AC005496) unknown protein [Arabidopsis thaliana]
Seq. No.
                   7898
                  10936 3.R1040
Contig ID
                  LIB3170-002-Q1-J1-H4
5'-most EST
```

thaliana]

5'-most EST

```
BLAST score
                   141
E value
                   1.0e-08
Match length
                   42
% identity
                   64
NCBI Description
                   (AC005496) unknown protein [Arabidopsis thaliana]
                   7899
Seq. No.
                   10936_5.R1040
Contig ID
5'-most EST
                   LIB3072-037-Q1-E1-G5
                   7900
Seq. No.
Contig ID
                   10938 1.R1040
5'-most EST
                   LIB3040-060-Q1-E1-A4
Seq. No.
                   7901
Contig ID
                   10941 1.R1040
5'-most EST
                   LIB3040-060-Q1-E1-A9
                   7902
Seq. No.
                   10947 1.R1040
Contig ID
5'-most EST
                   LIB3040-060-Q1-E1-B2
                   7903
Seq. No.
                   10948 1.R1040
Contig ID
5'-most EST
                   fC-gmse700654525r1
Method
                   BLASTX
NCBI GI
                   q4539423
BLAST score
                   1549
E value
                   1.0e-173
Match length
                   383
                   81
% identity
NCBI Description
                   (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
                   [Arabidopsis thaliana]
                   7904
Seq. No.
Contig ID
                   10948 2.R1040
5'-most EST
                   LIB3139-008-P1-N1-F6
                   7905
Seq. No.
                   10948_3.R1040
Contig ID
5'-most EST
                   fC-gmle700559917a1
Method
                   BLASTX
NCBI GI
                   g4539423
BLAST score
                   399
E value
                   2.0e-38
Match length
                   100
% identity
                   77
NCBI Description
                   (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
                   [Arabidopsis thaliana]
                   7906
Seq. No.
Contig ID
                   10948 4.R1040
5'-most EST
                   LIB3092-032-Q1-K1-F6
Seq. No.
                   7907
Contig ID
                   10948 5.R1040
```

 $eep70\overline{0}870309.h1$

```
7908
Seq. No.
                   10954 1.R1040
Contig ID
5'-most EST
                   LIB3051-044-Q1-K1-B3
                   BLASTX
Method
NCBI GI
                   g2583133
BLAST score
                   247
                   1.0e-20
E value
                   179
Match length
                   36
% identity
NCBI Description
                   (AC002387) unknown protein [Arabidopsis thaliana]
                   7909
Seq. No.
                   10954 2.R1040
Contig ID
5'-most EST
                   LIB3109-028-Q1-K1-D4
                   7910
Seq. No.
                   10954 3.R1040
Contig ID
                   leu701148605.hl
5'-most EST
                   7911
Seq. No.
                   10957 1.R1040
Contig ID
5'-most EST
                   leu70\overline{1}146515.h1
                   BLASTX
Method
NCBI GI
                   g2191136
BLAST score
                   173
E value
                   2.0e-16
Match length
                   176
                   34
% identity
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
Seq. No.
                   7912
                   10957 2.R1040
Contig ID
5'-most EST
                   LIB3040-045-Q1-E1-F2
Method
                   BLASTX
                   g2191136
NCBI GI
BLAST score
                   177
E value
                   7.0e-13
Match length
                   100
% identity
                   37
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
Seq. No.
                   7913
Contig ID
                   10962 1.R1040
5'-most EST
                   LIB3040-053-Q1-E1-A11
Method
                   BLASTN
                   g313026
NCBI GI
BLAST score
                   67
E value
                   4.0e-29
Match length
                   195
```

84

% identity

Method

BLASTX

```
NCBI Description L.esculentum rpl38 mRNA for ribosomal protein L38
                   7914
Seq. No.
                   10965 1.R1040
Contig ID
                   LIB3040-059-Q1-E1-D9
5'-most EST
                   7915
Seq. No.
                   10972 1.R1040
Contig ID
5'-most EST
                   LIB3106-048-Q1-K1-C3
                   7916
Seq. No.
                   10977 1.R1040
Contig ID
                  LIB3094-038-Q1-K1-H7
5'-most EST
                   7917
Seq. No.
                   10981 1.R1040
Contig ID
                   pmv700889551.h1
5'-most EST
Method
                   BLASTX
                   g2435511
NCBI GI
BLAST score
                   351
E value
                   5.0e-33
Match length
                   89
                   73
% identity
NCBI Description
                   (AF024504) contains similarity to prolyl 4-hydroxylase
                   alpha subunit [Arabidopsis thaliana]
Seq. No.
                   7918
Contig ID
                   10982 1.R1040
5'-most EST
                   uC-gmropic099a04b1
Method
                   BLASTN
NCBI GI
                   g3695058
BLAST score
                   132
E value
                   9.0e-68
Match length
                   344
                   90
% identity
NCBI Description
                  Lotus japonicus rac GTPase activating protein 1 mRNA,
                   complete cds
                   7919
Seq. No.
                   10989 1.R1040
Contig ID
5'-most EST
                  LIB3040-017-Q1-E1-A3
Method
                  BLASTX
NCBI GI
                   q2462834
BLAST score
                   356
E value
                   2.0e-33
Match length
                   173
% identity
                   47
NCBI Description
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   10993 1.R1040
Contig ID
5'-most EST
                   leu70\overline{1}154503.h1
                   7921
Seq. No.
                   10994 1.R1040
Contig ID
                   LIB3040-059-Q1-E1-A8
5'-most EST
```

E value

2.0e-35

```
NCBI GI
                  g4263713
BLAST score
                  593
E value
                  5.0e-61
Match length
                  200
% identity
                  (AC006223) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  7922
Seq. No.
                  10994 3.R1040
Contiq ID
5'-most EST
                  jex700903123.hl
Method
                  BLASTX
                  g4263713
NCBI GI
BLAST score
                  289
E value
                  4.0e-26
Match length
                  70
% identity
                  (AC006223) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  7923
Seq. No.
                  10996 1.R1040
Contig ID
5'-most EST
                  LIB3040-046-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  g2583135
BLAST score
                  578
E value
                  2.0e-59
Match length
                  159
                  71
% identity
NCBI Description
                  (AC002387) hypothetical protein [Arabidopsis thaliana]
                  >gi 3822216 (AF074948) FIL [Arabidopsis thaliana]
                  >gi 4322477 gb AAD16053 (AF087015) abnormal floral organs
                  protein [Arabidopsis thaliana]
Seq. No.
                  7924
Contig ID
                  10996 2.R1040
5'-most EST
                  LIB3170-001-Q1-K1-B1
                  BLASTX
Method
NCBI GI
                  g2583135
BLAST score
                  348
E value
                  7.0e-33
Match length
                  115
% identity
                  (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3822216 (AF074948) FIL [Arabidopsis thaliana]
                  >gi 4322477 gb_AAD16053_ (AF087015) abnormal floral organs
                  protein [Arabidopsis thaliana]
Seq. No.
                  7925
                  11001 1.R1040
Contig ID
5'-most EST
                  uC-gmropic062a09b1
                  7926
Seq. No.
                  11002 1.R1040
Contig ID
                  uC-gmflminsoy046e01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2464880
BLAST score
                  372
```

Match length

248

```
130
Match length
                   55
% identity
NCBI Description
                  (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                   7927
Contig ID
                   11002 2.R1040
                   fua701042774.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2464880
BLAST score
                   292
E value
                   3.0e-26
Match length
                   104
% identity
                   54
NCBI Description
                   (Z99707) putative protein [Arabidopsis thaliana]
                   7928
Seq. No.
                   11004 1.R1040
Contig ID
5'-most EST
                  LIB3170-015-Q1-K1-F6
                   7929
Seq. No.
                   11004 2.R1040
Contig ID
5'-most EST
                   zlv700807692.hl
                   7930
Seq. No.
Contig ID
                   11009 1.R1040
5'-most EST
                   LIB3170-053-Q1-K1-B9
                   BLASTX
Method
NCBI GI
                   q4455365
BLAST score
                   165
E value
                   3.0e-11
Match length
                   35
% identity
                   83
NCBI Description
                   (AL035524) putative protein [Arabidopsis thaliana]
                   7931
Seq. No.
Contig ID
                   11014 1.R1040
5'-most EST
                   jC-gmf102220081b10a1
                   7932
Seq. No.
                   11016_1.R1040
Contig ID
                   jC-gmro02910061a02a1
5'-most EST
Method
                   BLASTX
                   g2208908
NCBI GI
BLAST score
                   473
E value
                   3.0e-47
Match length
                   108
% identity
                   85
                   (AB004809) phosphate transporter [Catharanthus roseus]
NCBI Description
Seq. No.
                   7933
                   11017 1.R1040
Contig ID
5'-most EST
                  uC-gmropic063b09b1
Method
                  BLASTX
NCBI GI
                   g3461833
BLAST score
                   1056
E value
                   1.0e-115
```

% identity

89

```
% identity
                   75
                   (AC004138) putative expansin [Arabidopsis thaliana]
NCBI Description
                   7934
Seq. No.
                   11017 2.R1040
Contig ID
5'-most EST
                   fC-qmse700658228z1
Method
                   BLASTX
NCBI GI
                   q4027897
BLAST score
                   268
E value
                   4.0e-23
Match length
                   55
% identity
                   84
NCBI Description
                  (AF049353) alpha-expansin precursor [Nicotiana tabacum]
                   7935
Seq. No.
                   11017 3.R1040
Contig ID
5'-most EST
                  LIB3040-058-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                   q4027897
BLAST score
                   706
                   1.0e-74
E value
                   162
Match length
                   79
% identity
                   (AF049353) alpha-expansin precursor [Nicotiana tabacum]
NCBI Description
                   7936
Seq. No.
Contig ID
                   11018 1.R1040
5'-most EST
                  LIB3040-060-Q1-E1-A3
Method
                  BLASTX
NCBI GI
                   g2253442
BLAST score
                   260
E value
                   3.0e-22
Match length
                   62
                   66
% identity
NCBI Description
                   (AF007784) LTCOR11 [Lavatera thuringiaca]
Seq. No.
                  7937
                   11019 1.R1040
Contig ID
                   uC-gmrominsoy277b05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4158232
BLAST score
                   1716
                   0.0e + 00
E value
Match length
                   332
% identity
                   92
                   (Y18626) reversibly glycosylated polypeptide [Triticum
NCBI Description
                   aestivum]
Seq. No.
                   7938
                   11019 2.R1040
Contig ID
                   kl1701204287.h2
5'-most EST
Method
                  BLASTN
NCBI GI
                  q2218151
BLAST score
                   228
E value
                   1.0e-125
Match length
                   404
```

NCBI Description Vigna unguiculata type IIIa membrane protein cp-wap13 mRNA, complete cds Seq. No. 7939 11019 3.R1040 Contig ID 5'-most EST jC-gmst02400003d10d1 Method BLASTN NCBI GI g2218151 BLAST score 137 E value 6.0e-71 Match length 259 % identity 92 NCBI Description Vigna unquiculata type IIIa membrane protein cp-wap13 mRNA, complete cds 7940 Seq. No. 11029 1.R1040 Contig ID 5'-most EST q5666720 Method BLASTX NCBI GI q2495209 BLAST score 382 2.0e-36 E value Match length 105 % identity NCBI Description HYPOTHETICAL 12.9 KD PROTEIN SLR1417 >gi 1651819 dbj BAA16746 (D90900) hypothetical protein [Synechocystis sp.] Seq. No. 7941 Contig ID 11029 2.R1040 5'-most EST leu701148522.h1 Seq. No. 7942 Contig ID 11030 1.R1040 5'-most EST wrq700788995.h2 Method BLASTX NCBI GI g4263519 BLAST score 469 E value 6.0e-47 Match length 96 % identity NCBI Description (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana] 7943 Seq. No. Contig ID 11030 2.R1040 5'-most EST LIB3040-058-Q1-E1-G9 Method BLASTX NCBI GI g4263519

Method BLASTX
NCBI GI g4263519
BLAST score 393
E value 5.0e-38
Match length 79
% identity 97

NCBI Description (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis

thaliana]

Seq. No. 7944

5'-most EST

```
Contig ID
                   11035 1.R1040
5'-most EST
                   LIB3106-058-Q1-K1-A9
                   BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
                   1.0e-10
E value
Match length
                   36
                   100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   7945
Seq. No.
Contig ID
                   11037 1.R1040
5'-most EST .
                   hyd700727479.h1
Method
                   BLASTX
NCBI GI
                   q4567203
BLAST score
                   426
E value
                   1.0e-41
Match length
                   87
                   91
% identity
                   (AC007168) putative beta-hydroxyacyl-ACP dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   7946
Seq. No.
                   11044 1.R1040
Contig ID
5'-most EST
                   sat701015360.hl
Seq. No.
                   7947
                   11044 2.R1040
Contig ID
5'-most EST
                   LIB3055-003-Q1-N1-G2
                   7948
Seq. No.
Contig ID
                   11045 1.R1040
                   crh70\overline{0}850109.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1173624
BLAST score
                   1102
E value
                   1.0e-120
Match length
                   342
                   63
% identity
                   (U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid
NCBI Description
                   SM9108']
                   7949
Seq. No.
                   11045_2.R1040
Contig ID
                   LIB3170-020-Q1-K1-B5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1173624
BLAST score
                   259
E value
                   3.0e-22
Match length
                   77
% identity
                   66
NCBI Description
                   (U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid
                   SM9108']
Seq. No.
                   7950
                   11045 4.R1040
Contig ID
```

vwf700674610.hl

```
Seq. No.
                  7951
                  11053 1.R1040
Contig ID
5'-most EST
                  g5753161
                  7952
Seq. No.
Contig ID
                  11060 1.R1040
                  LIB3072-053-Q1-E1-G11
5'-most EST
                  BLASTX
Method
NCBI GI
                  g126078
BLAST score
                  277
                  2.0e-24
E value
Match length
                  117
                  30
% identity
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)
NCBI Description
                  >gi_81554_pir__S04046 embryonic abundant protein gD-34 -
                  upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea
                  protein [Gossypium hirsutum] >gi_167385 (M19389) storage
                  protein [Gossypium hirsutum] >gi_226556_prf_ 1601521F Lea
                  D-34 gene [Saguinus oedipus]
Seq. No.
                  7953
                  11061 1.R1040
Contig ID
5'-most EST
                  LIB3040-044-Q1-E1-A3
Method
                  BLASTX
NCBI GI
                  q2244822
BLAST score
                  328
E value
                  1.0e-30
Match length
                  85
% identity
                  72
                   (Z97336) RNA polymerase II fifth largest subunit homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  7954
Contig ID
                  11063 1.R1040
5'-most EST
                  LIB3092-008-Q1-K1-D1
Method
                  BLASTN
NCBI GI
                  q4104973
BLAST score
                  491
E value
                  0.0e+00
Match length
                  895
                  89
% identity
                  Pisum sativum spermidine synthase 2 (SPDSYN2) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  7955
                  11063 2.R1040
Contig ID
5'-most EST
                  LIB3052-014-Q1-N1-H2
Method
                  BLASTN
NCBI GI
                  g4104971
BLAST score
                  205
E value
                  1.0e-111
                  347
Match length
                  90
% identity
                  Pisum sativum spermidine synthase 1 (SPDSYN1) mRNA,
NCBI Description
```

complete cds

NCBI Description

```
7956
Seq. No.
                   11063 3.R1040
Contig ID
5'-most EST
                   asn701133255.hl
Method
                   BLASTN
NCBI GI
                   g4104973
BLAST score
                   34
E value
                   1.0e-09
Match length
                   50
% identity
                   92
NCBI Description
                   Pisum sativum spermidine synthase 2 (SPDSYN2) mRNA,
                   complete cds
                   7957
Seq. No.
Contig ID
                   11063 4.R1040
5'-most EST
                   jC-qmle01810063d11d1
Method
                   BLASTN
NCBI GI
                   g4104973
BLAST score
                   66
E value
                   1.0e-28
Match length
                   193
% identity
                   89
NCBI Description
                   Pisum sativum spermidine synthase 2 (SPDSYN2) mRNA,
                   complete cds
Seq. No.
                   7958
                   11063 5.R1040
Contig ID
5'-most EST
                   q4260078
Method
                   BLASTN
NCBI GI
                   q4104971
BLAST score
                   120
E value
                   8.0e-61
Match length
                   245
% identity
                   90
NCBI Description
                  Pisum sativum spermidine synthase 1 (SPDSYN1) mRNA,
                   complete cds
Seq. No.
                   7959
Contig ID
                   11065 1.R1040
5'-most EST
                   jC-gmle01810068a04a1
Method
                   BLASTX
NCBI GI
                   g3805842
BLAST score
                   285
E value
                   3.0e-25
Match length
                   161
% identity
                   43
NCBI Description
                   (AL031986) putative protein [Arabidopsis thaliana]
Seq. No.
                   11066 1.R1040
Contig ID
5'-most EST
                  LIB3040-057-Q1-E1-H1
Method
                  BLASTX
NCBI GI
                  g2119045
BLAST score
                   454
                   3.0e-45
E value
                  99
Match length
                   87
% identity
```

small nuclear ribonucleoprotein U1A - potato

Seq. No.

Contig ID 5'-most EST

7965

11075 1.R1040

LIB3170-017-Q1-J1-A11

```
protein, U1A [Solanum tuberosum]
Seq. No.
                   11069 1.R1040
Contig ID
                   jC-gmro02910052d01a1
5'-most EST
                   BLASTX ·
Method
NCBI GI
                   g537319
BLAST score
                   1386
                   1.0e-154
E value
Match length
                   309
% identity
                   83
                   (L36158) peroxidase [Medicago sativa]
NCBI Description
Seq. No.
                   7962
                   11072 1.R1040
Contig ID
5'-most EST
                   LIB3049-056-Q1-E1-H3
Method
                   BLASTX
NCBI GI
                   g3881724
BLAST score
                   291
E value
                   7.0e-26
                   90
Match length
% identity
                   58
NCBI Description
                   (Z69385) Similarity to Yeast JTA107 protein (PIR Acc. No.
                   S55137); cDNA EST yk290e3.3 comes from this gene; cDNA EST
                   yk290e3.5 comes from this gene [Caenorhabditis elegans]
Seq. No.
                   7963
                   11072 2.R1040
Contig ID
5'-most EST
                   LIB30\overline{4}0-057-Q1-E1-H9
Method
                   BLASTX
NCBI GI
                   g3881724
BLAST score
                   272
                   5.0e-24
E value
Match length
                   89
% identity
                   55
NCBI Description
                   (Z69385) Similarity to Yeast JTA107 protein (PIR Acc. No.
                   S55137); cDNA EST yk290e3.3 comes from this gene; cDNA EST
                   yk290e3.5 comes from this gene [Caenorhabditis elegans]
Seq. No.
                   7964
Contig ID
                   11074 1.R1040
5'-most EST
                   sat701014926.hl
Method
                   BLASTX
NCBI GI
                   q3834307
BLAST score
                   341
E value
                   7.0e-32
Match length
                   94
% identity
NCBI Description
                   (AC005679) Strong similarity to gene T10I14.120 gi 2832679
                   putative protein from Arabidopsis thaliana BAC gb AL021712.
                   ESTs gb N65887 and gb N65627 come from this gene.
                   [Arabidopsis thaliana]
```

>gi_1050840_emb_CAA90282_ (Z49990) UlsnRNP-specific

Seq. No.

7972

```
7966
Seq. No.
                   11077 1.R1040
Contig ID
                   LIB3170-017-Q1-J1-A12
5'-most EST
Seq. No.
                   11082 1.R1040
Contig ID
5'-most EST
                   LIB3040-057-Q1-E1-E9
Seq. No.
                   7968
                   11083 1.R1040
Contig ID
5'-most EST
                   LIB3040-031-Q1-E2-C12
Method
                   BLASTX
NCBI GI
                   q3283409
BLAST score
                   165
E value
                   4.0e-11
Match length
                   58
% identity
                   59
NCBI Description
                   (AF068754) heat shock factor binding protein 1 HSBP1 [Homo
                   sapiens] >gi_4557647_ref_NP_001528.1_pHSBP1_ heat shock
                   factor binding protein
Seq. No.
                   7969
                   11085_1.R1040
Contig ID
5'-most EST
                   LIB3074-036-Q1-K1-E2
Method
                   BLASTX
NCBI GI
                   q2739375
BLAST score
                   268
E value
                   2.0e-23
Match length
                   107
% identity
                   55
NCBI Description
                   (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   11085 3.R1040
5'-most EST
                   LIB3106-094-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   g2739375
BLAST score
                   152
E value
                   4.0e-10
Match length
                   46
% identity
NCBI Description
                   (AC002505) unknown protein [Arabidopsis thaliana]
                   7971
Seq. No.
Contig ID
                   11093 1.R1040
5'-most EST
                   LIB3106-057-Q1-K1-G9
Method
                   BLASTN
NCBI GI
                   g3603400
BLAST score
                   455
E value
                   0.0e+00
Match length
                   1073
% identity
                   86
                  Medicago sativa cinnamyl-alcohol dehydrogenase (MsaCadl)
NCBI Description
                  mRNA, complete cds
```

```
11093 3.R1040
Contig ID
5'-most EST
                   zhf70\overline{0}954121.h1
Method
                   BLASTN
NCBI GI
                   g556421
BLAST score
                   114
E value
                   3.0e-57
Match length
                   274
                   85
% identity
                   Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1)
NCBI Description
                  mRNA, complete cds
                   7973
Seq. No.
                   11095 1.R1040
Contig ID
5'-most EST
                   LIB3040-057-Q1-E1-G2
Seq. No.
                   7974
                   11100 1.R1040
Contig ID
5'-most EST
                  LIB3170-018-Q1-J1-A3
                   7975
Seq. No.
Contig ID
                   11102 1.R1040
                  LIB3107-042-Q1-K1-C6
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3738328
BLAST score
                   315
E value
                   5.0e-29
                  79
Match length
                   72
% identity
NCBI Description
                   (AC005170) putative serine carboxypeptidase [Arabidopsis
                   thaliana]
                   7976
Seq. No.
                   11102 2.R1040
Contig ID
5'-most EST
                  LIB3040-057-Q1-E1-D3
Method
                  BLASTX
NCBI GI
                   q4263777
BLAST score
                  234
E value
                   1.0e-19
Match length
                  84
% identity
NCBI Description
                   (AC006068) putative serine carboxypeptidase II [Arabidopsis
                   thaliana] >gi 4510391 gb AAD21479.1 (AC007017) putative
                   serine carboxypeptidase II [Arabidopsis thaliana]
Seq. No.
                   7977
                   11103_1.R1040
Contig ID
5'-most EST
                  LIB3040-057-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  q3004550
BLAST score
                  176
E value
                   2.0e-12
Match length
                  64
% identity
NCBI Description
                   (AC003673) hypothetical protein [Arabidopsis thaliana]
                   7978
Seq. No.
```

11109 1.R1040

Contig ID

```
5'-most EST
                   LIB3040-057-Q1-E1-E11
Method
                   BLASTX
NCBI GI
                   q586079
BLAST score
                   1015
                   1.0e-111
E value
Match length
                   196
                   97
% identity
NCBI Description
                   TUBULIN GAMMA-1 CHAIN >gi 460089 (U02069) gl-tubulin
                   [Arabidopsis thaliana]
                   7979
Seq. No.
                   11114 1.R1040
Contig ID
                   LIB3040-057-Q1-E1-B1
5'-most EST
                   7980
Seq. No.
                   11120 1.R1040
Contig ID
                   LIB3107-059-Q1-K1-D10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g266410
BLAST score
                   378
E value
                   4.0e-36
Match length
                   144
% identity
                   62
                   CDC2+/CDC28-RELATED PROTEIN KINASE R2 >gi 82507 pir S13934
NCBI Description
                   protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog - rice >gi_20194_emb_CAA41172_ (X58194) cdc2+/CDC28-related
                   protein kinase [Oryza sativa]
Seq. No.
                   7981
                   11122 1.R1040
Contig ID
5'-most EST
                   LIB3170-017-Q1-J1-A1
Seq. No.
                   7982
                   11126 1.R1040
Contig ID
5'-most EST
                   LIB3170-020-Q1-K1-A12
Seq. No.
                   7983
                   11127 1.R1040
Contiq ID
5'-most EST
                   LIB3040-057-Q1-E1-C4
Method
                   BLASTX
NCBI GI
                   g4508075
BLAST score
                   639
E value
                   2.0e-66
Match length
                   339
% identity
                   44
NCBI Description (AC005882) 50259 [Arabidopsis thaliana]
Seq. No.
                   7984
                   11128 1.R1040
Contig ID
                   LIB3139-062-P1-N1-H1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2388956
BLAST score
                   629
                   2.0e-65
E value
                   223
Match length
% identity
NCBI Description (Z98979) ribulose-phosphate 3-epimerase
```

5'-most EST

[Schizosaccharomyces pombe]

Seq. No. 7985 11128 2.R1040 Contig ID LIB3139-119-P1-N1-D7 5'-most EST BLASTX Method NCBI GI g861366 BLAST score 316 E value 4.0e-29 Match length 121 54 % identity (U28991) coded for by C. elegans cDNA cm21c7 NCBI Description [Caenorhabditis elegans] 7986 Seq. No. 11129 1.R1040 Contig ID 5'-most EST LIB3040-057-Q1-E1-C7 Seq. No. 7987 11134 1.R1040 Contig ID LIB3170-019-Q1-K1-A5 5'-most EST 7988 Seq. No. 11143 1.R1040 Contig ID 5'-most EST LIB3049-029-Q1-E1-A1 7989 Seq. No. 11145 1.R1040 Contig ID LIB3107-002-Q1-K1-E3 5'-most EST Method BLASTX NCBI GI g2388575 BLAST score 233 E value 2.0e-19 Match length 75 % identity NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana] Seq. No. 7990 11151 1.R1040 Contig ID 5'-most EST LIB3040-056-Q1-E1-F6 7991 Seq. No. 11156 1.R1040 Contig.ID LIB3170-020-Q1-K1-A5 5'-most EST Seq. No. 7992 11161 1.R1040 Contig ID 5'-most EST LIB3052-007-Q1-B1-E5 7993 Seq. No. 11168 1.R1040 Contig ID 5'-most EST LIB3040-056-Q1-E1-D8 Seq. No. 7994 11172 1.R1040 · Contig ID

LIB3049-008-Q1-E1-A6

NCBI GI

```
7995
Seq. No.
                   11172 2.R1040
Contig ID
5'-most EST
                   LIB3040-056-Q1-E1-C5
Method
                   BLASTX
NCBI GI
                   g4559384
BLAST score
                   215
E value
                   3.0e-17
Match length
                   62
% identity
                   68
NCBI Description
                   (AC006526) unknown protein [Arabidopsis thaliana]
Seq. No.
                   11172 3.R1040
Contig ID
5'-most EST
                   LIB3051-108-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   q4559384
BLAST score
                   164
E value
                   5.0e-11
Match length
                   65
% identity
                   (AC006526) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   7997
Contig ID
                   11183 1.R1040
5'-most EST
                   LIB3050-007-Q1-E1-H10
                   7998
Seq. No.
                   11184 1.R1040
Contig ID
5'-most EST
                   leu701152062.hl
                   BLASTX
Method
NCBI GI
                   q3785978
BLAST score
                   444
E value
                   5.0e-44
Match length
                   132
                   65
% identity
NCBI Description
                   (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   11185 1.R1040
5'-most EST
                   LIB3040-056-01-E1-B4
Seq. No.
                   8000
Contig ID
                   11190 1.R1040
5'-most EST
                   LIB3040-056-Q1-E1-C10
Method
                   BLASTX
NCBI GI
                   q2980795
BLAST score
                   825
E value
                   2.0e-88
Match length
                   177
% identity
NCBI Description
                   (AL022197) putative protein [Arabidopsis thaliana]
                   8001
Seq. No.
                   11192 1.R1040
Contig ID
5'-most EST
                   epx701104273.hl
Method
                   BLASTX
```

g4115916

BLAST score

E value

219

8.0e-18

```
BLAST score
                   145
E value
                   3.0e-09
Match length
                   96
% identity
                   46
NCBI Description
                   (AF118222) F3H7.9 gene product [Arabidopsis thaliana]
                   >gi_4539441_emb_CAB40029.1_ (AL049523) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   8002
                   11195 1.R1040
Contig ID
                   LIB3040-056-Q1-E1-A5
5'-most EST
                   8003
Seq. No.
                   11195 2.R1040
Contig ID
5'-most EST
                   qsv701051708.h1
                   8004
Seq. No.
                   11198 1.R1040
Contig ID
5'-most EST
                   LIB3040-055-Q1-E1-G6
Method
                   BLASTX
NCBI GI
                   g2208988
BLAST score
                   396
E value
                   9.0e-39
Match length
                   88
% identity
NCBI Description
                 (Y10117) signal recognition particle subunit 9 [Zea mays]
                   8005
Seq. No.
Contig ID
                   11204 1.R1040
5'-most EST
                   uC-gmflminsoy058d10b1
Method
                   BLASTN
NCBI GI
                   g294665
BLAST score
                   216
E value
                   1.0e-117
Match length
                   512
% identity
NCBI Description
                   Castor bean chloroplast beta-ketoacyl-ACP synthase mRNA,
                   complete cds
                   8006
Seq. No.
Contig ID
                   11211 1.R1040
5'-most EST
                   LIB3040-056-Q1-E1-A4
Method
                   BLASTX
NCBI GI
                   g4432814
BLAST score
                   408
E value
                   8.0e-40
Match length
                   92
% identity
NCBI Description
                   (AC006593) unknown protein [Arabidopsis thaliana]
                   8007
Seq. No.
                   11211 2.R1040
Contig ID
5'-most EST
                   uC-gmronoir007c10b1
Method
                   BLASTX
NCBI GI
                   g4432814
```

Seq. No.

8014

```
Match length
                   50
% identity
                   80
NCBI Description
                   (AC006593) unknown protein [Arabidopsis thaliana]
                   8008
Seq. No.
                   11217 1.R1040
Contig ID
5'-most EST
                   sat701010626.h1
Method
                   BLASTX
NCBI GI
                   g3786001
BLAST score
                   478
E value
                   2.0e-85
                   200
Match length
                   78
% identity
NCBI Description
                   (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                   11218 1.R1040
Contig ID
                   LIB3040-055-Q1-E1-F10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2335098
BLAST score
                   1103
E value
                   1.0e-121
Match length
                   331
% identity
                   63
NCBI Description
                   (AC002339) unknown protein [Arabidopsis thaliana]
Seq. No.
                   8010
                   11223 1.R1040
Contig ID
5'-most EST
                   LIB3040-055-Q1-E1-F7
Method
                   BLASTX
NCBI GI
                   g4165861
BLAST score
                   187
E value
                   6.0e-14
Match length
                   83
% identity
NCBI Description
                   (AF006603) histone deacetylase mHDA2 [Mus musculus]
Seq. No.
                   11231 1.R1040
Contig ID
5'-most EST
                   LIB3040-055-Q1-E1-C3
Seq. No.
                   8012
                   11233 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910068a07a1
Method
                   BLASTX
NCBI GI
                   g4049341
BLAST score
                   204
E value
                   9.0e-16
                   71
Match length
% identity
                   (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                   8013
Seq. No.
                   11235 1.R1040
Contig ID
                   LIB30\overline{4}0-055-Q1-E1-D1
5'-most EST
```

```
11237 1.R1040
Contig ID
5'-most EST
                   LIB3050-008-Q1-E1-F4
Method
                   BLASTX
NCBI GI
                   g461530
BLAST score
                   454
                   6.0e-45
E value
Match length
                   173
                   55
% identity
NCBI Description
                   N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG
                   >gi 159365 (L11348) ARD1 protein homologue [Leishmania
                   donovani]
                   8015
Seq. No.
                   11240 1.R1040
Contig ID
5'-most EST
                   LIB3170-013-Q1-K1-H4
Method
                   BLASTX
NCBI GI
                   q3184082
BLAST score
                   407
E value
                   2.0e-39
Match length
                   156
% identity
                   47
NCBI Description
                   (AL023781) N-terminal acetyltransferase 1
                   [Schizosaccharomyces pombe]
Seq. No.
                   8016
Contig ID
                   11242 1.R1040
5'-most EST
                   LIB3139-026-P1-N1-F7
Method
                   BLASTX
                   q3549670
NCBI GI
BLAST score
                   1829
E value
                   0.0e + 00
Match length
                   424
% identity
                   80
NCBI Description
                   (AL031394) putative protein [Arabidopsis thaliana]
                   8017
Seq. No.
Contig ID
                   11243 1.R1040
                                                           M_{\rm ext}^{\rm col}
                   LIB3170-014-Q1-J1-H2
5'-most EST
                   8018
Seq. No.
                   11245 1.R1040
Contig ID
5'-most EST
                   LIB3040-046-Q1-E1-H9
Seq. No.
                   8019
                   11258 1.R1040
Contig ID
                   LIB3040-055-Q1-E1-B12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4539355
BLAST score
                   152
                   8.0e-10
E value
Match length
                   53
% identity
NCBI Description
                   (AL049525) putative protein [Arabidopsis thaliana]
                   8020
Seq. No.
```

11270 1.R1040

g4291877

Contig ID 5'-most EST

NCBI Description

8025

Seq. No.

```
Method
                   BLASTX
NCBI GI
                   q1532167
BLAST score
                   200
E value
                   3.0e-15
Match length
                   65
% identity
                   51
                   (U63815) localized according to blastn similarity to EST
NCBI Description
                   sequences; therefore, the coding span corresponds only to
                   an area of similarity since the initation codon and stop
                   codon could not be precisely determined [Arabidopsis
                   thaliana]
Seq. No.
                   8021
                   11278 1.R1040
Contig ID
5'-most EST
                   LIB3107-060-Q1-K1-D12
Method
                   BLASTX
NCBI GI
                   g3831452
BLAST score
                   508
E value
                   2.0e-51
Match length
                   135
% identity
NCBI Description
                   (AC005700) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   11278 2.R1040
Contig ID
5'-most EST
                   zsg701127707.h1
Method
                   BLASTX
NCBI GI
                   q3831452
BLAST score
                   423
E value
                   1.0e-41
Match length
                   111
% identity
                   (AC005700) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8023
Contig ID
                   11283 1.R1040
5'-most EST
                  LIB3073-019-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   q3184288
BLAST score
                   223
E value
                   5.0e-18
Match length
                   60
% identity
                   70
NCBI Description
                   (AC004136) unknown protein [Arabidopsis thaliana]
                   8024
Seq. No.
Contig ID
                   11283 4.R1040
5'-most EST
                   vwf700675923.hl
Method
                   BLASTX
NCBI GI
                   q3184288
BLAST score
                   210
E value
                   5.0e-17
Match length
                   50
% identity
```

(AC004136) unknown protein [Arabidopsis thaliana]

```
11287 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir032c05b1
                   BLASTX
Method
NCBI GI
                   g2894598
BLAST score
                   441
                   1.0e-43
E value
                   93
Match length
% identity
                   85
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
                   8026
Seq. No.
                   11287 2.R1040
Contig ID
                   sat701010684.h1
5'-most EST
Method
                   BLASTX
                   g2894598
NCBI GI
                   387
BLAST score
E value
                   2.0e-37
Match length
                   81
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8027
                   11303 1.R1040
Contig ID
5'-most EST
                   pcp700989501.h1
                   8028
Seq. No.
                   11309 1.R1040
Contig ID
5'-most EST
                   LIB3040-053-Q1-E1-G7
Method
                   BLASTX
NCBI GI
                   g1439609
BLAST score
                   6,08
E value
                   4.0e-63
Match length
                   164
% identity
                   46
NCBI Description
                   (U62778) delta-tonoplast intrinsic protein [Gossypium
                   hirsutum]
                   8029
Seq. No.
                   11310 1.R1040
Contig ID
                   asn70\overline{1}139329.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2924257
BLAST score
                   114
E value
                   6.0e-57
                   394
Match length
% identity
                   90
NCBI Description
                  Tobacco chloroplast genome DNA
                   8030
Seq. No.
                   11312 1.R1040
Contig ID
5'-most EST
                   LIB3170-013-Q1-K1-G5
Seq. No.
                   8031
                   11316_1.R1040
Contig ID
                  LIB30\overline{4}0-053-Q1-E1-H9
5'-most EST
Seq. No.
                   8032
```

5'-most EST

```
11318 1.R1040
Contig ID
5'-most EST
                   LIB3072-050-Q1-K1-E12
                   8033
Seq. No.
                   11319 1.R1040
Contig ID
                   LIB3073-004-Q1-K1-G12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2281089
BLAST score
                   408
E value
                   1.0e-39
                   91
Match length
                   86
% identity
NCBI Description
                   (AC002333) Sm protein F isolog [Arabidopsis thaliana]
                   8034
Seq. No.
                   11322 1.R1040
Contig ID
5'-most EST
                   LIB3040-053-Q1-E1-D9
Seq. No.
                   8035
                   11326 1.R1040
Contig ID
5'-most EST
                   LIB3040-053-Q1-E1-E2
Method
                   BLASTX
NCBI GI
                   g3650037
BLAST score
                   989
E value
                   1.0e-107
Match length
                   214
% identity
                   89
                   (AC005396) auxin-responsive GH3-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   8036
Seq. No.
                   11329 1.R1040
Contig ID
                   LIB3049-017-Q1-E1-A7
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4263771
BLAST score
                   298
E value
                   5.0e-27
Match length
                  86
                   57
% identity
                   (AC006218) putative nonspecific lipid-transfer protein
NCBI Description
                  precursor [Arabidopsis thaliana]
                   8037
Seq. No.
                   11333_1.R1040
Contig ID
5'-most EST
                  LIB3094-079-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                   q4538911
BLAST score
                   398
E value
                   3.0e-38
Match length
                  175
% identity
                   50
NCBI Description
                   (AL049482) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   8038
                  11333 2.R1040
Contig ID
```

LIB3107-076-Q1-K1-C2

```
8039
Seq. No.
                   11336 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-047-Q1-K1-D3
                   8040
Seq. No.
                   11336 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy008d12b1
                   8041
Seq. No.
                   11336 3.R1040
Contig ID
5'-most EST
                   LIB3040-045-Q1-E1-C3
Seq. No.
                   8042
                   11341 1.R1040
Contig ID
5'-most EST
                   LIB3040-053-Q1-E1-B7
                   8043
Seq. No.
                   11343 1.R1040
Contig ID
                   k11701206623.h1
5'-most EST
                   8044
Seq. No.
                   11343 2.R1040
Contig ID
5'-most EST
                   ncj700983657.hl
Seq. No.
                   8045
                   11344 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220100e03a1
                   8046
Seq. No.
                   11348 1.R1040
Contig ID
5'-most EST
                   LIB3040-053-Q1-E1-D11
                   8047
Seq. No.
                   11356 1.R1040
Contig ID
5'-most EST
                   LIB3040-052-Q1-E1-H6
Method
                   BLASTN
NCBI GI
                   g2244991
BLAST score
                   44
E value
                   1.0e-15
Match length
                   112
% identity
                   85
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                   8048
Seq. No.
Contig ID
                   11363_1.R1040
5'-most EST
                   LIB3139-050-P1-N1-F10
Method
                   BLASTX
NCBI GI
                   g4220477
BLAST score
                   383
E value
                   6.0e-37
Match length
                   154
                   58
% identity
                   (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   8049
Seq. No.
```

11365_1.R1040

Contig ID.

5'-most EST

```
5'-most EST
                   rlr700896481.h1
Method
                   BLASTX
                   g2244846
NCBI GI
BLAST score
                   466
                   2.0e-46
E value
Match length
                   102
                   83
% identity
                   (Z97337) ferredoxin [Arabidopsis thaliana]
NCBI Description
                   8050
Seq. No.
Contig ID
                   11367 1.R1040
                   seb70\overline{0}650601.h1
5'-most EST
Seq. No.
                   8051
Contig ID
                   11370 1.R1040
                   LIB3138-062-Q1-N1-E3
5'-most EST
                   8052
Seq. No.
                   11372 1.R1040
Contig ID
5'-most EST
                   awf700840180.hl
Method
                   BLASTX
NCBI GI
                   g1172995
BLAST score
                   272
                   1.0e-23
E value
Match length
                   107
                   54
% identity
                   60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal
NCBI Description
                   protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus]
                   >gi 1093952 prf 2105193A ribosomal protein L22 [Rattus
                   norvegicus]
                   8053
Seq. No.
                   11378_1.R1040
Contig ID
                   LIB3170-076-Q1-K1-G3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4580461
BLAST score.
                   317
E value
                   4.0e-29
Match length
                   112
                   51
% identity
NCBI Description
                   (AC006081) unknown protein [Arabidopsis thaliana]
                   8054
Seq. No.
                   11378 2.R1040
Contig ID
                   hrw70\overline{1}060842.h1
5'-most EST
Method
                   BLASTX
                   g4580461
NCBI GI
BLAST score
                   147
E value
                   2.0e-09
                   77
Match length
% identity
                   (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   8055
Seq. No.
                   11386 1.R1040
Contig ID
```

LIB3049-028-Q1-E1-D1

% identity

NCBI Description

```
Method
                   BLASTX
NCBI GI
                   g2558660
BLAST score
                   196
E value
                   1.0e-14
Match length
                   178
% identity
                   31
NCBI Description
                   (AC002354) No definition line found [Arabidopsis thaliana]
Seq. No.
                   8056
                   11386 2.R1040
Contig ID
5'-most EST
                   eep700864234.hl
                   8057
Seq. No.
Contig ID
                   11389 1.R1040
5'-most EST
                   LIB3167-078-P1-K2-C12
Method
                   BLASTX
NCBI GI
                   q1362103
BLAST score
                   816
E value
                   3.0e-87
Match length
                   192
                   81
% identity
NCBI Description
                   ubiquitin conjugating enzyme - tomato
                   >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating
                   enzyme [Lycopersicon esculentum]
Seq. No.
Contig ID
                   11389 2.R1040
5'-most EST
                   pcp700990943.hl
Method
                   BLASTX
NCBI GI
                   q1362103
BLAST score
                   450
E value
                   6.0e-45
Match length
                   103
% identity
NCBI Description
                   ubiquitin conjugating enzyme - tomato
                   >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating
                   enzyme [Lycopersicon esculentum]
Seq. No.
                   8059
Contig ID
                   11396 1.R1040
5'-most EST
                   LIB3040-052-Q1-E1-C5
Seq. No.
                   8060
                   11400 1.R1040
Contig ID
5'-most EST
                   LIB3170-004-Q1-K1-D11
Seq. No.
                   8061
                   11407 1.R1040
Contig ID
5'-most EST
                   leu701154337.hl
Method
                   BLASTX
NCBI GI
                   q3885941
BLAST score
                   312
E value
                   1.0e-28
Match length
                   85
```

(AF095454) PII protein [Ricinus communis]

Seq. No.

8068

```
8062
Seq. No.
                  11416 1.R1040
Contig ID
5'-most EST
                  LIB3040-051-Q1-E1-G10
                  8063
Seq. No.
                  11419 1.R1040
Contig ID
                  LIB3040-051-Q1-E1-G2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2160694
BLAST score
                  620
E value
                  9.0e-65
Match length
                  141
% identity
                  83
NCBI Description
                  (U73528) B' regulatory subunit of PP2A [Arabidopsis
                  thaliana]
Seq. No.
                  8064
Contig ID
                  11427 1.R1040
5'-most EST
                  LIB3040-044-Q1-E1-H3
Method
                  BLASTX
NCBI GI
                  q2398533
BLAST score
                  519
E value
                  2.0e-52
Match length
                  113
                  92
% identity
NCBI Description
                  (Y13725) Transcription factor [Arabidopsis thaliana]
Seq. No.
Contig ID
                  11427 2.R1040
5'-most EST
                  uC-gmrominsoy258e01b1
Seq. No.
                  11431 1.R1040
Contig ID
5'-most EST
                  fde700875381.hl
Method
                  BLASTX
NCBI GI
                  g2894611.
                  210
BLAST score
                  7.0e-30°
E value
Match length
                  119
% identity
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
                  8067
Seq. No.
Contig ID
                  11433 1.R1040
5'-most EST
                  LIB3107-063-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  q3695408
BLAST score
                  268
E value
                  3.0e-23
Match length
                  86
% identity
NCBI Description
                  (AF096373) contains similarity to Solanum lycopersicum
                  (tomato) wound-induced protein (GB:X59882) [Arabidopsis
                  thaliana] >gi_4538956 emb_CAB39780.1 (AL049488) probable
                  wound-induced protein [Arabidopsis thaliana]
```

```
Contig ID
                  11433 2.R1040
5'-most EST
                  LIB3040-051-Q1-E1-C2
Method
                  BLASTX
                  g3695408
NCBI GI
BLAST score
                  270
E value
                  1.0e-23
Match length
                  86
% identity
                   63
                   (AF096373) contains similarity to Solanum lycopersicum
NCBI Description
                   (tomato) wound-induced protein (GB:X59882) [Arabidopsis
                  thaliana] >gi 4538956 emb CAB39780.1 (AL049488) probable
                  wound-induced protein [Arabidopsis thaliana]
                  8069
Seq. No.
                  11433 3.R1040
Contig ID
5'-most EST
                  LIB3093-036-Q1-K1-A1
Seq. No.
                  8070
Contig ID
                  11437 1.R1040
5'-most EST
                  LIB3040-051-Q1-E1-D10
                  8071
Seq. No.
                  11440 1.R1040
Contig ID
                  leu70\overline{1}156215.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q169364
BLAST score
                  111
E value
                  2.0e-55
Match length
                  210
                  89
% identity
                  Phaseolus vulgaris 5.8 Kb basic protein (PR4) gene,
NCBI Description
                  complete cds. >gi 217988 dbj D12914 PHVPVPR4 Phaseolus
                  vulgaris PvPR4 mRNA for 5.8 kb basic protein, complete cds
                  8072
Seq. No.
                  11440 2.R1040
Contig ID
5'-most EST
                  LIB3170-002-Q1-K1-H3
Method
                  BLASTN
NCBI GI
                  q169364
BLAST score
                  111
                  2.0e-55
E value
Match length
                  210
                  89
% identity
                  Phaseolus vulgaris 5.8 Kb basic protein (PR4) gene,
NCBI Description
                  complete cds. >gi 217988 dbj D12914_PHVPVPR4 Phaseolus
                  vulgaris PvPR4 mRNA for 5.8 kb basic protein, complete cds
                  8073
Seq. No.
                  11440 3.R1040
Contig ID
5'-most EST
                  LIB3049-047-Q1-E1-A9
Method
                  BLASTN
                  g169364
NCBI GI
                                                                            يه ۱۰ شو
BLAST score
                  123
E value
                  1.0e-62
Match length
                  209
% identity
                  91
```

. . .

NCBI Description Phaseolus vulgaris 5.8 Kb basic protein (PR4) gene,

Contig ID 5'-most EST

Method

NCBI GI

BLAST score

```
8074
Seq. No.
                   11448 1.R1040
Contig ID
5'-most EST
                   LIB3049-042-Q1-E1-G9
Method
                   BLASTX
NCBI GI
                   g3273828
                   1597
BLAST score
                   0.0e+00
E value
Match length
                   411
                   94
% identity
NCBI Description
                   (AF068686) nodule-enhanced malate dehydrogenase [Glycine
                   max]
                   8075
Seq. No.
                   11448 2.R1040
Contig ID
5'-most EST
                   gsv701053423.hl
Method
                   BLASTN
NCBI GI
                   g3273826
BLAST score
                   147
E value
                   6.0e-77
Match length
                   318
                   91
% identity
NCBI Description Glycine max nodule-enhanced malate dehydrogenase (Mdh)
                   gene, complete cds
                   8076
Seq. No.
                   11448 3.R1040
Contig ID
5'-most EST
                   gsv701043956.hl
                   BLASTN
Method
NCBI GI
                   q3273826
BLAST score
                   186
                   1.0e-100
E value
Match length
                   328
% identity
                   Glycine max nodule-enhanced malate dehydrogenase (Mdh)
NCBI Description
                   gene, complete cds
                   8077
Seq. No.
                   11468 1.R1040
Contig ID
5'-most EST
                   LIB3040-047-Q1-E1-H6
Method
                   BLASTX
                   g1173624
NCBI GI
BLAST score
                   308
E value
                   5.0e-28
                   71
Match length
% identity
                   (U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid
NCBI Description
                   SM9108']
Seq. No.
                   8078
```

complete cds. >gi_217988_dbj_D12914_PHVPVPR4 Phaseolus vulgaris PvPR4 mRNA for 5.8 kb basic protein, complete cds

11468 2.R1040

BLASTX

148

g2935525

LIB3040-026-Q1-E1-H6

```
2.0e-09
E value
Match length
                   76
                   49
% identity
                  (AF049067) cytochrome P450 [Pinus radiata]
NCBI Description
                   8079
Seq. No.
                   11479 1.R1040
Contig ID
5'-most EST
                   LIB3040-050-Q1-E1-G7
                   BLASTX
Method
NCBI GI
                   g2244935
BLAST score
                   285
E value
                   4.0e-25
                   106
Match length
                   57
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   8080
Seq. No.
                   11479 2.R1040
Contig ID
5'-most EST
                   LIB3170-016-Q1-K1-H1
Method
                   BLASTX
NCBI GI
                   g2244935
BLAST score
                   215
                   3.0e-17
E value
Match length
                   66
% identity
                   64
                   (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   8081
Seq. No.
                   11481 1.R1040
Contig ID
                   vzy700752646.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2494905
BLAST score
                   174
E value
                   2.0e-12
Match length
                   90
% identity
                   46
                   MICROTUBULE-ASSOCIATED PROTEIN YTM1 >gi 2132107 pir S67174
NCBI Description
                   hypothetical protein YOR272w - yeast (Saccharomyces
                   cerevisiae) >gi 1279699 emb CAA61778 (X89633) hypothetical
                   protein [Saccharomyces cerevisiae]
                   >gi_1420610_emb_CAA99497_ (Z75180) ORF YOR272w [Saccharomyces Cerevisiae] >gi_1928989 (U92821)
                   microtubule-associated protein [Saccharomyces cerevisiae]
Seq. No.
                   8082
                   11483 1.R1040
Contig ID
                   leu701149068.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2289907
BLAST score
                   557
E value
                   6.0e-57
                   206
Match length
                   55
% identity
                   (AC002397) C2F [Mus musculus]
NCBI Description
```

8083

11483_2.R1040

Seq. No.

Contig ID

```
5'-most EST
                  .leu701155519.h1
                   8084
Seq. No.
                   11497 1.R1040
Contig ID
5'-most EST
                   LIB3073-008-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   q2275216
BLAST score
                   235
E value
                   2.0e-19
Match length
                   64
% identity
                   69
NCBI Description
                   (AC002337) cytochrome c oxidase Vc subunit isolog
                   [Arabidopsis thaliana]
Seq. No.
                   8085
                   11497 2.R1040
Contig ID
5'-most EST
                   LIB3170-054-Q1-K1-G12
                   BLASTX
Method
NCBI GI
                   q2275216
BLAST score
                   231
                   3.0e-19
E value
                   64
Match length
% identity
                   67
NCBI Description
                   (AC002337) cytochrome c oxidase Vc subunit isolog
                   [Arabidopsis thaliana]
                   8086
Seq. No.
                   11501 1.R1040
Contig ID
5'-most EST
                   LIB3170-015-Q1-K1-E8
Seq. No.
                   8087
                   11505 1.R1040
Contig ID
5'-most EST
                   LIB3170-015-Q1-K1-E7
                   8088
Seq. No.
Contig ID
                   11513 1.R1040
5'-most EST
                  LIB3040-061-Q1-E11-G7
Method
                   BLASTX
NCBI GI
                   q3282674
BLAST score
                   414
E value
                   2.0e-40
Match length
                   99
                   77
% identity
NCBI Description
                   (AF036684) CCAAT-box binding factor HAP3 homolog
                   [Arabidopsis thaliana]
Seq. No.
                   8089
Contig ID
                   11513 2.R1040
5'-most EST
                  LIB3040-026-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                   q3282674
BLAST score
                   322
E value
                   1.0e-29
Match length
                   72
                   85
% identity
NCBI Description
                   (AF036684) CCAAT-box binding factor HAP3 homolog
                   [Arabidopsis thaliana]
```

Method

BLASTX

```
8090
Seq. No.
                   11517 1.R1040
Contig ID
                   epx70\overline{1}110032.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3004560
BLAST score
                   668
E value
                   5.0e-70
Match length
                   149
% identity
                   85
                   (AC003673) putative ATP binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   8091
Seq. No.
                   11517 2.R1040
Contig ID
5'-most EST
                   LIB3040-050-Q1-E1-C7
Method
                   BLASTX
NCBI GI
                   g3004560
BLAST score
                   287
E value
                   7.0e-26
Match length
                   75
% identity
NCBI Description
                   (AC003673) putative ATP binding protein [Arabidopsis
                   thaliana]
                   8092
Seq. No.
                   11518 1.R1040
Contig ID
5'-most EST
                   LIB3170-015-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   g3980254
BLAST score
                   299
E value
                   2.0e-29
Match length
                   109
% identity
NCBI Description
                   (AJ006053) peroxisomal membrane protein [Arabidopsis
                   thaliana]
Seq. No.
                   8093
                   11523 1.R1040
Contig ID
5'-most EST
                   jex700903169.h1
Seq. No.
                   11525 1.R1040
Contig ID
5'-most EST
                   LIB3040-049-Q1-E1-H12
Method
                   BLASTX
NCBI GI
                   q3024583
BLAST score
                   270
E value
                   9.0e-24
Match length
                   96
% identity
                   RT14 PROTEIN HOMOLOG >gi 2347196 (AC002338) RT14 protein
NCBI Description
                   isolog [Arabidopsis thaliana]
Seq. No.
                   8095
                   11532 1.R1040
Contig ID
5'-most EST
                   hyd700729012.h1
```

NCBI Description

```
NCBI GI
                  q1657617
BLAST score
                  604
                  1.0e-62
E value
Match length
                  135
                  83
% identity
NCBI Description
                  (U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236)
                  putative nuclear DNA-binding protein G2p [Arabidopsis
                  thaliana]
                  8096
Seq. No.
                  11532 2.R1040
Contig ID
5'-most EST
                  LIB3170-013-Q1-J1-D8
Method
                  BLASTX
NCBI GI
                  q1657617
BLAST score
                  416
E value
                  7.0e-41
Match length
                  105
% identity
                   (U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236)
NCBI Description
                  putative nuclear DNA-binding protein G2p [Arabidopsis
                  thaliana]
Seq. No.
                  8097
Contig ID
                  11533 1.R1040
                  LIB3040-050-Q1-E1-A5
5'-most EST
                  8098
Seq. No.
Contig ID
                  11538 1.R1040
                  LIB3170-013-01-K1-D12
5'-most EST
                  8099
Seq. No.
                  11538 2.R1040
Contig ID
                  LIB3109-050-Q1-K1-A1
5'-most EST
Method
                  BLASTX
                  g1706103
NCBI GI
BLAST score
                  331
E value
                  2.0e-30
Match length
                  243
                  34
% identity
NCBI Description
                  CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD
                  SUBUNIT (CPSF 100 KD SUBUNIT) >gi_1363022_pir__A56351
                  cleavage and polyadenylation specificity factor 100K chain
                  - bovine >gi_599683_emb_CAA53535_ (X75931) Cleavage and
                  Polyadenylation specificity factor (CPSF) 100kD subunit
                  [Bos taurus]
Seq. No.
                  8100
Contig ID
                  11557 1.R1040
5'-most EST
                  kl1701207775.h1
Method
                  BLASTX
                  q3747132
NCBI GI
BLAST score
                  489
E value
                  2.0e-49
Match length
                  124
% identity
                  71
```

(AF096776) expansin [Lycopersicon esculentum]

```
Seq. No.
                   8101
                   11561 1.R1040
Contig ID
5'-most EST
                   vzy700755696.hl
Method
                   BLASTX
NCBI GI
                   g2244939
BLAST score
                   203
E value
                   1.0e-24
Match length
                   181
% identity
                   (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11562 1.R1040
Contig ID
                   uaw70\overline{0}662405.h1
5'-most EST
                   8103
Seq. No.
Contig ID
                   11562 3.R1040
5'-most EST
                   zpv700759748.hl
Seq. No.
                   8104
                   11569 1.R1040
Contig ID
5'-most EST
                   LIB3074-039-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   g4467116
BLAST score
                   312
                   3.0e-28
E value
                   134
Match length
                   46
% identity
NCBI Description
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
                   8105
Seq. No.
                   11570 1.R1040
Contig ID
5'-most EST
                   LIB3040-049-Q1-E1-E2
                   8106
Seq. No.
                   11571 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy063e09b1
Method
                   BLASTX
NCBI GI
                   g3434975
BLAST score
                   392
E value
                   7.0e-38
Match length
                   172
                   54
% identity
NCBI Description
                   (AB008107) ethylene responsive element binding factor 5
                   [Arabidopsis thaliana]
                   8107
Seq. No.
Contig ID
                   11571 2.R1040
5'-most EST
                   LIB3040-049-Q1-E1-E3
Method
                   BLASTX
NCBI GI
                   g3434975
BLAST score
                   210
E value
                   1.0e-16
Match length
                   141
% identity
                   44
NCBI Description
                   (AB008107) ethylene responsive element binding factor 5
```

[Arabidopsis thaliana]

5'-most EST

```
Seq. No.
                   8108
Contig ID
                   11577 1.R1040
                                                       .....
5'-most EST
                   fC-gmse700669227a3
                  BLASTX
Method
NCBI GI
                  g3128167
BLAST score
                   796
                   1.0e-84
E value
                   483
Match length
                   43
% identity
                   (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3212874 (AC004005) hypothetical protein [Arabidopsis
                  thaliana]
                   8109
Seq. No.
                   11577 2.R1040
Contig ID
                  LIB3170-015-Q1-K1-D6
5'-most EST
Seq. No.
                   8110
                  11589 1.R1040
Contig ID
5'-most EST
                  gsv701054713.hl
Method
                  BLASTX
                  g3421109
NCBI GI
BLAST score
                  992
E value
                   1.0e-108
Match length
                  204
                   94
% identity
                   (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  8111
                  11589 2.R1040
Contig ID
                  LIB3106-114-Q1-K1-G7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3421109
BLAST score
                  776
E value
                   1.0e-82
Match length
                  171
% identity
                   (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
NCBI Description
                  thaliana]
                  8112
Seq. No.
                  11589 3.R1040
Contig ID
5'-most EST
                  LIB3049-056-Q1-E1-A10
Method
                  BLASTX
NCBI GI
                  g3421109
BLAST score
                  340
E value
                  3.0e-42
Match length
                  98
% identity
NCBI Description
                   (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
                  thaliana]
                  8113
Seq. No.
                  11589 4.R1040
Contig ID
```

kl1701204594.h2

NCBI Description

```
Method
                  BLASTX
NCBI GI
                  g3421109
BLAST score
                  616
                   3.0e-64
E value
Match length
                  127
% identity
                   93
                   (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
NCBI Description
                  thaliana]
                  8114
Seq. No.
Contig ID
                  11601 1.R1040
                  gsv701046451.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3850571
BLAST score
                  427
E value
                  8.0e-42
Match length
                  92
% identity
NCBI Description
                   (AC005278) Similar to gb_U85207 snRNP core Sm protein
                  homolog Sm-X5 from Mus musculus. EST gb AA612141 comes
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  8115
Contig ID
                  11601 2.R1040
5'-most EST
                  LIB3050-004-Q1-E1-E9
Method
                  BLASTX
NCBI GI
                  g3850571
BLAST score
                  233
E value
                  3.0e-29
                  79
Match length
% identity
NCBI Description
                   (AC005278) Similar to gb U85207 snRNP core Sm protein
                  homolog Sm-X5 from Mus musculus. EST gb AA612141 comes
                  from this gene. [Arabidopsis thaliana]
                  8116
Seq. No.
                  11603 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910060d01a1
Seq. No.
                  8117
                  11613 1.R1040
Contig ID
5'-most EST
                  LIB3074-004-Q1-K1-E9
                  8118
Seq. No.
Contig ID
                  11620 1.R1040
                  LIB3170-016-Q1-J1-D4
5'-most EST
                  8119
Seq. No.
                  11629 1.R1040
Contig ID
                  LIB3049-005-Q1-E1-G9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3044218
BLAST score
                  581
                  3.0e-60
E value
Match length
                  130
% identity
                  82
```

(AF057144) signal peptidase [Arabidopsis thaliana]

```
8120
Seq. No.
                   11631 1.R1040
Contig ID
                  LIB3087-008-Q1-K1-G5
5'-most EST
                   8121
Seq. No.
                   11632 1.R1040
Contig ID
                  LIB3040-045-Q1-E1-C11
5'-most EST
                   8122
Seq. No.
                   11635 1.R1040
Contig ID
                   uC-gmropic036b09b1
5'-most EST
Method
                   BLASTX
                   g4091080
NCBI GI
                   528
BLAST score
                   1.0e-53
E value
                   201
Match length
                   52
% identity
                  (AF045571) nucleic acid binding protein [Oryza sativa]
NCBI Description
                   8123
Seq. No.
                   11635 2.R1040
Contig ID
                   LIB3049-033-Q1-E1-D11
5'-most EST
                   BLASTX
Method
NCBI GI
                   q166410
                   319
BLAST score
                   2.0e-29
E value
                   91
Match length
                   71
% identity
                   (L07291) Alfin-1 [Medicago sativa]
NCBI Description
                   8124
Seq. No.
                   11635 3.R1040
Contig ID
                   leu701147577.hl
5'-most EST
Method
                   BLASTX
                   q166410
NCBI GI
                   287
BLAST score
                   9.0e-26
E value
                   62
Match length
% identity
                   (L07291) Alfin-1 [Medicago sativa]
NCBI Description
                   8125
Seq. No.
                   11637 1.R1040
Contig ID
                   LIB3106-061-Q1-K1-B6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2388578
BLAST score
                   861
                   1.0e-92
E value
Match length
                   202
                   81
% identity
                   (AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs
NCBI Description
                   gb_T75785,gb_R30580,gb_T04698 come from this gene.
                   [Arabidopsis thaliana]
                   8126
Seq. No.
```

11640_1.R1040

Contig ID

5'-most EST

```
5'-most EST
                   qsv701047317.h1
Seq. No.
                   8127
                   11641 1.R1040
Contig ID
                   jC-gmf102220113h02a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4512708
BLAST score
                   348
E value
                   9.0e-33
Match length
                   84
% identity
                   76
                   (AC006569) putative glutaredoxin [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   11641 2.R1040
5'-most EST
                   LIB3040-047-Q1-E1-H9
Method
                   BLASTX
NCBI GI
                   g4512708
BLAST score
                   326
E value
                   3.0e-30
Match length
                   83
% identity
                   75
NCBI Description (AC006569) putative glutaredoxin [Arabidopsis thaliana]
Seq. No.
                   8129
                   11656 1.R1040
Contig ID
5'-most EST
                   LIB3040-047-01-E1-F6
Method
                   BLASTX
NCBI GI
                   q4455325
BLAST score
                   415
E value
                   2.0e-40
Match length
                   142
% identity
NCBI Description
                   (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                   8130
Contig ID
                   11660 1.R1040
5'-most EST
                   LIB3051-031-Q1-K1-D8
                   8131
Seq. No.
Contig ID
                   11660 3.R1040
                   LIB3170-014-Q1-K1-C4
5'-most EST
Seq. No.
                   8132
Contig ID
                   11661 1.R1040
5'-most EST
                   LIB3040-047-Q1-E1-G12
Method
                   BLASTX
NCBI GI
                   q4490704
BLAST score
                   548
E value
                   6.0e-56
Match length
                   215
% identity
                   52
NCBI Description
                   (AL035680) putative protein [Arabidopsis thaliana]
Seq. No.
                   8133
                   11668 1.R1040
Contig ID
```

LIB3139-059-P1-N1-G6

```
BLASTX
Method
NCBI GI
                   q3080401
BLAST score
                   920
E value
                   1.0e-99
Match length
                   233
                   72
% identity
                   (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4455265_emb_CAB36801.1_ (AL035527) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   8134
                   11672 1.R1040
Contig ID
                   LIB3094-047-Q1-K1-A4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2865175
BLAST score
                   556
E value
                   8.0e-57
Match length
                   154
% identity
                   68
NCBI Description
                   (AB010945) AtRerlA [Arabidopsis thaliana]
Seq. No.
Contig ID
                   11672 2.R1040
5'-most EST
                   vzy700755937.hl
Method
                   BLASTX
NCBI GI
                   q2865177
BLAST score
                   555
E value
                   8.0e-57
Match length
                   183
                   57
% identity
NCBI Description
                   (AB010946) AtRerlB [Arabidopsis thaliana]
Seq. No.
                   8136
Contig ID
                   11672 3.R1040
5'-most EST
                   jC-gmst02400015f10a1
Method
                   BLASTX
NCBI GI
                   q2865175
BLAST score
                   168
E value
                   2.0e-11
Match length
                   49
                   59
% identity
NCBI Description
                   (AB010945) AtRer1A [Arabidopsis thaliana]
Seq. No.
                   8137
Contig ID
                   11672 4.R1040
5'-most EST
                   LIB3094-047-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   q2865175
BLAST score
                   390
E value
                   1.0e-37
Match length
                   119
% identity
NCBI Description
                   (AB010945) AtRerlA [Arabidopsis thaliana]
Seq. No.
                   8138
```

· · ·

11672 5.R1040

LIB3049-001-Q1-E1-H8

Contig ID 5'-most EST

BLAST score

E value

153

1.0e-09

```
BLASTX
Method
NCBI GI
                   g2865175
                   197
BLAST score
                   3.0e-15
E value
Match length
                   83
                   48
% identity
NCBI Description
                   (AB010945) AtRerlA [Arabidopsis thaliana]
                   8139
Seq. No.
                   11672 6.R1040
Contig ID
                   r1r70\overline{0}897411.h1
5'-most EST
Seq. No.
                   8140
                   11673 1.R1040
Contig ID
                   LIB3170-015-Q1-K1-C12
5'-most EST
                   8141
Seq. No.
                   11680 1.R1040
Contig ID
5'-most EST
                   LIB3072-023-Q1-E1-H11
Method
                   BLASTX
NCBI GI
                   g1723738
BLAST score
                   222
E value
                   5.0e-18
Match length
                   103
% identity
                   30
                   HYPOTHETICAL 55.1 KD PROTEIN IN TRX1-RTA1 INTERGENIC REGION
NCBI Description
                   >gi_2131699_pir__S64534 hypothetical protein YGR211w -
                   yeast (Saccharomyces cerevisiae) >gi 1323379 emb CAA97238
                   (Z72996) ORF YGR211w [Saccharomyces cerevisiae] >gi 3510466
                   (AF019769) zinc finger protein [Saccharomyces cerevisiae]
Seq. No.
                   8142
                   11693 1.R1040
Contig ID
5'-most EST
                   LIB3040-047-Q1-E1-C4
Seq. No.
                   8143
                   11693 2.R1040
Contig ID
                   LIB3093-037-Q1-K1-G5
5'-most EST
Seq. No.
                   8144
                   11694 1.R1040
Contig ID
                   ncj70\overline{0}979372.h1
5'-most EST
Method
                   BLASTX
                   g4455207
NCBI GI
BLAST score
                   443
E value
                   7.0e-44
Match length
                   91
% identity
                   (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8145
                   11695 1.R1040
Contig ID
5'-most EST
                   LIB3072-057-Q1-K1-G1
Method
                   BLASTX
NCBI GI
                   g1082054
```

```
Match length
                   142
% identity
                   30
                   (Z49859) copper transporter protein [Arabidopsis thaliana]
NCBI Description
                   8146
Seq. No.
                   11695 2.R1040
Contig ID
5'-most EST
                   94284406
                   8147
Seq. No.
                   11696 1.R1040
Contig ID
                   LIB3040-047-Q1-E1-C7
5'-most EST
Seq. No.
                   8148
                   11697 1.R1040
Contig ID
                   LIB3170-085-Q1-J1-C2
5'-most EST
                   8149
Seq. No.
                   11700 1.R1040
Contig ID
5'-most EST
                   LIB3050-015-Q1-E1-C4
Method
                   BLASTN
NCBI GI
                   g3449334
BLAST score
                   46
E value
                   1.0e-16
Match length
                   126
% identity
                   84
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   8150
                   11707 1.R1040
Contig ID
                   LIB3170-015-Q1-K1-C6
5'-most EST
                   8151
Seq. No.
                   11708 1.R1040
Contig ID
5'-most EST
                   LIB3170-016-Q1-K1-C7
                   8152
Seq. No.
                   11712 1.R1040
Contig ID
5'-most EST
                   LIB3170-015-Q1-J1-C7
Method
                   BLASTX
                   g4006878
NCBI GI
BLAST score
                   140
E value
                   1.0e-08
Match length
                   47
% identity
NCBI Description
                   (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
Seq. No.
                   8153
                   11716 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{4}0-046-Q1-E1-G9
Seq. No.
                   8154
                   11717 1.R1040
Contig ID
5'-most EST
                   LIB3040-047-Q1-E1-A7
Seq. No.
                   8155
```

11727_1.R1040

Contig ID

```
5'-most EST
                   LIB3040-046-Q1-E1-F9
Seq. No.
                   8156
Contig ID
                   11732 1.R1040
5'-most EST
                   LIB3170-016-Q1-K1-C2
Seq. No.
                   8157
                   11734 1.R1040
Contig ID
5'-most EST
                   LIB3170-015-Q1-K1-C2
Seq. No.
                   8158
                   11734 5.R1040
Contig ID
5'-most EST
                   leu701155165.hl
                   8159
Seq. No.
Contig ID
                   11734 8.R1040
5'-most EST
                   gsv701044315.h1
Seq. No.
                   8160
Contig ID
                   11737 1.R1040
                   jC-gmle01810092d05a1
5'-most EST
Method
                   BLASTX
                   g1699023
NCBI GI
BLAST score
                   215
E value
                   9.0e-17
Match length
                   225
% identity
NCBI Description
                   (U78866) putative arginine-aspartate-rich RNA binding
                   protein [Arabidopsis thaliana] >gi_1699051 (U78867)
                   putative aspartate-arginine-rich mRNA binding protein
                   [Arabidopsis thaliana]
                   8161
Seq. No.
                   11740 1.R1040
Contig ID
5'-most EST
                   gsv701044686.hl
                   8162
Seq. No.
Contig ID
                   11740 2.R1040
                   LIB3170-013-Q1-K1-E2
5'-most EST
                   8163
Seq. No.
Contig ID
                   11746 1.R1040
5'-most EST
                   LIB31\overline{0}9-001-Q1-K4-D1
Method
                   BLASTX
NCBI GI
                   g2760320
BLAST score
                   545
E value
                   2.0e-55
Match length
                   223
% identity
NCBI Description
                   (AC002130) F1N21.4 [Arabidopsis thaliana]
Seq. No.
                   8164
Contig ID
                   11755 1.R1040
5'-most EST
                   LIB3040-029-Q1-E1-E4
Method
                   BLASTN
NCBI GI
                   g3204128
```

200

BLAST score

```
E value
                   1.0e-108
Match length
                   404
% identity
                   87
NCBI Description
                  Cicer arietinum mRNA for histone H2A
                   8165
Seq. No.
                   11758 1.R1040
Contig ID
5'-most EST
                   LIB3040-046-Q1-E1-E5
Method
                   BLASTX
NCBI GI
                   q2281088
BLAST score
                   350
E value
                   6.0e-33
Match length
                   159
                   42
% identity
NCBI Description
                   (AC002333) indole-3-acetate beta-glucosyltransferase isolog
                   [Arabidopsis thaliana]
                   8166
Seq. No.
                   11762 1.R1040
Contig ID
5'-most EST
                   LIB3040-045-Q1-E1-H9
                   BLASTN
Method
NCBI GI
                   g633606
BLAST score
                   44
E value
                   3.0e-15
Match length
                   183
% identity
                   85
                  P.sativum mRNA for chloroplastic outer envelope membrane
NCBI Description
                  protein (OEP75)
Seq. No.
                   8167
Contig ID
                   11762 2.R1040
                   LIB3093-012-Q1-K1-H10
5'-most EST
                   BLASTN
Method
                   g633606
NCBI GI
BLAST score
                   57
E value
                   4.0e-23
Match length
                   230
% identity
                   86
                  P.sativum mRNA for chloroplastic outer envelope membrane
NCBI Description
                  protein (OEP75)
Seq. No.
                   8168
                   11762 3.R1040
Contig. ID
5'-most EST
                   gsv701050073.h1
Seq. No.
                   8169
Contig ID
                   11762 5.R1040
                   jC-gm\overline{l}e01810088c07d1
5'-most EST
Method
                   BLASTN
                   q633606
NCBI GI
BLAST score
                   34
E value
                   1.0e-09
Match length
                   50
% identity
                  P.sativum mRNA for chloroplastic outer envelope membrane
NCBI Description
```

protein (OEP75)

Match length

% identity

133 89

```
8170
Seq. No.
                   11763 1.R1040
Contig ID
                   pmv700888903.h1
5'-most EST
                   BLASTX
Method
                   q3096931
NCBI GI
BLAST score
                   301
E value
                   4.0e-27
Match length
                   78
% identity
                   (AL023094) putative ribosomal protein S16 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   8171
                   11768 1.R1040
Contig ID
                   zzp700834271.h1
5'-most EST
                   8172
Seq. No.
                   11774_1.R1040
Contig ID
5'-most EST
                   LIB30\overline{4}0-046-Q1-E1-B12
                   8173
Seq. No.
                   11785 1.R1040
Contig ID
                   LIB3040-045-Q1-E1-G8
5'-most EST
Seq. No.
                   8174
                   11788 1.R1040
Contig ID
5'-most EST
                   LIB3040-045-Q1-E1-H12
Method
                   BLASTN
                   g2244788
NCBI GI
BLAST score
                   56
E value
                   1.0e-22
Match length
                   197
                   88
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   8175
                   11788 2.R1040
Contig ID
5'-most EST
                   LIB3040-016-Q1-E1-G12
Method
                   BLASTN
NCBI GI
                   g2244788
BLAST score
                   60
E value
                   4.0e-25
Match length
                   197
                   89
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   8176
                   11788 3.R1040
Contig ID
5'-most EST
                   zsg701127979.h1
Method
                   BLASTN
NCBI GI
                   g2244788
BLAST score
                   47
E value
                   2.0e-17
```

% identity

NCBI Description

```
Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   8177
Seq. No.
Contig ID
                   11796 1.R1040
5'-most EST
                   LIB3170-031-Q1-K1-H3
                   BLASTN
Method
                   g3241927
NCBI GI
BLAST score
                   62
                   8.0e-26
E value
Match length
                   338
% identity
                   84
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MTE17, complete sequence [Arabidopsis thaliana]
                   8178
Seq. No.
                   11796_2.R1040
Contig ID
5'-most EST
                   kmv70\overline{0}740305.h1
Method
                   BLASTN
NCBI GI
                   g3241927
BLAST score
                   37
                   4.0e-11
E value
Match length
                   138
% identity
                   86
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MTE17, complete sequence [Arabidopsis thaliana]
                   8179
Seq. No.
                   11796 3.R1040
Contig ID
5'-most EST
                   LIB3093-003-Q1-K1-F4
Method
                   BLASTN
NCBI GI
                   g3241927
BLAST score
                   33
E value
                   1.0e-08
                   150
Match length
                   85
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   8180
                   11796 5.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-115-Q1-K1-G5
                   8181
Seq. No.
Contig ID
                   11796 6.R1040
5'-most EST
                   asn70\overline{1}142715.h1
                   8182
Seq. No.
                   11803 1.R1040
Contig ID
5'-most EST
                   LIB3074-033-Q1-K1-H3
Method
                   BLASTN
NCBI GI
                   g343492
BLAST score
                   107
                   3.0e-53
E value
Match length
                   188
                   94
```

Tobacco Leu-tRNA and Phe-tRNA genes

Seq. No.

8191

```
Seq. No.
                   8183
                   11805 1.R1040
Contig ID
                 LIB3106-043-Q1-K1-G7
5'-most EST
                   8184
Seq. No.
Contig ID
                  11807_1.R1040
                  LIB3040-045-Q1-E1-F6
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1370179
BLAST score
                   415
                   0.0e + 00
E value
Match length
                  591
                   93
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB5B
                   8185
Seq. No.
                   11807 2.R1040
Contig ID
5'-most EST
                   uC-gmronoir038c03b1
Method
                  BLASTX
NCBI GI
                   g4559380
BLAST score
                   315
                   3.0e-29
E value
                  89
Match length
% identity
                   62
                   (AC006526) putative auxin-responsive GH3 protein
NCBI Description
                   [Arabidopsis thaliana]
                   8186
Seq. No.
                   11812 1.R1040
Contig ID
5'-most EST
                  LIB3040-045-Q1-E1-C2
Method
                  BLASTX
                   g3249105
NCBI GI
BLAST score
                   424
E value
                   3.0e-41
Match length
                  188
% identity
                   53
                   (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                   8187
                   11812 2.R1040
Contig ID
5'-most EST
                  LIB3109-017-Q1-K1-H8
                   8188
Seq. No.
                   11818 1.R1040
Contig ID
5'-most EST
                  LIB3106-097-Q1-K1-E8
                   8189
Seq. No.
                   11818 2.R1040
Contig ID
5'-most EST
                  kl1701214013.h1
                  8190
Seq. No.
                  11819 1.R1040
Contig ID
                  LIB3094-077-Q1-K1-D2
5'-most EST
```

Seq. No.

8197 .

```
Contig ID
                  11821 1.R1040
5'-most EST
                  LIB3040-045-Q1-E1-D11
Method
                  BLASTN
NCBI GI
                  q470126
BLAST score
                  36
E value
                  1.0e-10
Match length
                  121
                  91
% identity
                  N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19
NCBI Description
Seq. No.
                  8192
Contig ID
                  11823 1.R1040
5'-most EST
                  LIB3170-068-Q1-J1-B9
Seq. No.
                  8193
Contig ID
                  11837 1.R1040
5'-most EST
                  kmv700742945.h1
Method
                  BLASTX
NCBI GI
                  g3915196
BLAST score
                  227
E value
                  2.0e-23
Match length
                  113
% identity
                  51
                  UBIQUITIN-CONJUGATING ENZYME E2-C (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 1493838 (U52949)
                  cyclin-specific ubiquitin carrier protein E2-C [Spisula
                  solidissima]
Seq. No.
                  8194
Contig ID
                  11847 1.R1040
                  LIB3107-062-Q1-K1-G9
5'-most EST
Method
                  BLASTN
NCBI GI
                  g11957
BLAST score
                  80
E value
                  9.0e-37
Match length
                  120
                  92
% identity
NCBI Description Rice complete chloroplast genome
Seq. No.
                  8195
                  11850 1.R1040
Contig ID
5'-most EST
                  LIB3040-044-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                  g4115916
BLAST score
                  191
E value
                  2.0e-14
Match length
                  84
% identity
                  (AF118222) F3H7.9 gene product [Arabidopsis thaliana]
NCBI Description
                  >gi 4539441 emb CAB40029.1 (AL049523) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  8196
Contig ID
                  11854 1.R1040
5'-most EST
                  jC-gmro02910016f04d1
```

Method

BLASTX

```
Contig ID
                   11858 1.R1040
5'-most EST
                   LIB30\overline{5}1-025-Q1-K1-D2
                   8198
Seq. No.
                   11861 1.R1040
Contig ID
                   trc700564152.h1
5'-most EST
Method
                   BLASTX
                   g1173257
NCBI GI
BLAST score
                   1195
E value
                   1.0e-131
                   264
Match length
                   86
% identity
                   40S RIBOSOMAL PROTEIN S4 >gi_1076674_pir_S47642 ribosomal
NCBI Description
                   protein S4 - potato >gi 457803 emb CAA54095 (X76651)
                   ribosomal protein S4 [Solanum tuberosum]
                   8199
Seq. No.
                   11868 1.R1040
Contig ID
5'-most EST
                   leu70\overline{1}151162.h1
Method
                   BLASTX
NCBI GI
                   g2407800
                   570
BLAST score
E value
                   9.0e-59
Match length
                   128
                   90
% identity
                   (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
                   8200
Seq. No.
                   11868 2.R1040
Contig ID
5'-most EST
                   zsg701117481.h1
Method
                   BLASTX
NCBI GI
                   g2407800
BLAST score
                   440
E value
                   9.0e-44
Match length
                   114
                   78
% identity
                   (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
                   8201
Seq. No.
                   11868 3.R1040
Contig ID
5'-most EST
                   LIB3040-044-Q1-E1-G2
Method
                   BLASTX
NCBI GI
                   g2407800
BLAST score
                   310
E value
                   2.0e-28
                   97
Match length
% identity
                   (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11869 1.R1040
Contig ID
5'-most EST
                   LIB3040-044-Q1-E1-G4
                   8203
Seq. No.
                   11871 1.R1040
Contig ID
5'-most EST
                   LIB3040-044-Q1-E1-G7
```

```
NCBI GI
                   g2243118
BLAST score
                   550
E value
                   2.0e-56
                   207
Match length
                   55
% identity
NCBI Description
                   (Y10984) glutathione synthetase [Brassica juncea]
                   8204
Seq. No.
                   11871 2.R1040
Contig ID
5'-most EST
                   LIB3109-029-Q1-K1-D1
                   BLASTX
Method
NCBI GI
                   g2243118
BLAST score
                   133
                   2.0e-13
E value
                   129
Match length
% identity
                   40
                   (Y10984) glutathione synthetase [Brassica juncea]
NCBI Description
                   8205
Seq. No.
                   11875 1.R1040
Contig ID
5'-most EST
                   LIB3040-044-Q1-E1-D12
                   8206
Seq. No.
                   11885 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810086e10d1
                   BLASTX
Method
NCBI GI
                   g2924258
BLAST score
                   2995
E value
                   0.0e + 00
Match length
                   751
                   79
% identity
                   (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]
NCBI Description
Seq. No.
                   8207
Contig ID
                   11895 1.R1040
5'-most EST
                   LIB3106-105-Q1-K1-H3
Method
                   BLASTX
NCBI GI
                   g2342735
BLAST score
                   480
E value
                   5.0e-48
Match length
                   124
% identity
                   80
                   (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                   8208
Seq. No.
                   11900 1.R1040
Contig ID
5'-most EST
                   dpv701099491.h1
Method
                   BLASTX
NCBI GI
                   g4566614
BLAST score
                   564
E value
                   1.0e-57
Match length
                   130
% identity
                   82
                   (AF112887) actin depolymerizing factor [Populus alba x
NCBI Description
```

Populus tremula]

```
11910 1.R1040
Contig ID
5'-most EST
                   LIB3107-010-Q1-K1-E6
Method
                   BLASTX
NCBI GI
                   g400983
BLAST score
                   640
E value
                   1.0e-66
Match length
                   215
% identity
                   63
                   50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11)
NCBI Description
                   >gi 279648 pir R5SP11 ribosomal protein L11 precursor -
                   spinach >gi 21313 emb CAA39950 (X56615) ribosomal protein
                   Ll1 [Spinacia oleracea]
                   8210
Seq. No.
                   11925 1.R1040
Contig ID
5'-most EST
                   vzy70\overline{0}756050.h1
Seq. No.
                   8211
                   11926 1.R1040
Contig ID
5'-most EST
                   LIB3040-043-Q1-E1-F9
Seq. No.
                   8212
                   11928 1.R1040
Contig ID
5'-most EST
                   qsv70\overline{1}052309.h1
Seq. No.
                   8213
                   11930 1.R1040
Contig ID
5'-most EST
                   LIB3040-043-Q1-E1-G2
Method
                   BLASTX
NCBI GI
                   g2088651
BLAST score
                   237
E value
                   2.0e-26
Match length
                   155
% identity
NCBI Description
                    (AF002109) hypersensitivity-related gene 201 isolog
                   [Arabidopsis thaliana]
Seq. No.
                   8214
                   11933 1.R1040
Contig ID
5'-most EST
                   LIB3040-017-Q1-E1-H7
Method
                   BLASTX
NCBI GI
                   g3874563
BLAST score
                   247
E value
                   5.0e-21
Match length
                   87
% identity
NCBI Description
                   (281042) similar to Yeast hypothetical protein YEY6 like;
                   cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5
                   comes from this gene; cDNA EST yk303h1.3 comes from this
                   gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...
                   >gi 3924825 emb CAB05549 (Z83113) similar to Yeast
                   hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes
                   from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5
                   comes from this gene; cDNA
```

Seq. No. 8215

```
11937 1.R1040
Contig ID
                   taw700654539.hl
5'-most EST
Method
                   BLASTX
                   g4337206
NCBI GI
BLAST score.
                   345
E value
                   2.0e-32
Match length
                   111
% identity
                   61
                   (AC006403) putative replication factor-A protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   11938 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400062f11d1
                   8217
Seq. No.
Contig ID
                   11940_1.R1040
5'-most EST
                   gsv701045940.hl
Method
                   BLASTX
NCBI GI
                   g1173074
BLAST score
                   179
                   9.0e-13
E value
Match length
                   111
                   37
% identity
                   60S ACIDIC RIBOSOMAL PROTEIN P2 (ALLERGEN CLA H 3) (CLA H
NCBI Description
                   III) >gi 1086177 pir S41866 ribosomal P2 protein -
                   Cladosporium herberum >gi 452606 emb CAA54470 (X77253)
                   ribosomal P2 protein [Cladosporium herbarum]
                   8218
Seq. No.
Contig ID
                   11952 1.R1040
5'-most EST
                   LIB3072-012-Q1-E1-C7
                   8219
Seq. No.
                   11955 1.R1040
Contig ID
5'-most EST
                   sat701011736.hl
Method
                   BLASTX
NCBI GI
                   q2398521
BLAST score
                   218
E value
                   3.0e-22
Match length
                   219
                   42
% identity
                   (Y13720) transcription factor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8220
                   11955 2.R1040
Contig ID
5'-most EST
                   LIB3040-043-Q1-E1-B11
                   8221
Seq. No.
                   11959 1.R1040
Contig ID
5'-most EST
                   rlr700900885.h1
                   BLASTX
Method
NCBI GI
                   g4115735
BLAST score
                   257
E value
                   5.0e-22
Match length
                   131
```

42

% identity

```
NCBI Description
                   (AB017627) acetyltransferase [Candida albicans]
                   8222
Seq. No.
                   11960 1.R1040
Contig ID
5'-most EST
                   LIB3040-043-Q1-E1-C10
Method
                   BLASTX
NCBI GI
                   g728827
                   202
BLAST score
                   9.0e-16
E value
Match length
                   90
                   50
% identity
NCBI Description
                  ALLANTOINASE PRECURSOR >gi 458126 (U03471) allantoinase
                   [Rana catesbeiana]
                   8223
Seq. No.
                   11963 1.R1040
Contig ID
5'-most EST
                   LIB3040-043-Q1-E1-C4
Method
                   BLASTX
NCBI GI
                   g1001630
                   330
BLAST score
                   2.0e-30
E value
                   95
Match length
% identity
                   62
NCBI Description
                   (D64002) hypothetical protein [Synechocystis sp.]
                   8224
Seq. No.
                   11968 1.R1040
Contig ID
5'-most EST
                   fua701039084.h1
Method
                   BLASTX
NCBI GI
                   g3367591
BLAST score
                   434
E value
                   6.0e-43
Match length
                  104
% identity
                   83
NCBI Description
                  (AL031135) putative protein [Arabidopsis thaliana]
Seq. No.
                   8225
                   11969 1.R1040
Contig ID
5'-most EST
                   pmv700894162.h1
                  BLASTX
Method
NCBI GI
                   g3292849
BLAST score
                   549
E value
                   3.0e-56
Match length
                  141
% identity
                   80
NCBI Description
                   (AJ007582) arginine methyltransferase [Arabidopsis
                  thaliana]
                   8226
Seq. No.
                  11971 1.R1040
Contig ID
5'-most EST
                  LIB3040-001-Q1-E1-H10
Method
                  BLASTX
NCBI GI
                  g730922
BLAST score
                  1445
                   0.0e + 00
E value
Match length
                  517
% identity
                   64
```

```
.....
NCBI Description T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)
                   (TCP20) (HTR3) >gi_627402_pir__S48087 chaperonin TCP20 -
                   human >gi_517065 (L27706) chaperonin-like protein [Homo
                   sapiens] >gi_4502643_ref_NP_001753.1_pCCT6_ chaperonin
                   containing T-complex subunit
Seq. No.
                   8227
Contig ID
                   11975 1.R1040
                   zhf700957834.hl
5'-most EST
                   8228
Seq. No.
                   11978 1.R1040
Contig ID
                  LIB3139-009-P1-N1-C11
5'-most EST
                   8229
Seq. No.
                   11983 1.R1040
Contig ID
5'-most EST
                  LIB3170-015-Q1-K1-A9
                   8230
Seq. No.
                   11985 1.R1040
Contig ID
5'-most EST
                  LIB3040-043-Q1-E1-A7
                   8231
Seq. No.
                   11992 1.R1040
Contig ID
                   zpv700759655.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3513744
BLAST score
                   332
E value
                   7.0e-31
                   143
Match length
                   33
% identity
NCBI Description
                   (AF080118) contains similarity to Medicago truncatula MtN3
                   (GB:Y08726) [Arabidopsis thaliana]
Seq. No.
                   8232
                   11993 1.R1040
Contiq ID
5'-most EST
                  LIB3040-042-Q1-E1-F12
                   8233
Seq. No.
Contig ID
                   11998 1.R1040
5'-most EST
                   LIB30\overline{4}0-042-Q1-E1-F9
Method
                   BLASTX
NCBI GI
                   g4102839
BLAST score
                   303
E value
                   1.0e-27
Match length
                  88
% identity
                   64
NCBI Description
                   (AF016713) LeOPT1 [Lycopersicon esculentum]
```

Contig ID 12008_1.R1040

5'-most EST LIB3040-042-Q1-E1-B6

Method BLASTX
NCBI GI g2736149
BLAST score 151
E value 1.0e-09
Match length 116

% identity NCBI Description (AF022108) putative replication initiator origin recognition complex subunit Orc4Lp [Homo sapiens] >gi_2906226 (AF047598) origin recognition complex subunit 4; Orc4p [Homo sapiens] >gi_4530597_gb_AAD22110.1 (AF132596) origin recognition complex subunit 4 [Homo sapiens] >gi_4505523_ref_NP_002543.1_pORC4L_ origin recognition complex, subunit 4 (yeast homolog)-like Seq. No. 8235 Contig ID 12011 1.R1040 seb700648931.h1 5'-most EST BLASTX Method NCBI GI g3335336 BLAST score 165 E value 4.0e-11 Match length 63 % identity (AC004512) Contains similarity to DnaJ gene YM8520.10 NCBI Description gb 825566 from from S. cerevisiae cosmid gb Z49705. ESTs gb Z47720 and gb Z29879 come from this gene. [Arabidopsis thaliana] 8236 Seq. No. 12018 1.R1040 Contig ID $zhf70\overline{0}954547.h1$ 5'-most EST BLASTX Method NCBI GI g1172556 BLAST score 315 7.0e-29 E value Match length 111 52 % identity 36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN NCBI Description (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir__B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin II [Solanum tuberosum] 8237 Seq. No. 12018 2.R1040 Contig ID 5'-most EST gsv701052324.hl Method BLASTX NCBI GI g1172556 BLAST score 142 E value 4.0e-09 Match length 48 % identity 36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN NCBI Description (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)

(POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir_B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin

II [Solanum tuberosum]

Seq. No. 8238

12028 1.R1040 Contig ID

```
5'-most EST
                   LIB3040-041-Q1-E1-H9
Method ·
                   BLASTX
                   g1076414
NCBI GI
BLAST score
                   641
E value
                   5.0e-67
Match length
                   195
                   64
% identity
NCBI Description
                   subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis
                   thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974)
                   subtilisin-like protease [Arabidopsis thaliana]
                   8239
Seq. No.
Contig ID
                   12029 1.R1040
                   gsv70\overline{1}046386.h1
5'-most EST
Seq. No.
                   8240
Contig ID
                   12031 1.R1040
5'-most EST
                   uC-gmflminsoy075g06b1
Method
                   BLASTX
NCBI GI
                   g2921873
BLAST score
                   677
E value
                   5.0e-71
Match length
                   245
                   52
% identity
NCBI Description
                   (AF047472) spleen mitotic checkpoint BUB3 [Homo sapiens]
                   >gi_2981231_gb_AAC06258_ (AF053304) mitotic checkpoint
                   component Bub3 [Homo sapiens] >gi 3639060 (AF081496)
                   kinetochore protein BUB3 [Homo sapiens]
                   8241
Seq. No.
Contig ID
                   12038 1.R1040
5'-most EST
                   leu70\overline{1}153034.h1
Method
                   BLASTX
                   g4388731
NCBI GI
BLAST score
                   283
E value
                   2.0e-25
Match length
                   94
% identity
NCBI Description
                   (AC006413) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   8242
Contig ID
                   12041 1.R1040
5'-most EST
                   LIB3170-009-Q2-K1-H4
                   8243
Seq. No.
                   12049 1.R1040
Contig ID
5'-most EST
                   LIB3040-016-Q1-E1-H2
Seq. No.
                   8244
                   12049 2.R1040
Contig ID
5'-most EST
                   LIB3040-041-Q1-E1-G10
Seq. No.
                   8245
Contig ID
                   12063 1.R1040
5'-most EST
                  LIB3040-041-Q1-E1-D7
Seq. No.
                   8246
```

E value

```
12076_1.R1040
Contig ID
5'-most EST
                   LIB3170-012-Q1-K1-H6
                   8247
Seq. No.
                   12080_1.R1040
Contig ID
5'-most EST
                   LIB3051-029-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   g4544434
BLAST score
                   518
E value
                   2.0e-52
Match length
                   142
% identity
                   73
NCBI Description
                   (AC006955) putative DNA-directed RNA polymerase II
                   [Arabidopsis thaliana]
Seq. No.
                   8248
Contig ID
                   12083 1.R1040
5'-most EST
                   LIB3092-062-Q1-K1-C9
                   BLASTN
Method
NCBI GI
                   g4558521
BLAST score
                   44
E value
                   3.0e-15
Match length
                   152
                   82
% identity
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC T10024,
                   complete sequence
                   8249
Seq. No.
                   12088 1.R1040
Contig ID
5'-most EST
                   hrw701059278.hl
Seq. No.
                   8250
                   12096 1.R1040
Contig ID
5'-most EST
                   LIB3040-040-Q1-E1-H8
Seq. No.
                   8251
Contig ID
                   12106 1.R1040
5'-most EST
                   LIB3072-056-Q1-K1-E11
Method
                   BLASTX
NCBI GI
                   q4335723
BLAST score
                   273
E value
                   4.0e-24
Match length
                   79
% identity
NCBI Description
                   (AC006248) putative thioredoxin M [Arabidopsis thaliana]
Seq. No.
                   8252
                   12115 1.R1040
Contig ID
5'-most EST
                   LIB3170-009-Q2-K1-G10
                   8253
Seq. No.
                   12121 1.R1040
Contig ID
                   seb700651777.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4115377
BLAST score
                   613
```

1.0e-63

```
174
Match length
% identity
                   70
NCBI Description
                   (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                   8254
                   12121 2.R1040
Contig ID
5'-most EST
                   k1170\overline{1}202752.h1
Method ·
                   BLASTX
NCBI GI
                   q4115377
BLAST score
                   221
E value
                   3.0e-18
Match length
                   55
% identity
NCBI Description
                   (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   12131 1.R1040
5'-most EST
                   uC-gmflminsoy075g05b1
Method
                   BLASTX
NCBI GI
                   q3004550
BLAST score
                   175
E value
                   8.0e-14
Match length
                   86
% identity
NCBI Description
                   (AC003673) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   8256
Contig ID
                   12134 1.R1040
5'-most EST
                   LIB3040-040-Q1-E1-E5
Method
                   BLASTX
NCBI GI
                   g3176668
BLAST score
                   809
E value
                   2.0e-86
Match length
                   214
% identity
                   86
NCBI Description
                   (AC004393) Similar to ribosomal protein L17 gb X62724 from
                   Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and
                   gb Z33937 come from this gene. [Arabidopsis thaliana]
Seq. No:
                   12136 1.R1040
Contig ID
                   LIB3170-010-Q1-J1-G9
5'-most EST
Seq. No.
Contig ID
                   12141 1.R1040
                   LIB30\overline{4}0-040-Q1-E1-B4
5'-most EST
                   8259
Seq. No.
                   12143 1.R1040
Contig ID
5'-most EST
                   LIB3049-012-Q1-E1-A7
Method
                   BLASTX
NCBI GI
                   g3510255
BLAST score
                   251
E value
                   4.0e-21
Match length
                   70
% identity
```

NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]

```
8260
Seq. No.
                   12148 1.R1040
Contig ID
                   leu701145636.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4567246
BLAST score
                   629
                   2.0e-65
E value
                   180
Match length
% identity
                   70
                   (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                   8261
Seq. No.
                   12149 1.R1040
Contig ID
5'-most EST
                   zzp700833747.h1
Method
                   BLASTX
NCBI GI
                   g217909
BLAST score
                   895
E value
                   1.0e-96
                   203
Match length
% identity
                   87
NCBI Description
                   (D14044) glycolate oxidase [Cucurbita sp.]
                   8262
Seq. No.
                   12149 2.R1040
Contig ID
                   jex700905933.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g217909
BLAST score
                   267
                   1.0e-23
E value
Match length
                   64
% identity
                   81
                   (D14044) glycolate oxidase [Cucurbita sp.]
NCBI Description
                   8263
Seq. No.
                   12151 1.R1040
Contig ID
5'-most EST
                   LIB3040-040-Q1-E1-B1.
                   8264
Seq. No.
                   12165 1.R1040
Contig ID
5'-most EST
                   LIB3139-059-P1-N1-E9
                   8265
Seq. No.
                   12165 2.R1040
Contig ID
5'-most EST
                   LIB31\overline{0}6-026-Q1-K1-E7
                   8266
Seq. No.
Contig ID
                   12169 1.R1040
5'-most EST
                   LIB3040-040-Q1-E1-A9
Method
                   BLASTX
                   q3242729
NCBI GI
                   907
BLAST score
E value
                   3.0e-98
Match length
                   173
% identity
                   (AC003040) curly leaf protein (polycomb-group) [Arabidopsis
NCBI Description
```

thaliana]

5'-most EST

```
8267
Seq. No.
                  12171_1.R1040
Contig ID
5'-most EST
                  LIB3138-083-P1-N1-C10
Method
                  BLASTX
                  g4455361
NCBI GI
BLAST score
                  368
E value
                  3.0e-60
Match length
                  185
% identity
                  61
NCBI Description
                   (AL035524) putative protein [Arabidopsis thaliana]
                  8268
Seq. No.
                  12175 1.R1040
Contig ID
5'-most EST
                  LIB3040-039-Q1-E1-F7
Method
                  BLASTN
NCBI GI
                  q166409
BLAST score
                  126
E value
                  3.0e-64
Match length
                  292
% identity
                  90
NCBI Description
                  Alfalfa nucleic acid binding protein (alfin-1) mRNA,
                  partial cds
                  8269
Seq. No.
                  12181 1.R1040
Contig ID
                  LIB3093-034-Q1-K1-D3
5'-most EST
                  BLASTX
Method
                  g1173027
NCBI GI
BLAST score
                  442
E value
                  1.0e-43
Match length
                  120
                  73
% identity
                  60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
NCBI Description
                  protein L31 [Nicotiana glutinosa]
Seq. No.
                  8270
                  12184 1.R1040
Contig ID
                  LIB3040-039-Q1-E1-G7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2144183
BLAST score
                  354
                  3.0e-33
E value
Match length
                  103
% identity
NCBI Description
                  DNA-directed RNA polymerase (EC 2.7.7.6) chain III -
                  Ecotype Columbia >gi_1184686 (U35049) RNA polymerase I(A)
                  and III(C) 14 kDa subunit [Arabidopsis thaliana]
                  >gi 1184688 (U35050) Arabidopsis thaliana RNA polymerase
                  I(A) and III(C) 14 kDa subunit [Arabidopsis thaliana]
                  >gi_3980382 (AC004561) RNA polymerase I(A) and III(C) 14
                  kDa subunit (AtRPAC14) [Arabidopsis thaliana]
Seq. No.
                  12192 1.R1040
Contig ID
```

LIB3170-054-Q1-K1-C2

Method

BLASTX

```
8272
Seq. No.
                   12192 2.R1040
Contig ID
5'-most EST
                   LIB3049-049-Q1-E1-G4
                   8273
Seq. No.
                   12200 1.R1040
Contig ID
5'-most EST
                   LIB3050-024-Q1-K1-E9
Seq. No.
                   8274
                   12200 2.R1040
Contig ID
5'-most EST
                   rca70\overline{1000961.h1}
                   BLASTX
Method
NCBI GI
                   a3242709
BLAST score
                   306
E value
                   1.0e-53
Match length
                   254
                   48
% identity
                   (AC003040) putative guanine nucleotide-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   8275
Seq. No.
                   12202 1.R1040
Contig ID
5'-most EST
                   leu701148856.h1
                   8276
Seq. No.
Contig ID
                   12207 1.R1040
5'-most EST
                   kmv70\overline{0}741774.h1
                   BLASTX
Method
NCBI GI
                   q3041738
BLAST score
                   512
E value
                   6.0e-52
Match length
                   140
% identity
                   69
NCBI Description
                   T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
                   (HIV-1 NEF INTERACTING PROTEIN) >gi_2559010 (AF026292)
                   chaperonin containing t-complex polypeptide 1, eta subunit;
                   CCT-eta [Homo sapiens]
Seq. No.
                   8277
Contig ID
                   12217 1.R1040
5'-most EST
                   trc700567909.hl
Method
                   BLASTX
NCBI GI
                   q4539403
BLAST score
                   360
E value
                   4.0e-34
Match length
                   144
% identity
                   51
NCBI Description
                   (AL049524) putative protein [Arabidopsis thaliana]
Seq. No.
                   12222 1.R1040
Contig ID
                   LIB3051-027-Q1-K1-E7
5'-most EST
                   8279
Seq. No.
                   12231 1.R1040
Contig ID
5'-most EST
                   jex70\overline{0}907994.h1
```

NCBI Description

```
NCBI GI
                   g3212871
                   474
BLAST score
                   3.0e-89
E value
Match length
                   186
                   87
% identity
                   (AC004005) putative translation initiation factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   8280
                   12231 2.R1040
Contig ID
5'-most EST
                   LIB3040-038-Q1-E1-H8
Method
                   BLASTX
                   q3212871
NCBI GI
BLAST score
                   264
E value
                   6.0e-23
                   55
Match length
% identity
                   85
NCBI Description
                   (AC004005) putative translation initiation factor
                   [Arabidopsis thaliana]
Seq. No.
                   8281
                   12231 3.R1040
Contig ID
5'-most EST
                   dpv70\overline{1}097109.h1
                   BLASTX
Method
                   g3212871
NCBI GI
BLAST score
                   249
E value
                   3.0e-21
Match length
                   53
                   85
% identity
NCBI Description
                   (AC004005) putative translation initiation factor
                   [Arabidopsis thaliana]
                   8282
Seq. No.
Contig ID
                   12232_1.R1040
5'-most EST
                   LIB30\overline{5}1-039-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   g2832645
BLAST score
                   164
E value
                   3.0e-11
                   55
Match length
                   73
% identity
NCBI Description
                   (AL021710) hypothetical protein [Arabidopsis thaliana]
                   8283
Seq. No.
                   12232 2.R1040
Contig ID
5'-most EST
                   LIB3106-039-Q1-K1-G7
Seq. No.
                   8284
Contig ID
                   12243 1.R1040
5'-most EST
                   LIB3170-010-Q1-K1-F12
                   BLASTX
Method
NCBI GI
                   q4454043
BLAST score
                   314
E value
                   4.0e-29
Match length
                   107
% identity
                   56
                   (AL035394) putative receptor kinase [Arabidopsis thaliana]
```

```
8285
Seq. No.
                  12244 1.R1040
Contig ID
                  uC-gmrominsoy097a11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2190419
BLAST score
                   480
                  5.0e-48
E value
                  150
Match length
                  58
% identity
NCBI Description
                   (Y13632) dem [Lycopersicon esculentum]
                  8286
Seq. No.
                  12255 1.R1040
Contig ID
5'-most EST
                  LIB3049-010-Q1-E1-D10
                  BLASTN
Method
                  g4159703
NCBI GI
BLAST score
                  57
E value
                  7.0e-23
Match length
                  325
                  85
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K5F14, complete sequence [Arabidopsis thaliana]
                  8287
Seq. No.
Contig ID
                  12255 2.R1040
5'-most EST
                  LIB3092-022-Q1-K1-C10
                  BLASTN
Method
                  g4159703
NCBI GI
BLAST score
                  57
                   6.0e-23
E value
Match length
                  151
                   90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K5F14, complete sequence [Arabidopsis thaliana]
Seq. No.
                  8288
Contig ID
                  12255 3.R1040
                  zhf700965132.h1
5'-most EST
Method
                  BLASTX
                  g2244797
NCBI GI
BLAST score
                  284
E value
                   4.0e-25
Match length .
                  84
                   65
% identity
NCBI Description
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
                  8289
Seq. No.
                  12255 4.R1040
Contig ID
5'-most EST
                  uC-gmropic006d07b1
Seq. No.
                  8290
Contig ID
                  12255 5.R1040
5'-most EST
                  jC-gmle01810068b06a1
Seq. No.
```

12255_6.R1040

Contig ID

5'-most EST Method

```
5'-most EST
                   jC-gmro02910002b01a1
                   8292
Seq. No.
Contig ID
                   12255 8.R1040
                   pxt70\overline{0}942169.h1
5'-most EST
                   8293
Seq. No.
                   12257 1.R1040
Contig ID
5'-most EST
                   LIB3170-009-Q2-K2-F7
                   8294
Seq. No.
                   12267 1.R1040
Contig ID
                   LIB3040-038-Q1-E1-D6
5'-most EST
                   8295
Seq. No.
                   12268 1.R1040
Contig ID
                   LIB3170-009-Q2-K1-F9
5'-most EST
                   8296
Seq. No.
Contig ID
                   12270 1.R1040
                   sat701012249.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g14162
BLAST score
                   41
E value
                   2.0e-13
Match length .
                   53
% identity
                   94
                   P.hybrida mitochondria genes rps19, Yrps3 and Yrpl16
NCBI Description
                   8297
Seq. No.
                   12271_1.R1040
Contig ID
5'-most EST
                   leu70\overline{1}147506.h1
                   BLASTX
Method
                   g169459
NCBI GI
BLAST score
                   239
E value
                   4.0e-20
Match length
                   93
% identity
                   49
                   (M18538) pop3 peptide [Populus balsamifera subsp.
NCBI Description
                   trichocarpa X Populus deltoides]
Seq. No.
                   8298
                   12274 1.R1040
Contig ID
5'-most EST
                   LIB3040-038-Q1-E1-A12
Method
                   BLASTX
NCBI GI
                   q4006872
BLAST score
                   301
E value
                   1.0e-27
Match length
                   65
% identity
NCBI Description
                   (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   8299
                   12277 1.R1040
Contig ID
```

LIB3072-021-Q1-E1-F5

BLASTX

NCBI Description

```
NCBI GI
                  q418507
                  342
BLAST score
                   6.0e-32
E value
Match length
                  156
% identity
                   46
                  S-ADENOSYLMETHIONINE: 2-DEMETHYLMENAQUINONE
NCBI Description
                  METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical
                  protein f161 - Escherichia coli >gi_305032 (L19201)
                  ORF f161 [Escherichia coli] >gi_1336002 (U56082)
                  S-adenosylmethionine: 2-demethylmenaquinone
                  methyltransferase [Escherichia coli] >gi_1790364 (AE000467)
                  menaquinone biosynthesis, unknown [Escherichia coli]
                  8300
Seq. No.
Contig ID
                  12277 2.R1040
                  LIB3138-064-Q1-N1-B10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q418507
BLAST score
                  165
                  2.0e-11
E value
                  53
Match length
% identity
                  58
NCBI Description
                  S-ADENOSYLMETHIONINE: 2-DEMETHYLMENAQUINONE
                  METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical
                  protein f161 - Escherichia coli >gi_305032 (L19201)
                  ORF_f161 [Escherichia coli] >gi_1336002 (U56082)
                  S-adenosylmethionine: 2-demethylmenaquinone
                  methyltransferase [Escherichia coli] >gi_1790364 (AE000467)
                  menaquinone biosynthesis, unknown [Escherichia coli]
Seq. No.
                  8301
                  12279 1.R1040
Contig ID
                  LIB3087-012-Q1-K1-E5
5'-most EST
Method
                  BLASTX
                  q2160182
NCBI GI
BLAST score
                  293
E value
                  4.0e-26
                  155
Match length
% identity
                   (AC000132) ESTs qb ATTS1236,qb T43334,qb N97019,qb AA395203
NCBI Description
                  come from this gene. [Arabidopsis thaliana]
                  8302
Seq. No.
                  12279 2.R1040
Contig ID
5'-most EST
                  LIB3107-057-Q1-K1-F1
Seq. No.
                  8303
Contig ID
                  12282 1.R1040
5'-most EST
                  LIB3074-011-Q1-E1-H7
Method
                  BLASTX
NCBI GI
                  q466160
BLAST score
                  372
E value
                  2.0e-35
Match length
                  83
% identity
```

HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771 pir_ S44903 ZK652.3 protein - Caenorhabditis

8309

```
elegans >g 289769 (L14429) putative [Caenorhabditis
                   elegansl
Seq. No.
                   8304
                   12282 2.R1040
Contig ID
                   LIB3049-025-Q1-E1-C1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g466160
BLAST score
                   372
E value
                   1.0e-35
Match length
                   83
% identity
                   86
                   HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
NCBI Description
                   >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis
                   elegans >gi 289769 (L14429) putative [Caenorhabditis
                   elegans]
Seq. No.
                   8305
Contig ID
                   12288 1.R1040
                   sat701013128.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1709798
BLAST score
                   1888
E value
                   0.0e + 00
Match length
                   388
% identity
                   96
NCBI Description
                   26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >qi 1155334
                   (U43398) POTATP1 [Solanum tuberosum]
Seq. No.
                   8306
                   12288 2.R1040
Contig ID
                   fua701042085.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1709798
BLAST score
                   453
E value
                   3.0e-45
Match length
                   102
                   90
% identity
                   26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >qi 1155334
NCBI Description
                   (U43398) POTATP1 [Solanum tuberosum]
                   8307
Seq. No.
                   12291_1.R1040
Contig ID
5'-most EST
                  LIB3040-037-Q1-E1-F8
Seq. No.
                   8308
                  12302 1.R1040
Contig ID
5'-most EST
                  leu701151648.h1
Method
                  BLASTX
NCBI GI
                  q1350548
BLAST score
                  350
E value
                  1.0e-32
Match length
                  115
                   57
% identity
NCBI Description
                  (L47609) heat shock-like protein [Picea glauca]
```

ر الماريخ . الماريخ .

BLAST score

```
12302_2.R1040
Contig ID
                   k1170\overline{1}204314.h2
5'-most EST
Method
                   BLASTX
                   g1350548
NCBI GI
BLAST score
                   334
                   8.0e-31
E value
                   108
Match length
                   57
% identity
NCBI Description
                    (L47609) heat shock-like protein [Picea glauca]
                   8310
Seq. No.
                   12302 3.R1040
Contig ID
                   LIB3170-029-Q1-K1-G12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1350548
BLAST score
                   281
                   4.0e-25
E value
                   85
Match length
% identity
                   60
NCBI Description
                    (L47609) heat shock-like protein [Picea glauca]
Seq. No.
                   8311
Contig ID
                   12302 4.R1040
5'-most EST
                   LIB3138-011-Q1-N2-B5
                   8312
Seq. No.
                   12302_5.R1040
Contig ID
                   LIB30\overline{9}3-001-Q1-K1-F10
5'-most EST
Method
                   BLASTX
                   g1350548
NCBI GI
BLAST score
                   277
E value
                   4.0e-25
                   93
Match length
% identity
                   59
NCBI Description
                   (L47609) heat shock-like protein [Picea glauca]
Seq. No.
                   8313
                   12305 1.R1040
Contiq ID
5'-most EST
                   LIB3040-037-Q1-E1-H5
                   8314
Seq. No.
Contig ID
                   12307 1.R1040
5'-most EST
                   epx70\overline{1}110127.h1
Method
                   BLASTX
NCBI GI
                   q3063450
BLAST score
                   204
E value
                   2.0e-23
Match length
                   108
% identity
                   62
NCBI Description
                   (AC003981) F22013.12 [Arabidopsis thaliana]
Seq. No.
                   8315
                   12310 1.R1040
Contig ID
                   gsv701045922.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g758643
```

```
1.0e-162
E value
Match length
                   487
% identity
                   90
                  P.sativum mRNA for nucleoside diphosphate kinase II
NCBI Description
Seq. No.
                   12320 1.R1040
Contig ID
5'-most EST
                   txt700733277.h1
Method
                   BLASTN
NCBI GI
                   g2921322
BLAST score
                   191
E value
                   1.0e-103
Match length
                  199
% identity
                   99
NCBI Description Glycine max beta-1,3-glucanase 7 (SGlu7) gene, partial cds
                  8317
Seq. No.
                   12335 1.R1040
Contig ID
5'-most EST
                   LIB3040-037-Q1-E1-C4
Seq. No.
                   8318
Contig ID
                   12336 1.R1040
5'-most EST
                  LIB3040-037-Q1-E1-A4
Seq. No.
                   8319
                   12337 1.R1040
Contig ID
5'-most EST
                   epx701107811.h1
Method
                  BLASTX
NCBI GI
                   g3810835
BLAST score
                   219
E value
                   2.0e-17
Match length
                   132
% identity
                   40
NCBI Description
                   (AL032684) putative RNA-binding protein
                   [Schizosaccharomyces pombe]
Seq. No.
                   8320
                   12337 2.R1040
Contig ID
                  sat701011382.hl
5'-most EST
Seq. No.
                   8321
                   12341 1.R1040
Contig ID
5'-most EST
                  LIB3040-036-Q1-E1-G8
                  8322
Seq. No.
                  12343 1.R1040
Contig ID
5'-most EST
                  LIB3040-017-Q1-E1-A5
                  8323
Seq. No.
                  12351 1.R1040
Contig ID
5'-most EST
                  uxk700670327.hl
Method
                  BLASTN
                  g2924257
NCBI GI
BLAST score
                  368
E value
                  0.0e+00
Match length
                  866
```

7-1

88

% identity

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 8324

Contig ID 12351 2.R1040

5'-most EST LIB3107-017-Q1-K1-B8

Method BLASTN
NCBI GI g12283
BLAST score 402
E value 0.0e+00
Match length 900
% identity 90

NCBI Description Spinach plastid psbB operon with genes for 10 kD

phosphoprotein associated with photosystem II (psbH), apocytochrome b6 and subunit 4 (petD) of cytochrome b6f

complex

Seq. No. 8325

Contig ID 12351_3.R1040 5'-most EST rca700998107.h1

Method BLASTN
NCBI GI g2924257
BLAST score 241
E value 1.0e-132
Match length 964

% identity 89

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 8326

Contig ID 12351 4.R1040

5'-most EST LIB3170-040-Q1-J1-D4

Method BLASTN
NCBI GI g2143322
BLAST score 157
E value 1.0e-82
Match length 305

% identity 91

NCBI Description P.deltoides chloroplast DNA for psbB operon

Seq. No. 8327

Contig ID 12351_6.R1040 5'-most EST rlr700898879.h1

Method BLASTN
NCBI GI g12150
BLAST score 163
E value 2.0e-86
Match length 223
% identity 93

NCBI Description Pea chloroplast gene for 15.2 kDA polypeptide from

cytochrome b-f complex

Seq. No. 8328

Contig ID 12352 1.R1040

5'-most EST LIB3040-036-Q1-E1-H9

Seq. No. 8329

Contig ID 12353_1.R1040 5'-most EST ncj700982094.h1

Method

NCBI GI

BLASTX

q4093155

```
Seq. No.
                   8330
Contig ID
                   12353 2.R1040
5'-most EST
                   hrw701061763.hl
Seq. No.
                   12354 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy042d02b1
Method
                   BLASTX
NCBI GI
                   q4539352
BLAST score
                   200
E value
                   2.0e-16
Match length
                   156
% identity
                   37
NCBI Description
                   (AL035539) putative protein [Arabidopsis thaliana]
                   8332
Seq. No.
Contig ID
                   12354 2.R1040
5'-most EST
                   LIB3051-038-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   q4539352
BLAST score
                   626
E value
                   4.0e-65
Match length
                   240
% identity
                   53
NCBI Description
                   (AL035539) putative protein [Arabidopsis thaliana]
                   8333
Seq. No.
Contig ID
                   12356 1.R1040
5'-most EST
                   LIB3170-009-Q2-K1-E12
Method
                   BLASTX
NCBI GI
                   q4220462
BLAST score
                   601
E value
                   1.0e-62
Match length
                   127
% identity
NCBI Description
                   (AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8)
                   gene from Arabidopsis thaliana containing Homeobox PF 00046
                   and bZIP PF_00170 domains. [Arabidopsis thaliana]
Seq. No.
                   8334
Contig ID
                   12357 1.R1040
5'-most EST
                   LIB3107-076-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g4093155
BLAST score
                   575
E value
                   5.0e-59
Match length
                   196
% identity
NCBI Description
                   (AF088281) phytochrome-associated protein 1 [Arabidopsis
                   thaliana]
                   8335
Seq. No.
                   12357 3.R1040
Contig ID
                   zhf700953009.h1
5'-most EST
```

% identity

```
BLAST score
                   166
                   1.0e-11
E value
Match length
                   48
% identity
                   69
                    (AF088281) phytochrome-associated protein 1 [Arabidopsis
NCBI Description
                   thaliana]
                   8336
Seq. No.
Contig ID
                   12360 1.R1040
5'-most EST
                   LIB30\overline{4}0-036-Q1-E1-E7
Method
                   BLASTX
NCBI GI
                   g3281868
BLAST score
                   532
E value
                   3.0e-54
Match length
                   133
% identity
NCBI Description
                   (AL031004) putative protein [Arabidopsis thaliana]
                   8337
Seq. No.
Contig ID
                   12365 1.R1040
5'-most EST
                   zzp70\overline{0}835138.h1
Method
                   BLASTX
NCBI GI
                   q2582971
BLAST score
                   218
E value
                   4.0e-18
Match length
                   76
                   59
% identity
NCBI Description
                   (D83711) TKRP125 [Nicotiana tabacum]
Seq. No.
                   8338
Contig ID
                   12375 1.R1040
5'-most EST
                   jC-gm\overline{f}102220106e09a1
Seq. No.
Contig ID
                   12380 1.R1040
5'-most EST
                   taw700660389.h1
                   8340
Seq. No.
Contig ID
                   12383 1.R1040
5'-most EST
                   LIB3107-016-01-K1-A2
Method
                   BLASTX
NCBI GI
                   g2983600
BLAST score
                   1036
E value
                   1.0e-113
Match length
                   399
% identity
NCBI Description
                   (AE000725) argininosuccinate synthase [Aquifex aeolicus]
Seq. No.
                   8341
                   12383 3.R1040
Contig ID
                   pmv700894244.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2983600
BLAST score
                   223
E value
                   5.0e-18
Match length
                   93
```

```
(AE000725) argininosuccinate synthase [Aquifex aeolicus]
NCBI Description
Seq. No.
                   8342
Contig ID
                   12383 4.R1040
                   qsv70\overline{1}044237.h1
5'-most EST
                   8343
Seq. No.
                   12387 1.R1040
Contig ID
5'-most EST
                  LIB3139-048-P1-N1-A2
                  BLASTN
Method
                   q1694899
NCBI GI
BLAST score
                   391
                   0.0e + 00
E value
Match length
                   583
% identity
                   92
NCBI Description
                  P.sativum mRNA for Copl protein
                  8344
Seq. No.
                   12388 1.R1040
Contig ID
5'-most EST
                   q5057689
Method
                   BLASTX
NCBI GI
                   q3193320
BLAST score
                   154
E value
                   7.0e-10
Match length
                   78
% identity
                   (AF069299) contains similarity to the subtilase family of
NCBI Description
                   serine proteases (Pfam: subtilase.hmm, score: 47.57);
                   strong similarity to Cucumis melo (muskmelon) cucumisin
                   (GB:D32206) [Arabidopsis thaliana]
                   8345
Seq. No.
Contig ID
                   12391 1.R1040
5'-most EST
                  LIB3170-010-Q1-J1-E7
Seq. No.
                   8346
Contig ID
                   12393 1.R1040
5'-most EST
                   zhf700963357.h1
                   8347
Seq. No.
Contig ID
                   12395 1.R1040
5'-most EST
                  LIB3040-036-Q1-E1-E11
Seq. No.
                   12406 1.R1040
Contig ID
5'-most EST
                  LIB3040-036-Q1-E1-B10
Seq. No.
                   8349
                   12407 1.R1040
Contiq ID
5'-most EST
                  LIB3040-036-Q1-E1-B11
Method
                  BLASTX
NCBI GI
                  g2245118
BLAST score
                  695
                  5.0e-73
E value
Match length
                  153
                   79
% identity
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
```

```
8350
Seq. No.
                  12407 2.R1040
Contig ID
5'-most EST
                  taw700657218.hl
                  BLASTX
Method
NCBI GI
                  q2245118
BLAST score
                  168
                  1.0e-11
E value
Match length
                  66
                  55
% identity
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
                  8351.
Seq. No.
                  12410 1.R1040
Contig ID
5'-most EST
                  LIB3170-010-01-K1-E6
Method ·
                  BLASTX
NCBI GI
                  q3510256
BLAST score
                  467
E value
                  3.0e-46
Match length
                  151
                  60
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  8352
                  12417 1.R1040
Contig ID
5'-most EST
                  LIB3040-008-Q1-E1-E11
                  8353
Seq. No.
                  12430 1.R1040
Contig ID
5'-most EST
                  LIB3170-009-Q2-K2-E3
                  8354
Seq. No.
                  12438 1.R1040
Contig ID
5'-most EST
                  pxt700946066.h1
Method
                  BLASTX
NCBI GI
                  q3219858
BLAST score
                  528
E value
                  1.0e-53
Match length
                  116
% identity
NCBI Description
                  DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE
                  >gi_2129724_pir__S71204 RNA polymerase II 13.6 kDa chain -
                  Arabidopsis thaliana >gi 881501 (U28048) RNA polymerase II
                  13.6 kDa subunit [Arabidopsis thaliana]
                  8355
Seq. No.
Contig ID
                  12438 2.R1040
5'-most EST
                  LIB3040-035-Q1-E1-D4
Method
                  BLASTX
NCBI GI
                  q3219858
BLAST score
                  331
E value
                  7.0e-31
                  79
Match length
% identity
                  DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE
NCBI Description
                  >gi 2129724 pir S71204 RNA polymerase II 13.6 kDa chain -
                  Arabidopsis thaliana >gi 881501 (U28048) RNA polymerase II
```

Contig ID

8356

12438 3.R1040

13.6 kDa subunit [Arabidopsis thaliana]

15-5

LIB3050-013-Q1-E1-H7 5'-most EST Method BLASTX q3219858 NCBI GI BLAST score 403 E value 2.0e-39 91 Match length % identity 84 NCBI Description DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE >gi 2129724 pir S71204 RNA polymerase II 13.6 kDa chain -Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II 13.6 kDa subunit [Arabidopsis thaliana] 8357 Seq. No. 12438 4.R1040 Contig ID bth700844772.h1 5'-most EST Method BLASTX g3219858 NCBI GI 169 BLAST score 3.0e-12 E value Match length 44 % identity 73 DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE NCBI Description >gi_2129724_pir__S71204 RNA polymerase II 13.6 kDa chain -Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II 13.6 kDa subunit [Arabidopsis thaliana] Seq. No. 8358 12439 1.R1040 Contig ID LIB3170-012-Q1-K1-E6 5'-most EST 8359 Seq. No. Contig ID 12443 1.R1040 5'-most EST LIB3170-011-Q1-K1-E7 8360 Seq. No. 12446 1.R1040 Contig ID 5'-most EST fua701040824.h1 Method **BLASTX** NCBI GI q1834379 BLAST score 183 E value 3.0e-13 Match length 98 % identity 43 NCBI Description (Y10551) ComAB [Bacillus licheniformis] 8361 Seq. No. 12452 1.R1040 Contig ID 5'-most EST zpv700763308.h1 Method BLASTN NCBI GI g4103986 109 BLAST score

6.0e-54

282

E value Match length

89 % identity Pisum sativum 5,10-methylenetetrahydrofolate NCBI Description dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase mRNA, complete cds 8362 Seq. No. 12452 2.R1040 Contig ID 5'-most EST bth700847483.h1 BLASTN Method NCBI GI g4103986 BLAST score 495 E value 0.0e + 00Match length 859 89 % identity Pisum sativum 5,10-methylenetetrahydrofolate NCBI Description dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase mRNA, complete cds 8363 Seq. No. 12468 1.R1040 Contig ID 5'-most EST uC-gmropic057h01b1 Method BLASTN NCBI GI g2062691 BLAST score 33 E value 6.0e-09 33 Match length % identity 61 NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete 8364 Seq. No.

Contig ID 12470_1.R1040

5'-most EST LIB3170-011-Q1-K1-E4

Seq. No. 8365

Contig ID 12473_1.R1040 5'-most EST pmv700892186.h1

Seq. No. 8366

Contig ID 12477_1.R1040

5'-most EST LIB3040-034-Q1-E1-H2

Method BLASTX
NCBI GI g2204234
BLAST score 522
E value 6.0e-53
Match length 183
% identity 56

NCBI Description (Y13862) enoyl-ACP reductase [Nicotiana tabacum]

Seq. No. 8367

Contig ID 12477_2.R1040 5'-most EST ssr700560123.h1

Seq. No. 8368

Contig ID 12480_1.R1040

5'-most EST LIB3050-005-Q1-K1-D7

```
Seq. No.
                   8369
                   12483 1.R1040
Contig ID
5'-most EST
                   LIB3040-035-Q1-E1-A1
                   8370
Seq. No.
                   12484 1.R1040
Contig ID
                   LIB3040-034-Q1-E1-G2
5'-most EST
                   8371
Seq. No.
                   12490 1.R1040
Contig ID
5'-most EST
                   LIB3170-010-Q1-K1-D2
                   8372
Seq. No.
                   12493 1.R1040
Contig ID
                   jC-gm\overline{l}e01810063h01a1
5'-most EST
Method
                   BLASTX
                   q2894599
NCBI GI
BLAST score
                   258
E value
                   4.0e-22
Match length
                   71
% identity
                   53
NCBI Description
                   (AL021889) putative protein [Arabidopsis thaliana]
                   8373
Seq. No.
Contig ID
                   12493 2.R1040
5'-most EST
                   jC-gmle01810010e01a1
Method
                   BLASTX
NCBI GI
                   g2894599
BLAST score
                   296
E value
                   1.0e-26
Match length
                   100
% identity
                   56
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   8374
Seq. No.
Contig ID
                   12493 3.R1040
5'-most EST
                   bth700848738.h1
Method
                   BLASTX
NCBI GI
                   q2894599
BLAST score
                   531
                   6.0e-57
E value
Match length
                   195
% identity
                   64
NCBI Description
                   (AL021889) putative protein [Arabidopsis thaliana]
                   8375
Seq. No.
Contig ID
                   12493 5.R1040
5'-most EST
                   LIB3138-033-Q1-N1-A4
Method
                   BLASTX
NCBI GI
                   q2894599
BLAST score
                   252
E value
                   1.0e-21
Match length
                   100
% identity
NCBI Description
                   (AL021889) putative protein [Arabidopsis thaliana]
```

5'-most EST

```
12500 1.R1040

⊗Contig ID

  5'-most EST
                     LIB3094-091-Q1-K1-E7
                     BLASTX
  Method
  NCBI GI
                     q3759184
  BLAST score
                     1082
  E value
                     1.0e-118
  Match length
                     290
  % identity
                     70
  NCBI Description
                     (AB018441) phi-1 [Nicotiana tabacum]
                     8377
  Seq. No.
                     12500 2.R1040
  Contig ID
  5'-most EST
                     zsg701122572.h1
  Method
                     BLASTX
  NCBI GI
                     q3759184
  BLAST score
                     336
                     2.0e-31
  E value
  Match length
                     109
  % identity
                     61
  NCBI Description
                     (AB018441) phi-1 [Nicotiana tabacum]
                     8378
  Seq. No.
  Contig ID
                     12500 3.R1040
  5'-most EST
                     LIB3139-084-P1-N1-G3
  Method
                     BLASTX
  NCBI GI
                     g3759184
  BLAST score
                     504
  E value
                     6.0e-51
                     163
  Match length
  % identity
                     60
  NCBI Description
                     (AB018441) phi-1 [Nicotiana tabacum]
                     8379
  Seq. No.
                     12500 6.R1040
  Contig ID
  5'-most EST
                     rlr700898648.h1
  Method
                     BLASTX
  NCBI GI
                     q3759184
  BLAST score
                     164
  E value
                     3.0e-11
  Match length
                     40
  % identity
                     78
  NCBI Description
                     (AB018441) phi-1 [Nicotiana tabacum]
                     8380
  Seq. No.
                     12500 7.R1040
  Contig ID
  5'-most EST
                     LIB3139-056-P1-N1-G1
  Method
                     BLASTX
  NCBI GI
                     q4325369
  BLAST score
                     248
  E value
                     7.0e-31
                     107
  Match length
  % identity
                     (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
  NCBI Description
                     8381
  Seq. No.
                     12508_1.R1040
  Contig ID
```

LIB3040-034-Q1-E1-G11

% identity

NCBI Description

49

```
Method
                   BLASTX
NCBI GI
                   g1703091
BLAST score
                   413
E value
                   3.0e-40
Match length
                   115
                   75
% identity
                   ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP)
NCBI Description
                   (NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KD SUBUNIT) (MTACP-1)
                   >gi_903689 (L23574) acyl carrier protein precursor
                   [Arabidopsis thaliana] >gi_3341682 (AC003672) acyl carrier
                   protein [Arabidopsis thaliana]
                   8382
Seq. No.
                   12511 1.R1040
Contig ID
                   jC-gmle01810059b09a1
5'-most EST
Method
                   BLASTX
                   q4262154
NCBI GI
BLAST score
                   495
E value
                   1.0e-49
Match length
                   154
% identity
                   67
                   (AC005275) putative protein phosphatase regulatory subunit
NCBI Description
                   [Arabidopsis thaliana]
                   8383
Seq. No.
Contig ID
                   12518 1.R1040
                   LIB3049-002-Q1-E1-C1
5'-most EST
Method
                   BLASTX
                   q4335763
NCBI GI
BLAST score
                   661
E value
                   9.0e-73
                   177
Match length
                   72
% identity
NCBI Description
                   (AC006284) unknown protein [Arabidopsis thaliana]
                   8384
Seq. No.
Contig ID
                   12518 2.R1040
5'-most EST
                   qsv701049114.h1
Method
                   BLASTX
NCBI GI
                   q4335763
BLAST score
                   151
E value
                   6.0e-10
Match length
                   44
% identity
NCBI Description
                   (AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.
                   8385
                   12520 1.R1040
Contig ID
                   LIB3167-010-P1-K1-D7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1402891
BLAST score
                   184
E value
                   3.0e-13
                   90
Match length
```

(X98130) unknown [Arabidopsis thaliana]

```
Seq. No.
                   8386
                   12520 2.R1040
Contig ID
                   smc70\overline{0}750345.h1
5'-most EST
Seq. No.
                   8387
                   12520 4.R1040
Contig ID
                   LIB31\overline{3}8-034-Q1-N1-B6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1402890
BLAST score
                   655
                   3.0e-68
E value
Match length
                   287
                   50
% identity
                   (X98130) unknown [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8388
                   12521 1.R1040
Contig ID
5'-most EST
                   k1170\overline{1}214785.h1
                   8389
Seq. No.
                   12521 2.R1040
Contig ID
5'-most EST
                   LIB3049-039-Q1-E1-B4
                   8390
Seq. No.
Contig ID
                   12524 1.R1040
5'-most EST
                   LIB3074-025-Q1-E1-H7
Method
                   BLASTX
NCBI GI
                   g2245131
                   902
BLAST score
E value
                   2.0e-97
Match length
                   262
% identity
                   73
NCBI Description
                   (Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   8391
Contig ID
                   12524_2.R1040
5'-most EST
                   jC-gmro02910004h11a1
Method
                   BLASTX
NCBI GI
                   q2245131
BLAST score
                   293
E value
                   4.0e-37
Match length
                   120
                   73
% identity
NCBI Description
                   (Z97344) hypothetical protein [Arabidopsis thaliana]
                   8392
Seq. No.
Contig ID
                   12527 1.R1040
5'-most EST
                   LIB3040-014-Q1-E1-A7
Method
                   BLASTN
NCBI GI
                   g914860
BLAST score
                   116
E value
                   3.0e-58
Match length
                   369
% identity
                   83
NCBI Description
                   M. varia mRNA for mitotic cyclin
```

E value

8.0e-24

```
Contig ID
                   12532 1.R1040
                   LIB3040-029-Q1-E1-F9
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4206101
BLAST score
                   152
                   1.0e-79
E value
                   176
Match length
                   97
% identity
NCBI Description
                   Glycine max retroelement diaspora gag-pol polyprotein
                   (gag-pol) pseudogene, partial sequence
Seq. No.
                   12541 1.R1040
Contig ID
                   uC-gmropic026d06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q464444
BLAST score
                   1087
                   1.0e-119
E value
                   238
Match length
% identity
                   PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                   COMPLEX 30 KD SUBUNIT) >gi_541889_pir__S39900 proteasome -
                   Arabidopsis thaliana >gi_1\overline{166830} (\overline{M98495}) proteasome
                   [Arabidopsis thaliana]
                   8395
Seq. No.
Contig ID
                   12541 2.R1040
                   uC-gmflminsoy093c02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4115377
BLAST score
                   1977
                   0.0e+00
E value
                   489
Match length
                   76
% identity
NCBI Description
                   (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                   8396
                   12541 3.R1040
Contig ID
                   LIB3170-058-Q1-K1-E5
5'-most EST
Method
                   BLASTX
NCBI GI
                   q464444
BLAST score
                   407
                   2.0e-39
E value
Match length
                   100
                   76
% identity
                   PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                   COMPLEX 30 KD SUBUNIT) >gi_541889_pir__S39900 proteasome -
                   Arabidopsis thaliana >gi 166830 (M98495) proteasome
                   [Arabidopsis thaliana]
Seq. No.
                   8397
Contig ID
                   12541 4.R1040
5'-most EST
                   iC-qmf102220054e09a1
Method
                   BLASTN
NCBI GI
                   g3421091
BLAST score
                   58.
```

```
146
Match length
                   85
% identity
                   Arabidopsis thaliana 20S proteasome subunit PAF1 (PAF1)
NCBI Description
                   mRNA, complete cds
                   8398
Seq. No.
                   12553 1.R1040
Contig ID
5'-most EST
                   LIB3073-023-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g3914555
BLAST score
                   337
                   1.0e-31
E value
Match length
                   86
                   85
% identity
NCBI Description
                   PUTATIVE RIBOSOME-BINDING FACTOR A, CHLOROPLAST PRECURSOR
                   >gi_3096942_emb_CAA18852.1_ (AL023094) putative protein
                   [Arabidopsis thaliana]
                   8399
Seq. No.
Contig ID
                   12555 1.R1040
                   LIB3040-033-Q1-E1-F3
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4262232
BLAST score
                   532
E value
                   5.0e-54
Match length
                   212
                   48
% identity
                   (AC006200) putative ribosomal protein L7 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   8400
                   12555 3.R1040
Contig ID
5'-most EST
                   LIB3049-026-Q1-E1-G7
Seq. No.
                   8401
Contig ID
                   12555 4.R1040
5'-most EST
                   fua701042636.hl
Seq. No.
                   8402
                   12561 1.R1040
Contig ID
5'-most EST
                   LIB3040-033-01-E1-G12
Seq. No.
                   8403
                   12565 1.R1040
Contig ID
5'-most EST
                   LIB3139-045-P1-N1-A6
Seq. No.
                   8404
                   12576 1.R1040
Contig ID
                   sat701014478.hl
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2502084
BLAST score
                   219
E value
                   1.0e-119
Match length
                   431
                   88
% identity
```

NCBI Description Vigna radiata adenosine triphosphatase mRNA, partial cds

5'-most EST

```
8405
Seq. No.
                   12576 2.R1040
Contig ID
5'-most EST
                   LIB3040-033-Q1-E1-D2
Method
                   BLASTN
NCBI GI
                   q2502084
BLAST score
                   223
E value
                   1.0e-122
Match length
                   524
% identity
                   87
NCBI Description
                   Vigna radiata adenosine triphosphatase mRNA, partial cds
Seq. No.
                   12578 1.R1040
Contig ID
5'-most EST
                   LIB3040-033-01-E1-D8
Method
                   BLASTX
NCBI GI
                   q3252868
BLAST score
                   978
E value
                   1.0e-106
Match length
                   332
% identity
                   57
                   (AF033536) putative zinc transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8407
Contig ID
                   12586 1.R1040
                   epx70\overline{1}109309.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3335335
BLAST score
                   414
E value
                   2.0e-40
Match length
                   139
% identity
                   60
NCBI Description
                   (AC004512) ESTs gb_F14113 and gb_T42122 come from this
                   region. [Arabidopsis thaliana]
Seq. No.
                   8408
Contig ID
                   12586 2.R1040
5'-most EST
                   LIB3040-032-Q1-E1-H6
Method
                   BLASTX
NCBI GI
                   q3335335
BLAST score
                   270
E value
                   1.0e-23
Match length
                   107
% identity
                   54
NCBI Description
                   (AC004512) ESTs gb_F14113 and gb_T42122 come from this
                   region. [Arabidopsis thaliana]
Seq. No.
                   8409
                   12590 1.R1040
Contig ID
5'-most EST
                   LIB3139-028-P1-N1-E11
                   8410
Seq. No.
                   12590 2.R1040
Contig ID
5'-most EST
                   LIB3055-010-Q1-N1-B6
                   8411
Seq. No.
                   12590_3.R1040
Contig ID
```

 $wrg70\overline{0}789462.h2$

12590 5.R1040 Contig ID 5'-most EST zpv700758707.h1

Seq. No.

8413 12604 1.R1040

Contig ID 5'-most EST

LIB3170-009-Q2-J1-D6

Seq. No.

8414

Contig ID 5'-most EST 12608 1.R1040

LIB3170-011-Q1-J1-C9

Seq. No.

8415

Contig ID 5'-most EST 12609 1.R1040 bth700849741.h1

Seq. No.

8416

Contig ID 5'-most EST 12613 1.R1040 vwf700674168.h1

Seq. No.

8417

Contig ID 5'-most EST 12613 2.R1040 vwf700673719.hl

Seq. No.

8418

Contig ID

12618 1.R1040

5'-most EST

LIB3040-032-01-E1-F6

Seq. No.

8419

Contig ID

12621 1.R1040

5'-most EST

LIB3040-032-Q1-E1-D8

Seq. No.

8420

Contig ID

12633 1.R1040

5'-most EST

LIB3040-032-Q1-E1-F4

Seq. No.

8421

Contig ID

12648 1.R1040

5'-most EST Method

LIB3040-020-01-E1-B5 BLASTX

NCBI GI

q2914702

BLAST score

322

2.0e-29

E value

Match length

222

% identity

50

NCBI Description

(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.

8422

Contig ID

12652 1.R1040

5'-most EST

LIB3051-048-Q1-K1-D8

Seq. No.

8423

Contig ID

12671 1.R1040

5'-most EST

LIB3170-012-Q1-K1-C1

Seq. No.

```
Contig ID
                   12679 1.R1040
5'-most EST
                   leu701155621.hl
Method
                   BLASTX
                   q4417304
NCBI GI
                   534
BLAST score
                   3.0e-54
E value
                   183
Match length
% identity
                   (AC006446) putative beta-1,4-mannosyl-glycoprotein
NCBI Description
                   beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis
                   thaliana]
                   8425
Seq. No.
                   12679 2.R1040
Contig ID
5'-most EST
                   LIB3056-013-Q1-N1-D7
Method
                   BLASTX
                   q4417304
NCBI GI
BLAST score
                   256
E value
                   9.0e-22
Match length
                   87
% identity
                   53
NCBI Description
                   (AC006446) putative beta-1,4-mannosyl-glycoprotein
                   beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis
                   thaliana]
                   8426
Seq. No.
                   12680 1.R1040
Contig ID
5'-most EST
                   k11701210069.h1
                   8427
Seq. No.
Contig ID
                   12680 2.R1040
5'-most EST
                   sat701005920.h1
Seq. No.
                   8428
                   12680 3.R1040
Contig ID
5'-most EST
                   trc700566611.h1
                   8429
Seq. No.
Contig ID
                   12690 1.R1040
5'-most EST
                   LIB3170-009-Q2-K1-B11
Seq. No.
                   8430
                   12697 1.R1040
Contig ID
5'-most EST
                  LIB3040-031-Q1-E2-E6
                   8431
Seq. No.
Contig ID
                   12698 1.R1040
5'-most EST
                  LIB3040-031-Q1-E2-E7
Method
                  BLASTX
NCBI GI
                   q2656003
BLAST score
                   333
E value
                   3.0e-31
                  91
Match length
% identity
                  (Z98980) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
```

8437

```
12708 1.R1040
Contig ID
                    LIB3094-025-Q1-K1-E12
5'-most EST
Seq. No.
                    8433
                    12708 2.R1040
Contig ID
5'-most EST
                    LIB3040-031-Q1-E2-C1
Method
                    BLASTX
                    g2865623
NCBI GI
BLAST score
                    668
                    5.0e-70
E value
Match length
                    169
                    76
% identity
                    (AF045286)
NCBI Description
                    GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                    [Arabidopsis thaliana]
                    8434
Seq. No.
                    12708 3.R1040
Contig ID
                    LIB3087-006-Q1-K1-F4
5'-most EST
Method
                    BLASTX
                    g2865623
NCBI GI
BLAST score
                   188
E value
                    4.0e-14
Match length
                    46
% identity
                    83
                    (AF045286)
NCBI Description
                    GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                    [Arabidopsis thaliana]
                    8435
Seq. No.
Contig ID
                    12713 1.R1040
                    6HA - 0\overline{2} - Q1 - B1 - E5
5'-most EST
Method
                    BLASTX
NCBI GI
                    g134794
BLAST score
                    513
E value
                    9.0e-52
Match length
                    173
% identity
                    MICROSOMAL SIGNAL PEPTIDASE 18 KD SUBUNIT (SPC18)
NCBI Description
                    >gi_108137_pir_ A35309 signal peptidase (EC 3.4.99.-) 18K
chain - dog >gi_164082 (J05466) microsomal signal peptidase
                    complex [Canis familiaris] >gi_4335939_gb_AAD17526_
                    (AF061737) microsomal signal peptidase [Homo sapiens]
Seq. No.
                    8436
Contig ID
                    12715 1.R1040
5'-most EST
                    ncj70\overline{0}987568.h1
Method
                    BLASTN
NCBI GI
                    g2351064
BLAST score
                    47
E value
                    3.0e-17
Match length
                    187
                    87
% identity
NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MDJ22, complete sequence [Arabidopsis thaliana]
```

 $\mathcal{F}_{i_1} \sim$

Match length

```
12716 1.R1040
Contig ID
5'-most EST
                   uaw700664678.hl
Method
                   BLASTX
                   g4468991
NCBI GI
BLAST score
                   183
E value
                   2.0e-13
                   104
Match length
% identity
                   39
NCBI Description
                   (AL035605) ribosomal-like protein [Arabidopsis thaliana]
                   8438
Seq. No.
                   12723 1.R1040
Contig ID
                   LIB3040-031-Q1-E1-H4
5'-most EST
Method
                   BLASTN
NCBI GI
                   q971167
BLAST score
                   114
                   3.0e-57
E value
                   254
Match length
% identity
                   86
NCBI Description
                   Pisum sativum Wando ornithine carbamoyltransferase mRNA,
                   complete cds
Seq. No.
                   8439
                   12728 1.R1040
Contig ID
5'-most EST
                   ssr700556271.h1
Method
                   BLASTX
NCBI GI
                   q4455213
BLAST score
                   1168
E value
                   1.0e-128
Match length
                   258
% identity
NCBI Description
                   (AL035440) glutamine amidotransferase/cyclase [Arabidopsis
                   thaliana]
Seq. No.
                   8440
                   12730 1.R1040
Contig ID
5'-most EST
                   LIB3040-031-Q1-E2-A7
Method
                   BLASTX
NCBI GI
                   q4455293
BLAST score
                   267
E value
                   3.0e-23
Match length
                   61
% identity
                   87
                   (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   12730 2.R1040
Contig ID
5'-most EST
                   kl1701213870.h1
Seq. No.
                   8442
                   12750 1.R1040
Contig ID
                  LIB3049-055-Q1-E1-F3
5'-most EST
Method
                  BLASTN
NCBI GI
                   g488564
BLAST score
                  170
E value
                   1.0e-90
```

```
% identity .
NCBI Description
                   Medicago sativa cultivar Chief histone H3.1 gene, 5' region
                    and complete cds
                    8443
Seq. No.
                    12752 1.R1040
Contig ID
5'-most EST
                    epx70\overline{1}104867.h1
Seq. No.
                    8444
Contig ID
                    12752 2.R1040
5'-most EST
                    LIB3050-025-Q1-K1-D2
                    8445
Seq. No.
Contig ID
                    12752 3.R1040
5'-most EST
                    LIB3093-037-01-K1-B6
                    8446
Seq. No.
                    12759 1.R1040
Contig ID
5'-most EST
                    LIB3040-031-Q1-E1-C9
                    8447
Seq. No.
                    12769 1.R1040
Contig ID
5'-most EST
                    LIB3040-030-Q1-E1-G5
Method
                    BLASTX
NCBI GI
                    g2829751
BLAST score
                    206
E value
                    5.0e-16
Match length
                    114
                    38
% identity
                   MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF)
NCBI Description
                   >gi_1850559 (U88035) macrophage migration inhibitory factor
[Brugia malayi] >gi_2190976 (AF002699) macrophage migration
                    inhibitory factor [Brugia malayi]
Seq. No.
                    8448
Contig ID
                    12774 1.R1040
5'-most EST
                    LIB3040-030-01-E1-H1
                    8449
Seq. No.
                    12784 1.R1040
Contig ID
5'-most EST
                    LIB3049-034-01-E1-E12
Seq. No.
                    8450
                    12789 1.R1040
Contig ID
5'-most EST
                    leu70\overline{1}149449.h1
Method
                    BLASTX
NCBI GI
                    q1718097
BLAST score
                    1090
E value
                    1.0e-119
Match length
                    340
% identity
                    58
NCBI Description
                   VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
                    (41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048 pir A55016
                    lysosomal membrane protein DVA41 - slime mold
                    (Dictyostelium discoideum) >gi 532733 (U13150) vacuolar
```

ATPase subunit DVA41 [Dictyostelium discoideum]

```
8451
Seq. No.
                   12793 1.R1040
Contig ID
                   bth700843731.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3763916
BLAST score
                    377
                   8.0e-36
E value
                   260
Match length
% identity
                    33
                    (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown
                   protein [Arabidopsis thaliana]
                   8452
Seq. No.
Contig ID
                   12796 1.R1040
5'-most EST
                    zzp70\overline{0}832237.h1
Method
                   BLASTX
NCBI GI
                   g4468813
BLAST score
                    387
E value
                    3.0e-37
                   202
Match length
% identity
                   39
                    (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
                   8453
Seq. No.
                   12796 2.R1040
Contig ID
5'-most EST
                   LIB3139-121-P1-N1-G4
                   8454
Seq. No.
                   12796 3.R1040
Contig ID
5'-most EST
                   gsv70\overline{1}045344.h1
                   8455
Seq. No.
                   12802 1.R1040
Contig ID
5'-most EST
                   LIB3040-030-Q1-E1-C5
Seq. No.
                   8456
                   12802 2.R1040
Contig ID
5'-most EST
                   leu70\overline{1}145651.h1
                   8457
Seq. No.
                   12802 4.R1040
Contig ID
5'-most EST
                   LIB3040-005-Q1-E1-A1
Seq. No.
                   8458
Contig ID
                   12808 1.R1040
5'-most EST
                   asn70\overline{1}135489.h1
                   8459
Seq. No.
                   12810 1.R1040
Contig ID
5'-most EST
                   LIB3170-012-Q1-K1-B10
                   8460
Seq. No.
                   12815 1.R1040
Contig ID
                   ncj70\overline{0}977424.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2731377
```

```
100
BLAST score
                   253
E value
                   1.0e-21
Match length
                   143
% identity
                   38
NCBI Description
                   (U28739) similar to alcohol dehydrogenase/ribitol
                   dehydrogenase [Caenorhabditis elegans]
Seq. No.
                   12817 1.R1040
Contig ID
5'-most EST
                   LIB3040-030-Q1-E1-A3
Method
                   BLASTN
NCBI GI
                   q2695738
BLAST score
                   56
E value
                   9.0e-23
Match length
                   68
% identity
                   96
NCBI Description
                   Pisum sativum mitochondrial tRNA-Gly gene and flanking
                   sequences
Seq. No.
                   8462
                   12819 1.R1040
Contig ID
5'-most EST
                   ncj70\overline{0}975520.h1
Seq. No.
                   8463
Contig ID
                   12820 1.R1040
5'-most EST
                   LIB3170-012-01-K1-B4
                   8464
Seq. No.
Contig ID
                   12831 1.R1040
5'-most EST
                   uC-gmrominsoy316e04b1
Method
                   BLASTX
NCBI GI
                   q4544409
BLAST score
                   1156
E value
                   1.0e-127
Match length
                   376
% identity
NCBI Description
                   (AC006955) putative transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   8465
                   12831 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy180c03b1
Method
                   BLASTX
NCBI GI
                   g4544409
BLAST score
                   194
E value
                   2.0e-14
Match length
                   69
                   59
% identity
                   (AC006955) putative transcription factor [Arabidopsis
NCBI Description
                   thalianal
```

Seq. No. 8466 Contig ID 12831_3.R1040

5'-most EST LIB3051-072-Q1-K1-E10

Method BLASTX NCBI GI g2244917 BLAST score 285

BLAST score

Method

NCBI GI

E value

```
E value
                   5.0e-25
Match length
                   139
% identity
                   45
NCBI Description
                   (Z97339) hypothetical protein [Arabidopsis thaliana]
                   8467
Seq. No.
                   12831 4.R1040
Contig ID
5'-most EST
                   LIB30\overline{9}3-034-Q1-K1-D7
Seq. No.
                   8468
Contig ID
                   12831 5.R1040
5'-most EST
                   uC-gmropic042d01b1
                   8469
Seq. No.
Contig ID
                   12831 6.R1040
5'-most EST
                   LIB3092-008-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2244917
BLAST score
                   161
E value
                   1.0e-10
Match length
                   65
% identity
NCBI Description
                   (Z97339) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   8470
                   12831 7.R1040
Contig ID
                   jex70\overline{0}905749.h1
5'-most EST
                   8471
Seq. No.
                   12840 1.R1040
Contig ID
5'-most EST
                   LIB3109-029-Q1-K1-G1
Method
                   BLASTX
NCBI GI
                   g3122357
BLAST score
                   370
E value
                   2.0e-35
Match length
                   98
% identity
                   70
                   PUTATIVE LIPOATE-PROTEIN LIGASE B (LIPOATE BIOSYNTHESIS
NCBI Description
                   PROTEIN B) >gi_2494127 (AC002376) Contains similarity to
                   Mycobacterium LIPB gene (gb_Q104041). [Arabidopsis
                   thaliana]
                   8472
Seq. No.
Contig ID
                   12856 1.R1040
5'-most EST
                   LIB3106-069-P1-K1-F8
Seq. No.
                   8473
                   12867 1.R1040
Contig ID
5'-most EST
                   LIB3051-006-Q1-K1-A11
Seq. No.
                   8474
Contig ID
                   12872 1.R1040
```

LIB3093-016-01-K1-F11

BLASTX

200

g1665817

2.0e-15

Seq. No.

8484

```
Match length
                   128
% identity
                   36
NCBI Description
                   (D87466) Similar to S.cerevisiae hypothetical protein L3111
                   (S59316) [Homo sapiens]
Seq. No.
                   8475
                   12873 1.R1040
Contig ID
5'-most EST
                   LIB3170-010-Q1-K1-A6
                   8476
Seq. No.
                   12873 2.R1040
Contig ID
                   LIB3107-006-Q1-K1-C10
5'-most EST
Seq. No.
                   8477
                   12875 1.R1040
Contig ID
5'-most EST
                   LIB3170-011-Q1-K1-A5
                   8478
Seq. No.
                   12882 1.R1040
Contig ID
5'-most EST
                   LIB3040-029-Q1-E1-B3
Seq. No.
                   8479
                   12883 1.R1040
Contig ID
5'-most EST
                   LIB3040-020-Q1-E1-B11
Method
                   BLASTX
NCBI GI
                   g4559346
BLAST score
                   407
E value
                   1.0e-39
Match length
                   122
% identity
                   61
                   (AC006585) early nodulin 16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8480
                   12883_2.R1040
Contig ID
5'-most EST
                   hrw701062307.h1
                   8481
Seq. No.
                   12884 1.R1040
Contig ID
5'-most EST
                   kmv70\overline{0}741435.h1
                   8482
Seq. No.
                   12898 1.R1040
Contig ID
5'-most EST
                   LIB3170-011-Q1-J1-A4
Seq. No.
                   8483
                   12905 1.R1040
Contig ID
5'-most EST
                   uC-gmropic016c07b1
Method
                   BLASTX
NCBI GI
                   g3355468
BLAST score
                   526
E value
                   2.0e-53
Match length
                   123 .
                   88
% identity
NCBI Description
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
                   thaliana]
```

```
12905 2.R1040
Contig ID
                   zhf70\overline{0}953832.h1
5'-most EST
                   BLASTX
Method
                   q3355468
NCBI GI
BLAST score
                   179
E value
                   3.0e-13
                   47
Match length
                   79
% identity
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   8485
Seq. No.
                   12908 1.R1040
Contig ID
                   LIB3040-028-Q1-E1-E5
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2224899
BLAST score
                   277
                   3.0e-24
E value
                  186
Match length
% identity
                   41
                   (U67133) DNA-binding protein PcMYB1 [Petroselinum crispum]
NCBI Description
                   8486
Seq. No.
                   12913 1.R1040
Contig ID
                   LIB3040-005-Q1-E1-G5
5'-most EST
Method
                   BLASTX
                   g1421741
NCBI GI
BLAST score
                   377
                   2.0e-36
E value
                   77
Match length
                   87
% identity
                   (U54770) cytochrome P450 homolog [Lycopersicon esculentum]
NCBI Description
                   8487
Seq. No.
                   12916 1.R1040
Contig ID
5'-most EST
                   LIB3040-028-Q1-E1-F7
Method
                   BLASTX
NCBI GI
                   g3360289
BLAST score
                   155
                   2.0e-15
E value
                   77
Match length
% identity
NCBI Description
                   (AF023164) leucine-rich repeat transmembrane protein kinase
                   1 [Zea mays]
                   8488
Seq. No.
                   12919 1.R1040
Contig ID
5'-most EST
                   LIB3170-005-Q1-K1-H6
Method
                   BLASTX
                   g2920587
NCBI GI
BLAST score
                   1416
E value
                   1.0e-157
Match length
                   539
% identity
                   (AF038362) TBP-associated factor 172 [Homo sapiens]
NCBI Description
                   >gi 2995136_emb_CAA04475_ (AJ001017) TAFII170 [Homo
```

sapiens]

Seq. No. 8489

Contig ID 12920 1.R1040

5'-most EST LIB30 $\frac{1}{4}$ 0-008-Q1-E1-B4

Method BLASTX
NCBI GI g2443886
BLAST score 314
E value 1.0e-28
Match length 87
% identity 76

NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No. 8490

Contig ID 12920 2.R1040 5'-most EST zhf700961575.h1

Seq. No. 8491

Contig ID 12920_5.R1040 5'-most EST zhf700964127.h1

Seq. No. 8492

Contig ID 12943 1.R1040

5'-most EST LIB3040-026-Q1-E1-D12

Method BLASTX
NCBI GI g2832625
BLAST score 759
E value 9.0e-81
Match length 221

% identity

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

 2.59×10^{3}

Seq. No. 8493

Contig ID 12959 1.R1040

5'-most EST LIB $30\overline{4}0-027-Q1-E1-G10$

Seq. No. 8494

Contig ID 12965 1.R1040

5'-most EST LIB3040-027-Q1-E1-G6

Method BLASTX
NCBI GI g2326363
BLAST score 301
E value 7.0e-36
Match length 121
% identity 65

NCBI Description (AJ001037) DNA-directed RNA polymerase [Arabidopsis

thaliana]

Seq. No. 8495

Contig ID 12970_1.R1040

5'-most EST LIB3040-027-Q1-E1-H2

Seq. No. 8496

Contig ID 12976_1.R1040 5'-most EST uaw700664514.h1

Method BLASTN NCBI GI g2760166

BLAST score 40

```
5.0e-13
E value
Match length
                   131
% identity
                   87
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBK20, complete sequence [Arabidopsis thaliana]
                   8497
Seq. No.
                   12977 1.R1040
Contig ID
                   LIB3040-027-Q1-E1-E4
5'-most EST
Method
                   BLASTN
NCBI GI
                   q2196463
BLAST score
                   213
                   1.0e-116
E value
Match length
                   537
                   86
% identity
                   Arabidopsis thaliana chloroplast trnC, rpoB & rpoCl genes
NCBI Description
                   8498
Seq. No.
                   12987 1.R1040
Contig ID
5'-most EST
                   LIB3051-009-Q1-E1-F7
Seq. No.
                   8499
                   12988 1.R1040
Contig ID
5'-most EST
                   epx701110320.hl
                   8500
Seq. No.
                   12992 1.R1040
Contig ID
                   LIB3106-025-Q1-K1-D7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1174870
BLAST score
                   268
                   2.0e-23
E value
Match length
                   68
% identity
                   75
NCBI Description
                   UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN
                   >gi_633685_emb_CAA55861_ (X79274) ubiquinol--cytochrome c
reductase [Solanum tuberosum]
                   8501
Seq. No.
                   12992 2.R1040
Contig ID
5'-most EST
                   LIB3053-002-Q1-B1-D1
Method
                   BLASTX
NCBI GI
                   g1174870
BLAST score
                   231
E value
                   3.0e-19
Match length
                   67
% identity
                   69
                   UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN
NCBI Description
                   >gi 633685 emb CAA55861 (X79274) ubiquinol--cytochrome c
                   reductase [Solanum tuberosum]
Seq. No.
                   8502
                   12992 3.R1040
Contig ID
5'-most EST
                   jC-gmro02800040c03a1
```

8503

12997 1.R1040

Seq. No.

Contig ID

Match length

66

```
5'-most EST
                   LIB3040-027-Q1-E1-D5
                   8504
Seq. No.
Contig ID
                   13023 1.R1040
5'-most EST
                   g4283734
Method
                   BLASTX
NCBI GI
                   q881625
BLAST score
                   575
E value
                   5.0e-59
Match length
                   125
% identity
                   83
NCBI Description
                   (U29432) 22.8 kDa protein [Ipomoea trifida]
                   8505
Seq. No.
                   13027 1.R1040
Contig ID
5'-most EST
                   qsv70\overline{1}044414.h1
Method
                   BLASTX
NCBI GI
                   q3292831
BLAST score
                   604
E value
                   2.0e-85
Match length
                   250
% identity
                   (AL031018) putative serine/threonine kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   8506
                   13027_2.R1040
Contig ID
5'-most EST
                   jC-qmle01810087q01a1
Method
                   BLASTX
NCBI GI
                   q2253010
BLAST score
                   542
E value
                   1.0e-55
Match length
                   144
% identity
                   68
NCBI Description
                   (Y14199) MAP3K delta-1 protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   8507
                   13030 1.R1040
Contig ID
5'-most EST
                   LIB3106-115-01-K1-E4
Method
                   BLASTX
NCBI GI
                   g2997684
BLAST score
                   270
E value
                   1.0e-23
Match length
                   67
% identity
                   (AF053302) putative transcriptional co-activator
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   8508
Contig ID
                   13032 1.R1040
                   LIB3170-007-Q1-K1-G11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4388832
BLAST score
                   255
E value
                   6.0e-22
```

NCBI Description

```
% identity
                   9.1
NCBI Description
                   (AC006528) putative DNA replication licensing factor with
                   an MCM family domain (prosite:PDOC00662) [Arabidopsis
                   thaliana]
                   8509
Seq. No.
                   13033 1.R1040
Contig ID
                   LIB3093-037-Q1-K1-F12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2826786
BLAST score
                   301
                   4.0e-27
E value
Match length
                   123
                   54
% identity
NCBI Description
                   (Y10905) RAPB protein [Oryza sativa]
                   8510
Seq. No.
                   13033 3.R1040
Contig ID
                   bth700849432.h1
5'-most EST
Seq. No.
                   8511
                   13034 1.R1040
Contig ID
5'-most EST
                   LIB3170-007-Q1-K1-G12
                   8512
Seq. No.
                   13036 1.R1040
Contig ID
5'-most EST
                   LIB3170-005-Q1-K1-G3
                   BLASTX
Method
                   g3582021
NCBI GI
BLAST score
                   473
E value
                   2.0e-47
Match length
                   149
% identity
                   60
NCBI Description
                   (Y09423) cytochrome P450 [Nepeta racemosa]
                   8513
Seq. No.
Contig ID
                   13041 1.R1040
5'-most EST
                   LIB3040-026-Q1-E1-D2
Method
                   BLASTX
NCBI GI
                   a3935184
BLAST score
                   194
E value
                   8.0e-15
Match length
                   93
% identity
                   49
NCBI Description
                   (AC004557) F17L21.27 [Arabidopsis thaliana]
Seq. No.
                   8514
                   13045 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810094d11a1
Method
                   BLASTX
NCBI GI
                   q3021285
BLAST score
                   250
E value
                   2.0e-21
                   75
Match length
% identity
```

(AL022347) hypothetical protein [Arabidopsis thaliana] >gi_3451058_emb CAA20454.1 (AL031326) hypothetical protein

NCBI Description

horikoshii]

Seq. No. 8515 Contig ID 13054 1.R1040 5'-most EST LIB3040-026-Q1-E1-C9 8516 Seq. No. 13060 1.R1040 Contig ID 5'-most EST jC-gmf102220141d09a1 Seq. No. 8517 13061 1.R1040 Contig ID 5'-most EST LIB3040-026-Q1-E1-B6 Seq. No. 8518 13063 1.R1040 Contig ID 5'-most EST uC-gmrominsoy299a01b1 8519 Seq. No. Contig ID 13075 1.R1040 5'-most EST -LIB3040-025-Q1-E1-H12 Seq. No. 8520 Contig ID 13079 1.R1040 5'-most EST LIB3093-036-Q1-K1-A2 BLASTN Method g11772 NCBI GI BLAST score 77 9.0e-35 E value Match length 365 % identity 88 NCBI Description Tobacco chloroplast tRNA-Ser and tRNA-Gln genes Seq. No. 8521 Contig ID 13079 2.R1040 5'-most EST LIB3170-071-Q1-K1-E12 Method BLASTN _g296156 NCBI GI BLAST score 77 E value 4.0e-35 Match length 204 % identity NCBI Description Spinach chloroplast psbK gene for low-molecular mass protein K of photosystem II Seq. No. 8522 Contig ID 13084 1.R1040 5'-most EST LIB3040-026-Q1-E1-A3 Method BLASTX NCBI GI q3257978 BLAST score 511 E value 2.0e-51 Match length 230 % identity

[Arabidopsis thaliana]

(AP000006) 249aa long hypothetical protein [Pyrococcus

E value

9.0e-34

```
Seq. No.
                   8523
                   13084 2.R1040
Contig ID
5'-most EST
                   leu701151015.h1
Method
                   BLASTX
NCBI GI
                   g2650133
BLAST score
                   153
E value
                   6.0e-10
Match length
                   55
% identity
NCBI Description
                   (AE001070) ribonuclease PH (rph) [Archaeoglobus fulgidus]
Seq. No.
                   13090 1.R1040
Contig ID
5'-most EST
                   LIB3040-025-Q1-E1-F10
                   8525
Seq. No.
Contig ID
                   13095 1.R1040
5'-most EST
                   LIB3040-025-Q1-E1-F9
Method
                   BLASTX
NCBI GI
                   q2832625
BLAST score
                   156
E value
                   1.0e-21
Match length
                   92
% identity
                   (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8526
                   13096 1.R1040
Contig ID
5'-most EST
                   jsh70\overline{1}063926.h1
Method
                   BLASTX
NCBI GI
                   q3647283
BLAST score
                   561
E value
                   1.0e-57
Match length
                   135
                   79
% identity
NCBI Description
                   (AJ011418) ubiquitin activating enzyme [Lycopersicon
                   esculentum]
Seq. No.
                   8527
                   13096 2.R1040
Contig ID
5'-most EST
                   bth700848190.h1
Method
                   BLASTX
NCBI GI
                   g4455237
BLAST score
                   359
E value
                   4.0e-34
Match length
                   144
% identity
                   55
NCBI Description
                   (AL035523) ubiquitin activating enzyme-like protein
                   [Arabidopsis thaliana]
                   8528
Seq. No.
                   13096 3.R1040
Contig ID
5'-most EST
                   LIB3049-034-Q1-E1-H1
Method
                   BLASTX
                   g4455237
NCBI GI
BLAST score
                   355
```

```
Match length
                    97
                    71
% identity
NCBI Description
                    (AL035523) ubiquitin activating enzyme-like protein
                    [Arabidopsis thaliana]
Seq. No.
                    8529
Contig ID
                    13098 1.R1040
5'-most EST
                    LIB3106-076-Q1-K1-C3
Method
                    BLASTX
NCBI GI
                    q548774
BLAST score
                    1027
E value
                    1.0e-112
Match length
                    240
                    83
% identity
                    60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
NCBI Description
                    ribosomal protein L7A [Oryza sativa]
Seq. No.
                    8530 -
Contig ID
                    13100 1.R1040
5'-most EST
                    LIB3170-005-Q1-J1-B2
Seq. No.
                    8531
Contig ID
                    13104 1.R1040
5'-most EST
                    LIB3170-006-Q1-K1-F4
                    8532
Seq. No.
                    13105 1.R1040
Contia ID
5'-most EST
                    LIB3040-025-Q1-E1-C8
Seq. No.
                    8533
                    13107 1.R1040
Contig ID
5'-most EST
                    q4313\overline{4}02
Method
                    BLASTX
NCBI GI
                    q3355468
BLAST score
                    517
E value
                    2.0e-52
Match length
                    122
% identity
NCBI Description
                    (AC004218) putative ribosomal protein L35 [Arabidopsis
                    thaliana]
Seq. No.
                    8534
                    13107 2.R1040
Contig ID
5'-most EST
                    94396\overline{4}98
Method
                    BLASTX
NCBI GI
                    g3355468
BLAST score
                    515
E value
                    4.0e-52
Match length
                    122
% identity
NCBI Description
                    (AC004218) putative ribosomal protein L35 [Arabidopsis
                    thaliana]
                    8535
Seq. No.
                    13110 1.R1040
Contig ID
```

LIB3107-003-Q1-K1-B4

```
Method
                   BLASTX
NCBI GI
                   a464981
BLAST score
                   752
E value
                   5.0e-80
Match length
                   147
                   93
% identity
NCBI Description
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
                   ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.
                   8536
Contig ID
                   13115 1.R1040
5'-most EST
                   leu701157895.hl
                   BLASTX
Method
NCBI GI
                   q4490308
BLAST score
                   1004
E value
                   1.0e-109
Match length
                   303
% identity
                   67
NCBI Description
                   (AL035678) putative protein [Arabidopsis thaliana]
                   8537
Seq. No.
                   13116 1.R1040
Contig ID
5'-most EST
                   bth700848141.h1
Method
                   BLASTX
NCBI GI
                   q3687243
BLAST score
                   256
E value
                   7.0e-22
Match length
                   67
% identity
NCBI Description
                   (AC005169) putative ribosomal protein [Arabidopsis
                   thaliana]
Seq. No.
                   8538
Contig ID
                   13116 2.R1040
5'-most EST
                   pmv700888753.h1
Method
                   BLASTX
NCBI GI
                   q3687243
BLAST score
                   254
E value
                   9.0e-22
Match length
                   66
% identity
NCBI Description
                   (AC005169) putative ribosomal protein [Arabidopsis
                   thaliana]
Seq. No.
                   8539
Contig ID
                   13121 1.R1040
5'-most EST
                   uC-qmflminsoy008b03b1
Seq. No.
                   13124 1.R1040
Contig ID
                   LIB3170-007-Q1-K1-F9
5'-most EST
Seq. No.
                   8541
                   13128_1.R1040
Contig ID
```

LIB3170-006-Q1-K1-F1

Contig ID 5'-most EST

```
Seq. No.
                   8542
                   13130 1.R1040
Contig ID
5'-most EST
                   zsq701123209.h1
Method
                   BLASTX
NCBI GI
                   g2559012
BLAST score
                   375
E value
                   1.0e-35
Match length
                   128
% identity
                   58
NCBI Description
                   (AF026293) chaperonin containing t-complex polypeptide 1,
                   beta subunit; CCT-beta [Homo sapiens] >gi 4090929
                   (AF026166) chaperonin-containing TCP-1 beta subunit homolog
                   [Homo sapiens]
                   8543
Seq. No.
                   13133 1.R1040
Contig ID
5'-most EST
                   LIB3170-007-Q1-K1-F12
Seq. No.
                   8544
Contig ID
                   13134 1.R1040
5'-most EST
                   leu70\overline{1}144349.h1
Method
                   BLASTN
NCBI GI
                   q4388705
BLAST score
                   37
E value
                   4.0e-11
Match length
                   142
                   89
% identity
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F20D21 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   8545
                   13134 3.R1040
Contig ID
5'-most EST
                   LIB3138-013-Q1-N1-G2
Method
                   BLASTX
NCBI GI
                   q4115731
BLAST score
                   160
E value
                   7.0e-11
Match length
                   86
% identity
                   44
NCBI Description
                   (AB017507) Apg12 [Homo sapiens]
Seq. No.
                   13137 1.R1040
Contig ID
5'-most EST
                   LIB3040-025-Q1-E1-C11
Seq. No.
                   13137 2.R1040
Contig ID
                   epx70\overline{1}105423.h1
5'-most EST
Seq. No.
                   8548
                   13140 1.R1040
Contig ID
5'-most EST
                   LIB3092-053-Q1-K1-D9
                   8549
Seq. No.
```

13147 1.R1040

g5676941

```
8550
Seq. No.
                  13147 2.R1040
Contig ID
5'-most EST
                  LIB3074-025-Q1-E1-D1
Method
                  BLASTN
NCBI GI
                  q728715
BLAST score
                   75
                  7.0e-34
E value
Match length
                  191
% identity
                  85
NCBI Description
                  S.oleracea mRNA for 6.1 kDa polypeptide of photosystem II
Seq. No.
                  8551
                  13147 4.R1040
Contig ID
5'-most EST
                  LIB3074-028-Q1-K1-A9
Method
                  BLASTX
NCBI GI
                  q2493694
BLAST score
                  180
E value
                   4.0e-13
Match length
                  98
% identity
                   42
                  PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII
NCBI Description
                   6.1 KD PROTEIN) >gi_1076268_pir__S53025 photosystem II
                  protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein
                  of photosystem II [Spinacia oleracea]
Seq. No.
                  8552
                  13149 1.R1040
Contig ID
5'-most EST
                  LIB3170-007-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  q3328587
BLAST score
                  334
E value
                   1.0e-33
Match length
                  165
% identity
NCBI Description
                   (AE001292) CMP-2-keto-3-deoxyoctulosonic acid synthetase
                   [Chlamydia trachomatis]
                  8553
Seq. No.
Contig ID
                  13151 1.R1040
5'-most EST
                  LIB3040-024-Q1-E1-G5
Seq. No.
                  13158 1.R1040
Contig ID
5'-most EST
                  LIB3138-015-Q1-N2-E2
Seq. No.
Contig ID
                  13158 2.R1040
5'-most EST
                  uC-qmflminsoy043f05b1
Seq. No.
                  13158 3.R1040
Contig ID
5'-most EST
                  leu701154395.hl
Seq. No.
                  13159 1.R1040
Contig ID
```

uC-gmropic041a09b1

```
8558
Seq. No.
                   13159 2.R1040
Contig ID
5'-most EST
                   vwf700677224.hl
                   8559
Seq. No.
                   13160 1.R1040
Contig ID
                   jex70\overline{0}906127.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3402690
BLAST score
                   233
                   4.0e-19
E value
                   94
Match length
% identity
NCBI Description
                   (AC004697) hypothetical protein, 3' partial [Arabidopsis
                   thaliana]
                   8560
Seq. No.
                   13161 1.R1040
Contig ID
                   zzp700832222.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1352663
BLAST score
                   183
E value
                   3.0e-13
Match length
                   48
% identity
                   73
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC
NCBI Description
                   SUBUNIT >gi_1076388_pir__S52659 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 3 - Arabidopsis thaliana
                   >qi 466441 (M96841) Ser/Thr protein phosphatase
                   [Arabidopsis thaliana]
                   >gi_4559341_gb_AAD23003.1 AC007087 22 (AC007087)
                   serine/threonine protein phosphatase PP2A-3 catalytic
                   subunit [Arabidopsis thaliana]
                   >qi 4567320 gb AAD23731.1 AC005956 20 (AC005956)
                   serine/threonine protein phosphatase [Arabidopsis thaliana]
                   8561
Seq. No.
                   13161 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy136h01b1
Method
                   BLASTX
NCBI GI
                   q1352664
BLAST score
                   776
E value
                   1.0e-82
Match length
                   160
                   91
% identity
NCBI Description
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC
                   SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase
                   (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana
                   >gi 473259 (U08047) Ser/Thr protein phosphatase
                   [Arabidopsis thaliana] >gi 4204949 (U60136)
                   serine/threonine protein phosphatase 2A-4 catalytic subunit
                   [Arabidopsis thaliana]
                   8562
Seq. No.
                   13169 1.R1040
Contig ID
```

kmv700737865.hl

NCBI GI

```
8563
Seq. No.
                   13173 1.R1040
Contig ID
5'-most EST
                   LIB3051-027-Q1-K1-G8
Method
                   BLASTX
NCBI GI
                   g4056425
BLAST score
                   744
                   9.0e-79
E value
Match length
                   164
% identity
                   82
                   (AC005322) ESTs gb H36249, gb AA59732 and gb AA651219 come
NCBI Description
                   from this gene. [Arabidopsis thaliana]
                   8564
Seq. No.
                   13173 2.R1040
Contig ID
                   LIB3170-006-Q1-K1-E8
5'-most EST
                   8565
Seq. No.
                   13178 1.R1040
Contig ID
5'-most EST
                   LIB3072-051-Q1-E1-C1
Method
                   BLASTN
NCBI GI
                   g2764803
'BLAST score
                   146
E value
                   2.0e-76
Match length
                   366
% identity
                   85
                  G.max mRNA for epoxide hydrolase
NCBI Description
Seq. No.
                   8566
                   13182 1.R1040
Contig ID
5'-most EST
                   LIB3040-023-Q1-E1-G8
Method
                   BLASTX
NCBI GI
                   g3702329
BLAST score
                   156
E value
                   2.0e-10
Match length
                   50
% identity
                   (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   8567
Seq. No.
                   13183 1.R1040
Contig ID
5'-most EST
                   hrw701056967.h1
Method
                   BLASTX
NCBI GI
                   g2811026
BLAST score
                   357
E value
                   9.0e-34
Match length
                   80
% identity
                   TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi 1946375 (U93215)
NCBI Description
                   TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]
                   >gi 2347204 (AC002338) TCP1-chaperonin cofactor A isolog
                   [Arabidopsis thaliana]
                   8568
Seq. No.
                   13183 2.R1040
Contig ID
5'-most EST
                   LIB3040-023-Q1-E1-G9
Method
                   BLASTX
```

g2811026

```
BLAST score
                   353
E value
                   1.0e-33
Match length
                   78
% identity
                   88
                   TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi 1946375 (U93215)
NCBI Description
                   TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]
                   >gi 2347204 (AC002338) TCP1-chaperonin cofactor A isolog
                   [Arabidopsis thaliana]
Seq. No.
                   8569
                   13200 1.R1040
Contig ID
                   LIB3170-006-Q1-K1-C2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4567248
BLAST score
                   888
E value
                   1.0e-95
                   303
Match length
                   57
% identity
NCBI Description
                   (AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.
                   8570
                   13214 1.R1040
Contig ID
5'-most EST
                   LIB3138-061-Q1-N1-C5
Seq. No.
                   8571
                   13214 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810027g04d1
Seq. No.
                   8572
                   13214 3.R1040
Contig ID
5'-most EST
                   LIB3170-005-Q1-K1-D8
Seq. No.
                   8573
Contig ID
                   13214 4.R1040
5'-most EST
                   jC-qmle01810061e02a1
Seq. No.
                   8574
                   13216 1.R1040
Contig ID
5'-most EST
                   uxk70\overline{0}672719.h1
Seq. No.
                   8575
                   13216 2.R1040
Contig ID
                   uxk70\overline{0}672738.h1
5'-most EST
                   8576
Seq. No.
                   13216 3.R1040
Contig ID
                   awf70\overline{0}840091.h1
5'-most EST
                   8577
Seq. No.
                   13222 1.R1040
Contig ID
5'-most EST
                   LIB3107-002-Q1-K1-B3
                   8578
Seq. No.
                   13227 1.R1040
Contig ID
                   LIB3170-006-Q1-J1-C12
5'-most EST
```

8579

Seq. No.

Method

BLASTX

```
Contig ID
                   13235 1.R1040
5'-most EST
                   LIB3040-022-Q1-E1-H5
Method
                   BLASTX
NCBI GI
                   g2232057
BLAST score
                   232
E value
                   5.0e-19
Match length
                   69
% identity
                   67
                   (AF000177) CaSm [Homo sapiens]
NCBI Description
                   8580
Seq. No.
                   13235 2.R1040
Contig ID
                   jex700905452.hl
5'-most EST
Seq. No.
                   8581
                   13242 1.R1040
Contig ID
5'-most EST
                   LIB3049-052-Q1-E1-G2
Seq. No.
                   8582
                   13244_1.R1040
Contig ID
5'-most EST
                   LIB3170-004-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   g4490737
BLAST score
                   509
E value
                   2.0e-51
Match length
                   184
                   34
% identity
NCBI Description
                   (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   13256 1.R1040
Contig ID
5'-most EST
                   LIB3040-022-Q1-E1-G3
Seq. No.
                   8584
                   13260 1.R1040
Contig ID
5'-most EST
                   epx70\overline{1}105025.h1
Seq. No.
                   8585
Contig ID
                   13266 1.R1040
5'-most EST
                   wrg700786736.h2
                   8586
Seq. No.
                   13270 1.R1040
Contig ID
5'-most EST
                   LIB3170-005-Q1-K1-H4
Seq. No.
                   8587
                   13274 1.R1040
Contig ID
5'-most EST
                   LIB3170-006-Q1-J1-E6
                   8588
Seq. No.
                   13285 1.R1040
Contig ID
5'-most EST
                   LIB3040-022-Q1-E1-A10
                   8589
Seq. No.
Contig ID
                   13288 1.R1040
5'-most EST
                   LIB30\overline{4}0-022-Q1-E1-A6
```

Method

BLASTX

```
NCBI GI
                    q465602
BLAST score
                    261
E value
                    1.0e-22
Match length
                    98
% identity
                    57
                    HYPOTHETICAL 32.9 KD PROTEIN IN NFO-FRUA INTERGENIC REGION
NCBI Description
                    >gi_405885 (U00007) yeiN [Escherichia coli] >gi_1788490
                    (AE000306) orf, hypothetical protein [Escherichia coli]
                    >gi 744200 prf 2014253BL yeiN gene [Escherichia coli]
                    8590
Seq. No.
                    13295 1.R1040
Contig ID
5'-most EST
                    uC-qmronoir057d05b1
Seq. No.
                    8591
                    13295 2.R1040
Contig ID
                    LIB30\overline{5}1-025-Q1-K1-G11
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3786008
BLAST score
                    175
E value
                    2.0e-12
Match length
                    127
% identity
                    39
NCBI Description
                    (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                    8592
Contig ID
                    13300 1.R1040
5'-most EST
                    LIB3055-012-Q1-N1-B12
Method
                    BLASTX
NCBI GI
                    g3335060.
BLAST score
                    609
E value
                    5.0e-63
                    225
Match length
% identity
NCBI Description
                    (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
                    thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
                    8593
Seq. No.
                    13300 2.R1040
Contig ID
5'-most EST
                    LIB3040-021-Q1-E1-F2
Method
                    BLASTX
NCBI GI
                    g3098571
BLAST score
                    519
E value
                    2.0e-52
Match length
                    214
% identity
                    47
                    (AF049028) BURP domain containing protein [Brassica napus]
NCBI Description
Seq. No.
                    13300 4.R1040
Contig ID
                    seb70\overline{0}651485.h1
5'-most EST
                    8595
Seq. No.
                    13304 1.R1040
Contig ID
5'-most EST
                    awf70\overline{0}840276.h1
```

```
q3132470
NCBI GI
BLAST score
                   179
E value
                   5.0e-13
Match length
                   96
% identity
                   50
                   (AC003096) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   13304 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy084b04b1
Seq. No.
                   13308 1.R1040
Contig ID
5'-most EST
                   hrw701060302.h1
Method
                   BLASTX
NCBI GI
                   g2739376
BLAST score
                   263
E value
                   8.0e-23
Match length
                   90
% identity
                   58
NCBI Description
                   (AC002505) putative permease [Arabidopsis thaliana]
Seq. No.
                   8598
                   13316 1.R1040
Contig ID
5'-most EST
                   kl1701208551.hl
Method
                   BLASTX
NCBI GI
                   g2132842
BLAST score
                   344
E value
                   4.0e-32
Match length
                   118
% identity
                   53
                   probable membrane protein YOL077c - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi_1419909_emb_CAA99087_ (Z74819) ORF YOL077c
                   [Saccharomyces cerevisiae]
Seq. No.
                   8599
                   13323 1.R1040
Contig ID
5'-most EST
                  hrw701060978.hl
Seq. No.
                   8600
                   13324 1.R1040
Contig ID
5'-most EST
                  LIB3040-021-Q1-E1-D4
Seq. No.
                   8601
                   13335 1.R1040
Contig ID
                  LIB3170-007-Q1-K1-C5
5'-most EST
Method
                  BLASTX
NCBI GI
                   q499693
BLAST score
                   491
E value
                   2.0e-49
Match length
                  167
% identity
                  (L32095) cyclophilin [Vicia faba]
NCBI Description
                   8602
Seq. No.
                   13337 1.R1040
Contig ID
```

LIB3040-021-Q1-E1-A4

E value

3.0e - 31

```
8603
Seq. No.
                  13339 1.R1040
Contig ID
5'-most EST
                  LIB3170-006-Q1-K1-C1
                  BLASTX
Method
NCBI GI
                  g2344897
                  150
BLAST score
                   1.0e-09
E value
Match length
                  100
                   43
% identity
NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.
                   8604
                   13342 1.R1040
Contig ID
5'-most EST
                  rlr700897809.h1
                  BLASTX
Method
NCBI GI
                  q4158232
BLAST score
                   548
                   4.0e-56
E value
Match length
                  110
% identity
                   88
                   (Y18626) reversibly glycosylated polypeptide [Triticum
NCBI Description
                  aestivum]
                   8605
Seq. No.
Contig ID
                  13345 1.R1040
                  LIB3040-021-Q1-E1-C12
5'-most EST
Method
                  BLASTX
                  q2739371
NCBI GI
                   293
BLAST score
E value
                   2.0e-26
                   68
Match length
% identity
                  84
NCBI Description
                  (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
                  8606
Contig ID
                  13364 1.R1040
5'-most EST
                  uC-gmflminsoy036f09b1
Method
                  BLASTX
NCBI GI
                  g2244834
BLAST score
                  186
E value
                   1.0e-13
Match length
                  96
                                                            4:
% identity
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  8607
Contig ID
                  13381 1.R1040
5'-most EST
                  LIB3040-020-Q1-E1-E1
                  8608
Seq. No.
                  13385 1.R1040
Contig ID
5'-most EST
                  LIB3040-020-Q1-E1-C6
Method
                  BLASTX
NCBI GI
                  g4263701
BLAST score
                  335
```

110 Match length % identity 64 (AC006223) hypothetical protein [Arabidopsis thaliana] NCBI Description 8609 Seq. No. 13388 1.R1040 Contig ID LIB3049-028-Q1-E1-G3 5'-most EST BLASTX Method NCBI GI g3650030 BLAST score 255 1.0e-21 E value Match length 78 % identity 59 (AC005396) unknown protein [Arabidopsis thaliana] NCBI Description 8610 Seq. No. 13396 1.R1040 Contig ID 5'-most EST LIB3040-020-Q1-E1-D8 8611 Seq. No. Contig ID 13415 1.R1040 5'-most EST LIB3040-020-Q1-E1-C1 8612 Seq. No. Contig ID 13416 1.R1040 5'-most EST LIB3040-019-Q1-E1-F7 Method BLASTX g4249662 NCBI GI BLAST score 275 2.0e-46 E value Match length 118 % identity (AF089810) Altered Response to Gravity [Arabidopsis NCBI Description thaliana] 8613 Seq. No. Contig ID 13421 1.R1040 5'-most EST LIB3040-019-Q1-E1-G11 8614 Seq. No. 13422 1.R1040 Contig ID 5'-most EST LIB3106-111-Q1-K1-F11 Method BLASTX g132918 NCBI GI 334 BLAST score 5.0e-31 E value Match length 75 % identity 87 NCBI Description 50S RIBOSOMAL PROTEIN L35, CHLOROPLAST PRECURSOR (CL35) >gi_81486_pir__A36107 ribosomal protein L35 precursor,

Seq. No. 8615

Contig ID 13422_2.R1040

5'-most EST LIB3040-011-Q1-E1-B5

Method BLASTX

L35 [Spinacia oleracea]

chloroplast - spinach >gi 170139 (M60449) ribosomal protein

E value

Match length % identity

NCBI Description

48

thaliana]

The International Contract of the Contract of

```
NCBI GI
                  q132918
BLAST score
                  314
E value
                  1.0e-28
Match length
                  102
% identity
                  73
                  50S RIBOSOMAL PROTEIN L35, CHLOROPLAST PRECURSOR (CL35)
NCBI Description
                  >gi 81486 pir A36107 ribosomal protein L35 precursor,
                  chloroplast - spinach > gi 170139 (M60449) ribosomal protein
                  L35 [Spinacia oleracea]
                  8616
Seq. No.
Contig ID
                  13426 1.R1040
                  LIB3109-018-Q1-K1-A4
5'-most EST
Seq. No.
                  8617
Contig ID
                  13427 1.R1040
                  LIB3073-021-Q1-K1-C1
5'-most EST
Seq. No.
                  8618
                  13433 1.R1040
Contig ID
                  bth700848210.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2144099
BLAST score
                  188
                  3.0e-14
E value
                  77
Match length
                  42
% identity
NCBI Description
                  Set alpha isoform - rat >gi 545263 bbs 143660 (S68589) Set
                  alpha isoform=leukemogenesis protein {alternatively
                  spliced} [rats, neonatal kidney, Peptide, 289 aa] [Rattus
                  sp.] >gi 741750 prf 2008109A set gene [Rattus norvegicus]
                  8619
Seq. No.
Contig ID
                  13439 1.R1040
                  LIB3073-003-Q1-K1-F3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g585960
BLAST score
                  206
E value
                  4.0e-16
Match length
                  42
% identity
                  93
NCBI Description
                  PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT
                  >gi 433665 emb CAA81412 (Z26753) Sec61 beta-subunit
                  homolog [Arabidopsis thaliana]
                  8620
Seq. No.
                  13442 1.R1040
Contig ID
5'-most EST
                  zzp700836203.hl
Method
                  BLASTX
NCBI GI
                  g3885334
                  182
BLAST score
                  2.0e-13
```

(AC005623) putative argonaute protein [Arabidopsis

```
8621
Seq. No.
                   13446 1.R1040
Contig ID
5'-most EST
                   LIB3040-019-Q1-E1-F12
                   8622
Seq. No.
                   13452 1.R1040
Contig ID
                   LIB30\overline{4}0-019-Q1-E1-B8
5'-most EST
                   BLASTX
Method
                   g1914685
NCBI GI
                   352
BLAST score
E value
                   2.0e-33
                   74
Match length
% identity
                   89
                   (Y12014) RAD23 protein, isoform II [Daucus carota]
NCBI Description
                   8623
Seq. No.
                   13456 1.R1040
Contig ID
                   LIB3170-007-Q1-K1-B6
5'-most EST
                   8624
Seq. No.
                   13467 1.R1040
Contig ID
                   LIB3040-018-Q1-E1-H11
5'-most EST
                   8625
Seq. No.
                   13475 1.R1040
Contig ID
5'-most EST
                   LIB3065-003-Q1-N1-G12
                   8626
Seq. No.
                   13476 1.R1040
Contig ID
                   zhf700963568.h1
5'-most EST
Method
                   BLASTX
                   g4101589
NCBI GI
                   571
BLAST score
E value
                   1.0e-58
Match length
                   205
                   52
% identity
NCBI Description
                   (AF005050) aspartyl aminopeptidase [Homo sapiens]
                   8627
Seq. No.
                   13479 2.R1040
Contig ID
                   asn70\overline{1}133559.h2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g132964
BLAST score
                   212
                   9.0e-17
E value
Match length
                   52
% identity
                   73
NCBI Description
                   60S RIBOSOMAL PROTEIN L29 (P23) >gi_71376_pir__R6RT43
                   ribosomal protein RL43 - rat >gi_57145_emb_CAA43146_
                   (X60744) ribosomal protein [Rattus norvegicus]
                   >gi_312208_emb_CAA48344_ (X68283) rat ribosomal protein L29
                   [Rattus norvegicus]
                   8628
Seq. No.
Contig ID
                   13488 1.R1040
```

LIB3040-018-Q1-E1-F3

```
Seq. No.
                   8629
Contig ID
                   13489 1.R1040
5'-most EST
                   LIB3051-117-Q1-K1-F11
Method
                   BLASTX
NCBI GI
                   g1705678
BLAST score
                   1079
                   1.0e-161
E value
                   312
Match length
                   72
% identity
                   CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                   PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
                   valosin-containing protein [Glycine max]
Seq. No.
                   8630
                   13490 1.R1040
Contig ID
5'-most EST
                   gsv701054670.hl
                   8631
Seq. No.
                   13495 1.R1040
Contig ID
5'-most EST
                   LIB3040-018-Q1-E1-E5
Method
                   BLASTX
                   g3805765
NCBI GI
BLAST score
                   224
                   3.0e-18
E value
Match length
                   54
% identity
                   76
NCBI Description
                   (AC005693) putative protein kinase [Arabidopsis thaliana]
                   8632
Seq. No.
                   13498 1.R1040
Contig ID
                   smc70\overline{0}750158.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2501538
BLAST score
                   153
                   6.0e-10
E value
Match length
                   91
% identity
                   40
NCBI Description
                   HYPOTHETICAL 51.0 KD PROTEIN SLL0996
                   >gi_1652230_dbj_BAA17153_ (D90904) hypothetical protein
                   [Synechocystis sp.]
                   8633
Seq. No.
                   13500 1.R1040
Contig ID
5'-most EST
                   LIB3040-018-Q1-E1-C4
                   8634
Seq. No.
Contig ID
                   13501 1.R1040
5'-most EST
                   LIB3040-018-Q1-E1-C6
Method
                   BLASTX
NCBI GI
                   q3122853
BLAST score
                   383
                   1.0e-36
E value
Match length
                   250
% identity
                   WD-REPEAT PROTEIN SAZD >gi 1082863 pir A49367 transducin
NCBI Description
                   homolog sazD - human >gi_414536 (U\overline{0}260\overline{9}) transducin-like
```

protein [Homo sapiens]

NCBI GI

```
8635
Seq. No.
                   13512 1.R1040
Contig ID
                   LIB3170-005-Q1-J1-B3
5'-most EST
                   8636
Seq. No.
Contig ID
                   13514 1.R1040
                   LIB3049-051-Q1-E1-A9
5'-most EST
                   BLASTX
Method
                   g2135057
NCBI GI
BLAST score
                   416
                   2.0e-40
E value
                   226
Match length
                   41
% identity
                   EB1 - human >gi_998357 (U24166) EB1 [Homo sapiens]
NCBI Description
                   8637
Seq. No.
                   13520 1.R1040
Contig ID
                   LIB3170-006-Q1-J1-A1
5'-most EST
                   8638
Seq. No.
                   13524 1.R1040
Contig ID
                   LIB3139-075-P1-N1-G4
5'-most EST
                   8639
Seq. No.
                   13524 2.R1040
Contig ID
5'-most EST
                   LIB3051-117-Q1-K1-B9
                   8640
Seq. No.
                   13525 1.R1040
Contig ID
                   LIB3040-018-Q1-E1-B2
5'-most EST
                   8641
Seq. No.
                   13532 1.R1040
Contig ID
                   LIB30\overline{4}0-018-Q1-E1-A2
5'-most EST
                   8642
Seq. No.
Contig ID
                   13534 1.R1040
                   jC-gmle01810009a09a1
5'-most EST
                   8643
Seq. No.
                   13534 2.R1040
Contig ID
5'-most EST
                   LIB3040-017-Q1-E1-G10
                   8644
Seq. No.
                   13534 3.R1040
Contig ID
5'-most EST
                   LIB3092-044-Q1-K1-G11
                   8645
Seq. No.
                   13538 1.R1040
Contig ID
                   trc700566156.hl
5'-most EST
                   8646
Seq. No.
Contig ID
                   13547 1.R1040
                   g5677<del>6</del>07
5'-most EST
Method
                   BLASTX
```

g3935148

```
786
BLAST score
                   6.0e-84
E value
                   228
Match length
                   73
% identity
NCBI Description
                   (AC005106) T25N20.12 [Arabidopsis thaliana]
                   8647
Seq. No.
                   13551_1.R1040
Contig ID
                   LIB3170-061-Q1-J1-E1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3599418
BLAST score
                   63
E value
                   1.0e-26
Match length
                   80
                   95
% identity
NCBI Description
                   Glycine max alternative oxidase precursor (Aox1) gene,
                   nuclear gene encoding mitochondrial protein, complete cds
                   8648
Seq. No.
                   13558 1.R1040
Contig ID
5'-most EST
                   zsg701124685.h1
                   BLASTX
Method
NCBI GI
                   g4580466
BLAST score
                   372
E value
                   2.0e-35
Match length
                   100
% identity
                   74
                   (AC006081) putative 50S ribosomal protein L4 [Arabidopsis
NCBI Description
                   thaliana]
                   8649
Seq. No.
                   13558 2.R1040
Contig ID
                   LIB3040-017-Q1-E1-F2
5'-most EST
                   8650
Seq. No.
Contig ID
                   13575 1.R1040
5'-most EST
                   LIB3040-017-Q1-E1-D2
                   8651
Seq. No.
                   13577 1.R1040
Contig ID
5'-most EST
                   LIB3040-017-Q1-E1-D7
                   8652
Seq. No.
                   13579 1.R1040
Contig ID
5'-most EST
                   LIB3040-017-Q1-E1-C12
Method
                   BLASTX
NCBI GI
                   q3201610
BLAST score
                   323
E value
                   5.0e-30
                   70
Match length
```

170

Seq. No. 8653

% identity
NCBI Description

Contig ID 13583_1.R1040

5'-most EST LIB3170-002-Q1-K1-H8

Method BLASTX

(AC004669) unknown protein [Arabidopsis thaliana]

* j. j.

```
q2565436
NCBI GI
BLAST score
                   423
E value
                   2.0e-41
Match length
                   91
                   88
% identity
NCBI Description
                   (AF028842) DegP protease precursor [Arabidopsis thaliana]
Seq. No.
                   8654
                   13608 1.R1040
Contig ID
                   asn701135465.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2213595
BLAST score
                   481
                   5.0e-48
E value
                   219
Match length
                   44
% identity
                  (AC000348) T7N9.15 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8655
                   13608 2.R1040
Contig ID
5'-most EST
                  bth700849093.h1
Method
                  BLASTX
NCBI GI
                   g2213595
BLAST score
                   244
E value
                   4.0e-28
                   112
Match length
                   58
% identity
                   (AC000348) T7N9.15 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8656
                   13608 3.R1040
Contig ID
5'-most EST
                  pxt700944327.h1
Method
                  BLASTX
NCBI GI
                   g2190992
BLAST score
                   220
E value
                   3.0e-18
Match length
                   65
% identity
                   69
                   (AF004358) glutathione S-transferase TSI-1 [Aegilops
NCBI Description
                   tauschii]
Seq. No.
                   8657
                   13609 1.R1040
Contig ID
5'-most EST
                  rlr700895595.h1
Method
                  BLASTX
NCBI GI
                  q4006860
BLAST score
                   666
E value
                   8.0e-70
                  184
Match length
                   69
% identity
NCBI Description
                   (Z99707) thiol-disulfide interchange like protein
                   [Arabidopsis thaliana]
                  8658
Seq. No.
                  13616 1.R1040
Contig ID
```

LIB3170-003-Q1-J1-H12

NCBI Description

```
Seq. No.
                   8659
                   13620_1.R1040
Contig ID
                   LIB3073-019-Q1-K1-A5
5'-most EST
                   8660
Seq. No.
Contig ID
                   13620 2.R1040
                   zvp70\overline{0}764268.h1
5'-most EST
                   8661
Seq. No.
Contig ID
                   13622 1.R1040
5'-most EST
                   LIB3040-016-Q1-E1-F4
Method
                   BLASTX
NCBI GI
                   g542070
BLAST score
                   154
E value
                   4.0e-10
Match length
                   56
% identity
NCBI Description
                   cytochrome P450 77A1 - eggplant
                   8662
Seq. No.
                   13625 1.R1040
Contig ID
5'-most EST
                   LIB3170-001-Q1-J1-H2
Seq. No.
                   8663
Contig ID
                   13628 1.R1040
5'-most EST
                   jC-gmro02910070d03a1
                   BLASTX
Method
NCBI GI
                   g1084415
BLAST score
                   439
E value
                   5.0e-43
Match length
                   245
% identity
                   40
NCBI Description
                   RNA-binding protein - Wood tobacco >gi 624925 dbj BAA05170
                   (D26182) RNA-binding glycine rich protein (RGP-2)
                   [Nicotiana sylvestris]
                   8664
Seq. No.
Contig ID
                   13636 1.R1040
5'-most EST
                   uC-gmronoir016d01b1
Method
                   BLASTX
NCBI GI
                   g2832642
BLAST score
                   144
E value
                   1.0e-08
Match length
                   100
% identity
NCBI Description
                   (AL021710) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   13638 1.R1040
5'-most EST
                   leu701150379.h1
                   BLASTX
Method
                   g2213536
NCBI GI
BLAST score
                   650
E value
                   7.0e-68
Match length
                   206
% identity
                   66
                  (X98738) DNA-binding protein PD1 [Pisum sativum]
```

Seq. No. 8666

Contig ID 13639_1.R1040

5'-most EST LIB3170-003-Q1-K1-H7

Seq. No. 8667

Contig ID 13642 1.R1040

5'-most EST LIB3170-003-Q1-K1-H8

Seq. No. 8668

Contig ID 13652 1.R1040

5'-most EST LIB3040-015-Q1-E1-H9

Seq. No. 8669

Contig ID 13658 1.R1040

5'-most EST jC-gmf102220130c11a1

Method BLASTX
NCBI GI g1929998
BLAST score 295
E value 1.0e-26
Match length 101
% identity 58

NCBI Description (U77463) NADPH-dependent HC-toxin reductase [Hordeum

vulgare]

Seq. No. 8670

Contig ID 13666_1.R1040

5'-most EST LIB3170-028-Q1-K1-G7

Seq. No. 8671

Contig ID 13666 2.R1040

5'-most EST LIB3040-013-Q1-E1-F1

Seq. No. 8672

Contig ID 13666_3.R1040 5'-most EST kl1701211343.h1

Seq. No. 8673

Contig ID 13667 1.R1040

5'-most EST LIB3040-015-Q1-E1-F9

Method BLASTX
NCBI GI g3122873
BLAST score 239
E value 5.0e-20
Match length 103
% identity 44

NCBI Description TRANSCRIPTION INITIATION PROTEIN SPT4 HOMOLOG 1 >gi_1209779

(U43923) similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens]

ras potential N-terminal zinc-ringer [Homo sapiens]

>gi_1401053 (U38818) SUPT4H [Homo sapiens] >gi_1401055
(U38817) SUPT4H [Homo sapiens] >gi_1401066 (U43154) Supt4h
[Mus musculus] >gi_3779194 (U96809) chromatin structural

protein homolog [Mus musculus]

>gi 4507311 ref_NP_003159.1_pSUPT4H1_ suppressor of Ty

(S.cerevisiae) 4 homolog

Seq. No. 8674

Match length

134

```
Contig ID
                  13674 1.R1040
                  uaw700663720.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g544150
BLAST score
                  106
E value
                  1.0e-10
Match length
                  157
                  32
% identity
                  DEK PROTEIN >gi 284375 pir S26059 probable transforming
NCBI Description
                  protein (dek) - human >gi 30503 emb CAA45536 (X64229)
                  putative oncogene [Homo sapiens] >gi_4007163_emb_CAA21138_
                   (AL031774) dek (putative oncogene) [Homo sapiens]
                  >gi_4503249_ref_NP_003463.1_pD6S231E_ DEK gene
                  8675
Seq. No.
Contig ID
                  13674 2.R1040
5'-most EST
                  jC-gmle01810030d12d1
Seq. No.
                  8676
Contig ID
                  13676 1.R1040
5'-most EST
                  LIB3040-015-Q1-E1-D10
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  92
                  3-0e-44
E value
                  222
Match length
                  85
% identity
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
Contig ID
                  13681 1.R1040
5'-most EST
                  LIB3040-015-Q1-E1-D6
Seq. No.
                  8678
Contig ID
                  13684 1.R1040
5'-most EST
                  LIB3040-015-Q1-E1-D9
Seq. No.
                  8679
Contig ID
                  13686 1.R1040
5'-most EST
                  LIB3040-015-Q1-E1-E10
                  BLASTX
Method
NCBI GI
                  g2392769
BLAST score
                  281
E value
                  7.0e-25
                  94
Match length
% identity
NCBI Description
                  (AC002534) putative histone deacetylase [Arabidopsis
                  thaliana]
                  8680
Seq. No.
                  13687 1.R1040
Contig ID
5'-most EST
                  zhf700960830.h1
Method
                  BLASTX
NCBI GI
                  g3341685
BLAST score
                  403
E value
                  4.0e-39
```

```
% identity
                   64
                   (AC003672) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   13720_1.R1040
Contig ID
                   LIB3170-002-Q1-K1-G6
5'-most EST
Seq. No.
                   8682
                   13724 1.R1040
Contig ID
5'-most EST
                   qsv701047493.h1
                   BLASTX
Method
                                                  q170753
NCBI GI
BLAST score
                   753
E value
                   7.0e-80
                   185
Match length
% identity
                   74
                   (M95819) initiation factor (iso) 4F p28 subunit [Triticum
NCBI Description
                   aestivum]
Seq. No.
                   8683
                   13730 1.R1040
Contig ID
5'-most EST
                   LIB3049-002-Q1-E1-F10
Method
                   BLASTX
NCBI GI
                   g2262102
BLAST score
                   255
E value
                   2.0e-21
                   202
Match length
% identity
                   39
                   (AC002343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   8684
Seq. No.
                   13734 1.R1040
Contig ID
                   LIB3051-109-Q1-K1-G3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1174779
BLAST score
                   1918
E value
                   0.0e + 00
Match length
                   449
                   83
% identity
                   TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi 166894
NCBI Description
                   (M81620) tryptophan synthase beta-subunit [Arabidopsis
                   thaliana] >gi_4490703_emb_CAB38837.1 (AL035680) tryptophan
                   synthase beta-subunit (TSB2) [Arabidopsis thaliana]
Seq. No.
                   8685
                   13734 2.R1040
Contig ID
5'-most EST
                   ssr700560895.hl
                   BLASTX
Method
NCBI GI
                   g1174779
BLAST score
                   200
E value
                   8.0e-16
Match length
                   72
% identity
                  TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi_166894
NCBI Description
                   (M81620) tryptophan synthase beta-subunit [Arabidopsis
```

thaliana] >gi 4490703 emb CAB38837.1 (AL035680) tryptophan

synthase beta-subunit (TSB2) [Arabidopsis thaliana]

BLAST score

278

```
8686
Seq. No.
                  13736 1.R1040
Contig ID
5'-most EST
                  LIB3170-017-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  q1524370
BLAST score
                  526
E value
                  1.0e-66
Match length
                  191
                   65
% identity
NCBI Description
                  (X92491) TOM20 [Solanum tuberosum]
                  8687
Seq. No.
                   13750 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910060f05d1
                  8688
Seq. No.
Contig ID
                  13753 1.R1040
5'-most EST
                  LIB3040-014-Q1-E1-D9
Method
                  BLASTN
NCBI GI
                  q3599418
BLAST score
                  80
E value
                  8.0e-37
Match length
                  322
                  88
% identity
NCBI Description
                  Glycine max alternative oxidase precursor (Aox1) gene,
                  nuclear gene encoding mitochondrial protein, complete cds
                  8689
Seq. No.
                  13755 1.R1040
Contig ID
5'-most EST
                  qsf700698435.hl
                  BLASTN
Method
NCBI GI
                  q1063683
BLAST score
                  34
E value
                  2.0e-09
Match length
                  46
% identity
                  93
                  Arabidopsis thaliana glycine-rich protein (AtGRP2b) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  8690
Contig ID
                  13758 1.R1040
5'-most EST
                  LIB3073-005-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  q3510256
BLAST score
                  352
E value
                  5.0e-33
Match length
                  151
% identity
                  49
NCBI Description
                  (AC005310) unknown protein [Arabidopsis thaliana]
                  8691
Seq. No.
                  13758 2.R1040
Contig ID
5'-most EST
                  LIB3040-014-Q1-E1-E2
Method
                  BLASTX
NCBI GI
                  g3510256
```

Contig ID

```
E value
                   2.0e-24
Match length
                   103
                   56
% identity
NCBI Description
                  (AC005310) unknown protein [Arabidopsis thaliana]
                   8692
Seq. No.
                   13758 4.R1040
Contig ID
                   pcp700995143.hl
5'-most EST
                   BLASTX
Method
                   q3510256
NCBI GI
BLAST score
                   227
                   1.0e-18
E value
Match length
                   112
                   51
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                   8693
Seq. No.
                   13773 1.R1040
Contig ID
                   LIB3170-004-Q1-K1-G7
5'-most EST
                   8694
Seq. No.
                   13779 1.R1040
Contig ID
5'-most EST
                   asn70\overline{1}141901.h1
                   8695
Seq. No.
                   13780 1.R1040
Contig ID
5'-most EST
                   LIB3170-001-Q1-K1-F11
                   8696
Seq. No.
                   13781 1.R1040
Contig ID
5'-most EST
                   LIB3040-013-Q1-E1-F9
                   8697
Seq. No.
Contig ID
                   13785 1.R1040
                   LIB3138-075-P1-N1-B4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4218124
BLAST score
                   176
E value
                   1.0e-12
Match length
                   44
% identity
                   (AL035353) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   8698
Seq. No.
Contig ID
                   13786 1.R1040
5'-most EST
                   LIB3040-013-Q1-E1-H12
Method
                   BLASTN
NCBI GI
                   g1888556
BLAST score
                   175
E value
                   1.0e-93
Match length
                   295
                   90
% identity
                  Lupinus angustifolius diadenosine
NCBI Description
                   5',5'''-P1,P4-tetraphosphate hydrolase mRNA, complete cds
Seq. No.
```

13790 1.R1040

Match length

198

```
5'-most EST
                   jC-gmro02910074h12a1
Method
                   BLASTN
NCBI GI
                   g2345147
BLAST score
                   288
E value
                   1.0e-161
Match length
                   447
% identity
                   92
NCBI Description
                   Pisum sativum developmentally regulated GTP binding protein
                   (PsDRG1) mRNA, complete cds
                   8700
Seq. No.
Contig ID
                   13792 1.R1040
5'-most EST
                   LIB3170-002-Q1-K1-F9
                   8701
Seq. No.
                   13801 1.R1040
Contig ID
5'-most EST
                   eep70\overline{0}865294.h1
Method
                   BLASTX
NCBI GI
                   g4115377
BLAST score
                   1076
E value
                   1.0e-118
Match length
                   268
                   74
% identity
NCBI Description
                   (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                   8702
                   13812 1.R1040
Contig ID
5'-most EST
                   LIB3107-068-Q1-K1-A5
Method
                   BLASTN
NCBI GI
                   g343348
BLAST score
                   384
E value
                   0.0e + 00
Match length
                   450
% identity
                   98
NCBI Description
                   Glycine max mitochondrial DNA sequence, transcription
                   initiation motif
Seq. No.
                   8703
Contiq ID
                   13813 1.R1040
5'-most EST
                   vzy700754146.h1
Seq. No.
                   8704
                   13823 1.R1040
Contig ID
5'-most EST
                   LIB3170-009-Q1-J1-F9
Seq. No.
                   8705
                   13825 1.R1040
Contig ID
5'-most EST
                   fua701042577.h1
Seq. No.
                   8706
                   13827 1.R1040
Contig ID
5'-most EST
                  LIB3056-013-Q1-N1-G10
Method
                  BLASTX
NCBI GI
                   g2511590
BLAST score
                   928
E value
                   1.0e-100
```

```
% identity
NCBI Description
                   (Y13692) multicatalytic endopeptidase complex, proteasome
                   component, beta subunit [Arabidopsis thaliana] >gi 3421111
                   (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis
                   thaliana]
Seq. No.
                   8707
                   13828 1.R1040
Contig ID
                  jex70\overline{0}909345.h1
5'-most EST
Seq. No.
                   8708
                   13828 2.R1040
Contig ID
5'-most EST
                   jC-qmst02400032f03a1
                   8709
Seq. No.
                   13828 3.R1040
Contig ID
                   LIB3040-013-Q1-E1-D2
5'-most EST
Seq. No.
                   8710
                   13829 1.R1040
Contig ID
                   zhf70\overline{0}960810.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2673910
BLAST score
                   147
E value
                   5.0e-09
                   39
Match length
% identity
                   (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   13830 1.R1040
Contig ID
                   LIB3170-002-Q1-K1-F3
5'-most EST
Seq. No.
                   8712
                   13838 1.R1040
Contig ID
5'-most EST
                   rry700808304.h1
Method
                   BLASTX
NCBI GI
                   g3335366
BLAST score
                   270
E value
                   1.0e-23
Match length
                   91
% identity
                   (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                   8713
Seq. No.
                   13847 1.R1040
Contig ID
                   LIB3170-002-Q1-K1-F5
5'-most EST
                   8714
Seq. No.
                   13853 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400049g08a1
                   8715
Seq. No.
                   13853 2.R1040
Contig ID
5'-most EST
                   gsv701052150.hl
```

Seq. No.

NCBI GI .

ï., .

g4008441

```
Contig ID
                   13858 1.R1040
5'-most EST
                  LIB3040-012-Q1-E1-F5
Method
                  BLASTX
NCBI GI
                   g3142294
BLAST score
                  1676
                   0.0e + 00
E value
Match length
                   374
% identity
                   91
NCBI Description
                   (AC002411) Strong similarity to initiation factor eIF-2,
                   gb U37354 from S. pombe. ESTs gb T41979, gb N37284 and
                   gb N37529 come from this gene. [Arabidopsis thaliana]
                   8717
Seq. No.
                   13858 2.R1040
Contig ID
                   k1170\overline{1}205184.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2832707
BLAST score
                  227
E value
                   8.0e-19
Match length
                  56
                   84
% identity
NCBI Description
                   (AL021713) translation initiation factor eIF-2 gamma
                   chain-like protein [Arabidopsis thaliana]
Seq. No.
                   8718
                   13863 1.R1040
Contig ID
                   uC-qmflminsoy003c10b1
5'-most EST
Method
                  BLASTX
                  q4008441
NCBI GI
BLAST score
                   458
E value
                   2.0e-45
Match length
                  143
% identity
                   62
NCBI Description
                   (AL034488) predicted using Genefinder; cDNA EST yk433c6.3
                   comes from this gene; cDNA EST EMBL:D72601 comes from this
                   gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST
                  yk433c6.5 comes from this gene [Caenorhabditis elegans]
Seq. No.
                   8719
Contig ID
                   13863 2.R1040
5'-most EST
                  ckk70\overline{0}605883.h2
Method
                  BLASTX
NCBI GI
                  q4008441
BLAST score
                  212
E value
                   5.0e-28
Match length
                  100
% identity
                   (AL034488) predicted using Genefinder; cDNA EST yk433c6.3
NCBI Description
                  comes from this gene; cDNA EST EMBL: D72601 comes from this
                   gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST
                  yk433c6.5 comes from this gene [Caenorhabditis elegans]
                  8720
Seq. No.
                  13863 3.R1040
Contig ID
5'-most EST
                  LIB3051-002-Q1-E1-F4
Method
                  BLASTX
```

NCBI GI

BLAST score

```
BLAST score
                   340
                   6.0e-32
E value
Match length
                   105
                   62
% identity
                   (AL034488) predicted using Genefinder; cDNA EST yk433c6.3
NCBI Description
                   comes from this gene; cDNA EST EMBL: D72601 comes from this
                   gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST
                   yk433c6.5 comes from this gene [Caenorhabditis elegans]
                   8721
Seq. No.
                   13868 1.R1040
Contig ID
                   zzp700835456.h1
5'-most EST
                   8722
Seq. No.
                   13872 1.R1040
Contig ID
5'-most EST
                   g4313\overline{4}89
Seq. No.
                   8723
                   13872 2.R1040
Contig ID
5'-most EST
                   k1170\overline{1}207410.h1
Seq. No.
                   8724
                   13872 3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy194h08b1
Seq. No.
                   8725
                   13873 1.R1040
Contig ID
5'-most EST
                   LIB3040-012-Q1-E1-C1
Seq. No.
                   8726
                   13877 1.R1040
Contig ID
5'-most EST
                   LIB3040-012-Q1-E1-C5
Method
                   BLASTN
NCBI GI
                   g1150683
BLAST score
                   105
                   7.0e-52
E value
Match length
                   220
                   92
% identity
NCBI Description V.radiata atpB, rbcL and trnK genes
                   8727
Seq. No.
                   13884 1.R1040
Contig ID
5'-most EST
                   bth700843663.h1
Method
                   BLASTX
NCBI GI
                   g4539351
BLAST score
                   181
E value
                   2.0e-13
Match length
                   101
                   46
% identity
NCBI Description
                   (AL035539) putative protein [Arabidopsis thaliana]
                   8728
Seq. No.
                   13884 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910004e02a1
Method
                   BLASTX
```

g4539351

278

E value

3.0e - 39

```
1.0e-24
E value
Match length
                   107
                   61
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   8729
Seq. No.
Contig ID
                   13889 1.R1040
                  LIB3170-004-Q1-K1-F1
5'-most EST
                   8730
Seq. No.
                   13891 1.R1040
Contig ID
5'-most EST
                  LIB3040-011-Q1-E1-H5
Method
                  BLASTX
NCBI GI
                   g2245124
BLAST score
                  734
                   1.0e-77
E value
Match length
                  241
% identity
                   65
NCBI Description
                  (Z97343) protein kinase [Arabidopsis thaliana]
Seq. No.
                   8731
                   13891 3.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy008c09b1
Method
                  BLASTX
NCBI GI
                  q2245124
BLAST score
                  167
                   1.0e-11
E value
                  74
Match length
% identity
                   53
NCBI Description
                  (Z97343) protein kinase [Arabidopsis thaliana]
Seq. No.
                   8732
                   13900 1.R1040
Contig ID
5'-most EST
                  fde700876566.h1
Method
                  BLASTX
NCBI GI
                  q4522012
                  706
BLAST score
E value
                  2.0e-74
Match length
                  234
% identity
                   58
                  (AC007069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  8733
Seq. No.
                  13902 1.R1040
Contig ID
5'-most EST
                  LIB3170-002-Q1-K1-E3
                  8734
Seq. No.
                  13903 1.R1040
Contig ID
5'-most EST
                  LIB3170-001-Q1-K1-E4
                  8735
Seq. No.
                  13906 1.R1040
Contig ID
5'-most EST
                  asn701134208.hl
                  BLASTX
Method
NCBI GI
                  g349379
BLAST score
                  342
```

NCBI Description

thaliana]

```
Match length
                   134
% identity
                   65
NCBI Description
                   (L22847) HAHB-1 [Helianthus annuus]
                   8736
Seq. No.
                   13907 1.R1040
Contig ID
5'-most EST
                   LIB3170-002-Q1-K1-E5
Seq. No.
                   8737
                   13922 1.R1040
Contig ID
5'-most EST
                   LIB3040-011-Q1-E1-B3
                   8738
Seq. No.
                   13926 1.R1040
Contig ID
5'-most EST
                   LIB3040-011-Q1-E1-B8
                   8739
Seq. No.
                   13928 1.R1040
Contig ID
5'-most EST
                   LIB3170-002-Q1-K1-E2
                   8740
Seq. No.
                   13930 1.R1040
Contig ID
5'-most EST
                   leu701152715.h1
                   8741
Seq. No.
Contig ID
                   13931 1.R1040
                   LIB3074-019-Q1-E1-H1
5'-most EST
                   BLASTX
Method
                   q2407233
NCBI GI
BLAST score
                   280
E value
                   2.0e-24
Match length
                   101
% identity
                   48
                   (AF017750) similar to Haemophilus influenzae product
NCBI Description
                   encoded by Genbank Accession Number U32796 [Haemophilus
                   ducreyi]
                   8742
Seq. No.
                   13931 2.R1040
Contig ID
5'-most EST
                   jC-qmle01810043e07a1
Seq. No.
Contig ID
                   13931 4.R1040
5'-most EST
                   hrw701061635.h1
                   8744
Seq. No.
Contig ID
                   13935_1.R1040
5'-most EST
                   fC-gmse700671588a3
Method
                   BLASTX
NCBI GI
                   q2583129
BLAST score
                   1833
E value
                   0.0e + 00
Match length
                   394
% identity
```

(AC002387) putative methionine aminopeptidase [Arabidopsis

```
8745
Seq. No.
Contig ID
                  13936_1.R1040
                  LIB3049-034-Q1-E1-F3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4539457
BLAST score
                  327
                  4.0e-60
E value
                  278
Match length
% identity
                  53
NCBI Description
                   (AL049500) heat shock transcription factor-like protein
                   [Arabidopsis thaliana]
                  8746
Seq. No.
                  13936 2.R1040
Contig ID
                  LIB3093-034-Q1-K1-D8
5'-most EST
                  BLASTX
Method
                  g4539457
NCBI GI
BLAST score
                  600
E value
                   7.0e-62
Match length
                  237
                  57
% identity
NCBI Description
                   (AL049500) heat shock transcription factor-like protein
                   [Arabidopsis thaliana]
                  8747
Seq. No.
Contig ID
                  13937 1.R1040
5'-most EST
                  LIB3170-004-Q1-K1-E7
Method
                  BLASTX
                  g3873408
NCBI GI
                  200
BLAST score
                  3.0e-15
E value
Match length
                  90
                  41
% identity
                   (L76926) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  8748
Contig ID
                  13954 1.R1040
5'-most EST
                  jC-gmst02400074e06a1
                  8749
Seq. No.
                  13973 1.R1040
Contig ID
5'-most EST
                  LIB3170-001-Q1-K1-D8
Method
                  BLASTX
                              ...
NCBI GI
                  g2760323
BLAST score
                  1146
E value
                  1.0e-126
Match length
                  284
                  73
% identity
NCBI Description
                  (AC002130) F1N21.8 [Arabidopsis thaliana]
                  8750
Seq. No.
                  13974 1.R1040
Contig ID
5'-most EST
                  LIB3170-002-Q1-J1-D8
Seq. No.
                  8751
```

, e + 1s

13989 1.R1040

Contig ID

```
5'-most EST
                    LIB3170-003-Q1-J1-E2
 Method
                    BLASTN
                    g3599418
 NCBI GI
.BLAST score
                    104
 E value
                    7.0e-52
                    135
 Match length
                    94
 % identity
                    Glycine max alternative oxidase precursor (Aox1) gene,
 NCBI Description
                    nuclear gene encoding mitochondrial protein, complete cds
                    8752.
 Seq. No.
 Contig ID
                    14001 1.R1040
 5'-most EST
                    LIB3094-062-Q1-K1-C7
                    BLASTN
 Method
 NCBI GI
                    g2062691
 BLAST score
                    34
                    3.0e-09
 E value
                    34
 Match length
                    62
 % identity
                    Human sodium phosphate transporter (NPT4) mRNA, complete
 NCBI Description
                    8753
 Seq. No.
                    14001 2.R1040
 Contig ID
 5'-most EST
                    LIB3040-010-Q1-E1-A10
 Seq. No.
                    8754
 Contig ID
                    14004 1.R1040
                    LIB3170-001-Q1-J1-D4
 5'-most EST
                    8755
 Seq. No.
                    14013 1.R1040
 Contig ID
                    LIB3049-039-Q1-E1-D11
 5'-most EST
                    8756
 Seq. No.
                    14047_1.R1040
 Contig ID
 5'-most EST
                    LIB30\overline{5}0-024-Q1-K1-C5
Method
                    BLASTX
                    g3236242
 NCBI GI
 BLAST score
                    428
                    6.0e-42
 E value
 Match length
                    103
 % identity
                    84
                    (AC004684) putative ribosomal protein L36 [Arabidopsis
 NCBI Description
                    thaliana]
                    8757
 Seq. No.
 Contig ID
                    14047 2.R1040
 5'-most EST
                    LIB3093-027-Q1-K1-H11
 Method
                    BLASTX
 NCBI GI
                    g3236242
 BLAST score
                    407
 E value
                    1.0e-39
 Match length
                    99
                    83
 % identity
 NCBI Description
                    (AC004684) putative ribosomal protein L36 [Arabidopsis
```

thaliana]

```
8758
Seq. No.
                  14047 3.R1040
Contig ID
5'-most EST
                  LIB3049-049-Q1-E1-E6
Method
                  BLASTX
NCBI GI
                  q1710546
BLAST score
                  437
E value
                   4.0e-43
                  106
Match length
% identity
                   79
                  60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative
NCBI Description
                   ribosomal protein [Daucus carota]
                   8759
Seq. No.
                   14047 4.R1040
Contig ID
5'-most EST
                   vwf700675179.hl
                  BLASTX
Method
                  g1710546
NCBI GI
BLAST score
                   346
                   6.0e-33
E value
Match length
                  75
% identity
                  89
                  60S RIBOSOMAL PROTEIN L36 >gi 1276967 (U47095) putative
NCBI Description
                  ribosomal protein [Daucus carota]
Seq. No.
                   8760
Contig ID
                   14049 1.R1040
5'-most EST
                  LIB3040-009-Q1-E1-B11
                   8761
Seq. No.
                  14057 1.R1040
Contig ID
5'-most EST
                  LIB3040-009-Q1-E1-C5
                   8762
Seq. No.
                   14058 1.R1040
Contig ID
5'-most EST
                   eep70\overline{0}870490.h1
Method
                  BLASTX
NCBI GI
                  g1532168
BLAST score
                   251
E value
                   2.0e-21
Match length
                   66
% identity
                   73
NCBI Description
                   (U63815) localized according to blastn similarity to EST
                   sequences; therefore, the coding span corresponds only to
                  an area of similarity since the initation codon and stop
                  codon could not be precisely determined [Arabidopsis
                  thaliana]
Seq. No.
                   8763
                  14066 1.R1040
Contig ID
                  LIB3170-006-Q1-K1-H7
5'-most EST
Method
                  BLASTX
NCBI GI
                  a2829910
BLAST score
                   440
                   2.0e-43
E value
Match length
                  234
```

% identity

BLAST score

196

```
NCBI Description
                   (AC002291) Unknown protein, contains regulator of
                  chromosome condensation motifs [Arabidopsis thaliana]
                  8764
Seq. No.
                  14068 1.R1040
Contig ID
                  LIB3167-023-P4-K4-E8
5'-most EST
                  8765
Seq. No.
                  14076 1.R1040
Contig ID
                  ncj700988351.hl
5'-most EST
                  BLASTX
Method
                  g3342798
NCBI GI
                  453
BLAST score
                  7.0e-45
E value
Match length
                  132
% identity
                   (AF061240) glutamine cyclotransferase precursor [Carica
NCBI Description
                  papaya]
                  8766
Seq. No.
                  14076 2.R1040
Contig ID
5'-most EST
                  g5606901
Method
                  BLASTX
                  g3342798
NCBI GI
BLAST score
                  251
                   6.0e-27
E value
Match length
                  166
% identity
                   53
                   (AF061240) glutamine cyclotransferase precursor [Carica
NCBI Description
                  papaya]
                  8767
Seq. No.
                  14082 1.R1040
Contig ID
                  LIB3049-007-Q1-E1-E9
5'-most EST
                  8768
Seq. No.
                   14082 2.R1040
Contig ID
5'-most EST
                  LIB3040-008-Q1-E1-F5
                  8769
Seq. No.
                  14086 1.R1040
Contig ID
                  LIB3049-009-Q1-E1-F4
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3881507
BLAST score
                   461
                   2.0e-45
E value
                  147
Match length
% identity
                   (Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST
NCBI Description
                  yk375c3.3 comes from this gene [Caenorhabditis elegans]
                  8770
Seq. No.
                   14086 2.R1040
Contig ID
5'-most EST
                   gsv701046761.hl
                  BLASTX
Method
                  g3881507
NCBI GI
```

```
٠. ـ
E value
                   5.0e-15
                   53
Match length
                   60
% identity
                   (Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST
NCBI Description
                   yk375c3.3 comes from this gene [Caenorhabditis elegans]
                   8771
Seq. No.
                   14092 1.R1040
Contig ID
                   LIB3170-039-Q1-K2-F2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2924520
BLAST score
                   754
E value
                   6.0e-80
                   273
Match length
                   82
% identity
NCBI Description
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
                   [Arabidopsis thaliana]
Seq. No.
                   8772
                   14096 1.R1040
Contig ID
5'-most EST
                   LIB31\overline{0}6-067-P1-K1-C6
Method
                   BLASTX
                   q2618688
NCBI GI
                   430
BLAST score
E value
                   2.0e-42
                   99
Match length
% identity
                   77
                   (AC002510) putative esterase D [Arabidopsis thaliana]
NCBI Description
                   8773
Seq. No.
                   14104 1.R1040
Contig ID
5'-most EST
                   gsv701049590.hl
Method
                   BLASTX
NCBI GI
                   g2194132
BLAST score
                   485
                   7.0e-49
E value
Match length
                   156
% identity
                   (AC002062) No definition line found [Arabidopsis thaliana]
NCBI Description
                   8774
Seq. No.
                   14105 1.R1040
Contig ID
5'-most EST
                   pxt700945486.h1
                   BLASTX
Method
                   g4314389
NCBI GI
BLAST score
                   326
E value
                   3.0e-30
Match length
                   91
                   68
% identity
NCBI Description
                   (AC006232) putative transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   8775
                   14114 1.R1040
Contig ID
                   LIB3170-002-Q1-K1-C4
5'-most EST
```

Seq. No.

NCBI GI

```
Contig ID
                   14116 1.R1040
                   LIB30\overline{5}1-067-Q1-K1-B5
5'-most EST
Method
                   BLASTN
                   g2351065
NCBI GI
BLAST score
                   43
E value
                   1.0e-14
                   130
Match length
                   74
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MHF15, complete sequence [Arabidopsis thaliana]
                   8777
Seq. No.
                   14120 1.R1040
Contig ID
                   LIB3107-017-Q1-K1-C12
5'-most EST
                   8778
Seq. No.
Contig ID
                   14120 2.R1040
5'-most EST
                   q4307297
Method
                   BLASTX
NCBI GI
                   q1938549
BLAST score
                   203
                   1.0e-15
E value
Match length
                   122
                   42
% identity
                   (U97016) similar to drosophila Rlc1 gene product
NCBI Description
                   (NID:g563361) and S. cerevisiae mitochondrial 60S ribosomal \cdot
                   protein L4 (YML4) (NID:g459259) [Caenorhabditis elegans]
                   8779
Seq. No.
                   14122 1.R1040
Contig ID
                   jC-qmro02910011b12a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2583120
BLAST score
                   262
                   2.0e-40
E value
Match length
                   143
                   47
% identity
NCBI Description
                   (AC002387) putative receptor-like protein kinase
                   [Arabidopsis thaliana]
                   8780
Seq. No.
Contig ID
                   14128 1.R1040
                   LIB3049-032-Q1-E1-D9
5'-most EST
                   8781
Seq. No.
                   14137 1.R1040
Contig ID
5'-most EST
                   LIB3040-008-Q1-E1-A2
                   8782
Seq. No.
                   14137 2.R1040
Contig ID
                   LIB3106-105-Q1-K1-E2
5'-most EST
                   8783
Seq. No.
                   14146 1.R1040
Contig ID
                   LIB3049-025-Q1-E1-B1
5'-most EST
                   BLASTX
Method
```

g3184100

```
270
BLAST score
                  2.0e-23
E value
Match length
                  72
% identity
                  67
                  (AL023777) rna binding protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                  8784
                  14146 2.R1040
Contig ID
                  asn701142530.h1
5'-most EST
                  8785
Seq. No.
                  14164 1.R1040
Contig ID
5'-most EST
                  LIB3040-007-Q1-E1-A8
                  BLASTX
Method
                  g3269289
NCBI GI
BLAST score
                  371
E value
                  2.0e-35
Match length
                  112
% identity
                  66
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                  8786
                  14164 2.R1040
Contig ID
5'-most EST
                  zsg701123057.hl
Method
                  BLASTX
                  q3269289
NCBI GI
BLAST score
                  369
                  3.0e-35
E value
Match length
                  137
% identity
                   69
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                  8787
Seq. No.
                   14174 1.R1040
Contig ID
5'-most EST
                  LIB3073-026-Q1-K1-G11
                  8788
Seq. No.
                   14174 2.R1040
Contig ID
5'-most EST
                  LIB3170-004-Q1-K1-C1
Seq. No.
                  8789
                   14176 1.R1040
Contig ID
5'-most EST
                  LIB3170-003-Q1-K1-C1
Seq. No.
                  8790
Contig ID
                   14204 1.R1040
5'-most EST
                   zpv700760194.hl
Method
                  BLASTX
NCBI GI
                  q3367536
BLAST score
                  521
E value
                   7.0e-53
Match length
                  117
% identity
NCBI Description
                   (AC004392) Contains similarity to symbiosis-related like
                  protein F1N20.80 gi_2961343 from A. thaliana BAC
```

[Arabidopsis thaliana]

gb AL022140. EST gb T04695 comes from this gene.

```
Seq. No.
                  8791
Contig ID
                  14204 2.R1040
5'-most EST
                  LIB3109-050-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q3367536
BLAST score
                  520
E value
                  6.0e-53
Match length
                  117
                  88
% identity
NCBI Description
                   (AC004392) Contains similarity to symbiosis-related like
                  protein F1N20.80 gi_2961343 from A. thaliana BAC
                  gb_AL022140. EST gb_T04695 comes from this gene.
                   [Arabidopsis thaliana]
                  8792
Seq. No.
                  14204 3.R1040
Contig ID
                  epx701109088.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3367536
BLAST score
                  316
E value
                  4.0e-29
Match length
                  85
                  79
% identity
NCBI Description
                   (AC004392) Contains similarity to symbiosis-related like
                  protein F1N20.80 gi_2961343 from A. thaliana BAC.
                  gb AL022140. EST gb T04695 comes from this gene.
                   [Arabidopsis thaliana]
                  8793
Seq. No.
                  14205 1.R1040
Contig ID
5'-most EST
                  LIB3170-004-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2708743
BLAST score
                  222
                  4.0e-18
E value
Match length
                  142
% identity
NCBI Description
                   (AC003952) putative Tal-1-like reverse transcriptase
                   [Arabidopsis thaliana]
                  8794
Seq. No.
Contig ID
                  14212 1.R1040
5'-most EST
                  LIB3040-006-Q1-E1-F7
                  8795
Seq. No.
Contig ID
                  14215 1.R1040
5'-most EST
                  zzp700831774.hl
Method
                  BLASTX
NCBI GI
                  g4510386
BLAST score
                  550
E value
                  4.0e-56
Match length
                  161
% identity
NCBI Description
                   (AC007017) unknown protein [Arabidopsis thaliana]
```

Seq. No.

```
14215 2.R1040
Contig ID
5'-most EST
                   LIB3170-002-Q1-K1-A10
Method
                   BLASTX
                                                             144
NCBI GI
                   g4510387
BLAST score
                   396
                   2.0e-38
E value
Match length
                   122
                   62
% identity
NCBI Description
                   (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                   8797
                   14218 1.R1040
Contig ID
5'-most EST
                   LIB3040-006-Q1-E1-C1
Seq. No.
                   8798
                   14224 1.R1040
Contig ID
                   LIB3139-052-P1-N1-A5
5'-most EST
                   8799
Seq. No.
Contig ID
                   14227 1.R1040
                   LIB3040-006-Q1-E1-D12
5'-most EST
                   8800
Seq. No.
                   14230 1.R1040
Contig ID
                   LIB30\overline{4}0-005-Q1-E1-H5
5'-most EST
                   BLASTX
Method ·
                   g3377813
NCBI GI
BLAST score
                   328
E value
                   3.0e-30
Match length
                   150
                   49
% identity
                   (AF076275) No definition line found [Arabidopsis thaliana]
NCBI Description
                   8801
Seq. No.
                   14231 1.R1040
Contig ID
5'-most EST
                   zhf700953828.h1
                   BLASTX
Method
                   g3063442
NCBI GI
BLAST score
                   181
                   6.0e-13
E value
                   84
Match length
% identity
NCBI Description
                   (AC003981) F22013.6 [Arabidopsis thaliana]
                   8802
Seq. No.
                   14233_1.R1040
Contig ID
                   LIB3040-005-Q1-E1-H9
5'-most EST
Method
                   BLASTX
NCBÍ GI
                   g3377813
BLAST score
                   426
E value
                   1.0e-41
                   202
Match length
                   47
% identity
                   (AF076275) No definition line found [Arabidopsis thaliana]
NCBI Description
```

14240 1.R1040

Seq. No.

Contig ID

Seq. No.

```
pmv700889748.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4455754
                                                                     3000
BLAST score
                  164
                   6.0e-11
E value
                  160
Match length
                  28
% identity
                   (AL035478) hypothetical protein SC2G5.30 [Streptomyces
NCBI Description
                   coelicolor]
                  8804
Seq. No.
                   14242 1.R1040
Contig ID
                   jC-gmro02910025g01d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4220485
BLAST score
                   455
                   4.0e-45
E value
Match length
                   139
                   64
% identity
                   (AC006069) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
                   8805
Seq. No.
                   14245 1.R1040
Contig ID
                   LIB3170-002-Q1-K1-A11
5'-most EST
                   8806
Seq. No.
Contig ID
                   14251 1.R1040
                   jC-gmst02400071e04a1
5'-most EST
Method
                   BLASTX
                   q4006827
NCBI GI
BLAST score
                   686
                   2.0e-72
E value
Match length
                   182
                   71
% identity
                   (AC005970) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                   8807
Seq. No.
Contig ID
                   14252 1.R1040
                   LIB3051-037-Q1-K1-C6
5'-most EST
Method
                   BLASTN
                   g3821780
NCBI GI
                   37
BLAST score
                   5.0e-11
E value
Match length
                   37
                   100
% identity
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   8808
Seq. No.
                   14252 2.R1040
Contig ID
                   LIB3040-005-Q1-E1-F9
5'-most EST
                   8809
Seq. No.
                   14282 1.R1040
Contig ID
                   LIB3040-005-Q1-E1-A12
5'-most EST
                   8810
```

```
14283 1.R1040
                                                                       8
Contig ID
5'-most EST
                  LIB3170-003-Q1-K1-A1
                  BLASTX
Method
NCBI GI
                  g3645899
BLAST score
                  173
                  1.0e-12
E value
Match length
                  60
% identity
                  58
NCBI Description (U68408) 5' end not determined experimentally [Zea mays]
                  8811
Seq. No.
Contig ID
                  14299 1.R1040
5'-most EST
                  txt700733446.h1
                  8812
Seq. No.
                  14300 1.R1040
Contig ID
5'-most EST
                  LIB3170-018-Q1-K1-G10
Seq. No.
                  8813
                  14302 1.R1040
Contig ID
                  LIB3170-086-Q1-J1-B7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2739387
BLAST score
                  225
E value
                  4.0e-18
Match length
                  116
                  43
% identity
NCBI Description
                  (AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  8814
                  14306 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220094a10a1
Method
                  BLASTX
NCBI GI
                  q1173121
BLAST score
                  217
                  4.0e-17
E value
Match length
                  116
% identity
NCBI Description
                  ATP-DEPENDENT RNA HELICASE ROK1 >gi_2131186_pir__S59649
                  ATP-dependent RNA helicase ROK1 - yeast (Saccharomyces
                  cerevisiae) >gi_607182_emb_CAA84384_ (Z34901) ATP-dependent
                  RNA helicase [Saccharomyces cerevisiae]
                  >gi_971382_emb_CAA59758_ (X85757) putative ATP dependent
                  RNA helicase [Saccharomyces cerevisiae]
                  >gi 1322774 emb CAA96883 (Z72693) ORF YGL171w
                  [Saccharomyces cerevisiae]
                  8815
Seq. No.
                  14313 1.R1040
Contig ID
5'-most EST
                  LIB3040-004-Q1-E1-G11
Method
                  BLASTN
NCBI GI
                  q2398828
BLAST score
                  76
E value
                  2.0e-34
Match length
                  184
% identity
NCBI Description
                  Solanum tuberosum mRNA for mitochondrial uncoupling protein
```

Seq. No.

Contig ID

8821

14326 3.R1040

```
Seq. No.
                  8816
                  14322 1.R1040
Contig ID
                  vzy700754492.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3881978
BLAST score
                  1322
E value
                  1.0e-146
                  324
Match length
% identity
                  81
NCBI Description (Y11348) annexin-like protein [Medicago sativa]
Seq. No.
                  8817
                  14322 2.R1040
Contig ID
                  LIB30\overline{5}1-116-Q1-K1-F3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3881978
                  432
BLAST score
                  1.0e-42
E value
                  110
Match length
                  33
% identity
                  (Y11348) annexin-like protein [Medicago sativa]
NCBI Description
Seq. No.
                  8818
                  14323 1.R1040
Contig ID
5'-most EST
                  LIB3107-044-Q1-K1-D3
                  8819
Seq. No.
Contig ID
                  14326 1.R1040
5'-most EST
                  uC-gmflminsoy070e10b1
Method
                  BLASTX
NCBI GI
                  g2492668
                  275
BLAST score
E value
                  4.0e-24
Match length
                  176
% identity
                  ACTIN >gi 1419540 emb CAA67388 (X98885) beta-actin [Fucus
NCBI Description
                  vesiculosus]
                  8820
Seq. No.
Contig ID
                  14326 2.R1040
5'-most EST
                  LIB3107-009-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g728795
BLAST score
                  187
E value
                  1.0e-13
                  90
Match length
% identity
                  CENTRACTIN (ACTIN-LIKE PROTEIN) >gi 626122 pir S48973
NCBI Description
                  centractin ACT3 - yeast (Saccharomyces cerevisiae)
                  >gi_500679 (U10398) Arplp: Actin-related protein, of the
                  dynactin complex [Saccharomyces cerevisiae]
                  >gi 557670 emb CAA56206 (X79811) centractin [Saccharomyces
                  cerevisiae]
```

Contig ID

5'-most EST

```
5'-most EST
                   LIB3107-034-Q1-K1-H6
Seq. No.
                   8822
                   14326 5.R1040
Contig ID
                   sat701010945.hl
5'-most EST
Seq. No.
                   8823
                   14342 1.R1040
Contig ID
                   jC-qmst02400042h11a1
5'-most EST
Method
                   BLASTX
                   q2388913
NCBI GI
BLAST score
                   141
                   1.0e-08
E value
Match length
                   104
% identity
                   42
NCBI Description
                   (Z98974) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
Contig ID
                   14344 1.R1040
5'-most EST
                   LIB3170-020-Q1-J1-G12
Seq. No.
                   8825
Contig ID
                   14351 1.R1040
5'-most EST
                   uC-gmropic083h01b1
Method
                   BLASTX
NCBI GI
                   q4544453
BLAST score
                   376
E value
                   4.0e-36
Match length
                   105
% identity
NCBI Description
                  (AC006592) hypothetical protein [Arabidopsis thaliana]
                   8826
Seq. No.
Contig ID
                   14351 2.R1040
5'-most EST
                   LIB3170-019-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   g4544453
BLAST score
                   280
E value
                   1.0e-31
Match length
                  89
% identity
                   81
NCBI Description
                  (AC006592) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   8827
Contig ID
                   14357 1.R1040
5'-most EST
                  kl1701209107.hl
Method
                  BLASTX
NCBI GI
                   g4521249
BLAST score
                   468
E value
                   2.0e-46
Match length
                  268
% identity
NCBI Description
                   (AB013912) DNA helicase [Mus musculus]
                  8828
Seq. No.
                  14358 1.R1040
```

LIB3040-004-Q1-E1-A1

```
8829
Seq. No.
Contig ID
                  14359 1.R1040
                  LIB3040-004-Q1-E1-A11
5'-most EST
Method
                  BLASTX
                  q3980034
NCBI GI
BLAST score
                  286
                  2.0e-25
E value
                  81
Match length
                   65
% identity
                   (AL033514) predicted using Genefinder; cDNA EST EMBL:D71127
NCBI Description
                   comes from this gene; cDNA EST EMBL:D73731 comes from this
                  gene [Caenorhabditis elegans]
Seq. No.
                   8830
                   14362 1.R1040
Contig ID
                   zhf70\overline{0}959092.h1
5'-most EST
                   8831
Seq. No.
                   14377 1.R1040
Contig ID
                   uC-qmrominsoy203b10b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455224
BLAST score
                   357
E value
                   2.0e-37
Match length
                  188
                   46
% identity
                   (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8832
                   14382 1.R1040
Contig ID
                   LIB3040-003-Q1-E1-G4
5'-most EST
Seq. No.
                   8833
                   14386 1.R1040
Contig ID
                   ncj700985656.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2257503
BLAST score
                   437
E value
                   8.0e-43
Match length
                   272
% identity
                   (AB004535) BEM46 PROTEIN [Schizosaccharomyces pombe]
NCBI Description
                   8834
Seq. No.
                   14386 2.R1040
Contiq ID
                   k1170\overline{1}213588.h1
5'-most EST
                   8835
Seq. No.
                   14387 1.R1040
Contig ID
                   LIB3040-003-Q1-E1-D1
5'-most EST
                   8836
Seq. No.
                   14398 1.R1040
Contig ID
                   LIB3170-079-Q1-J1-G1
5'-most EST
```

Seq. No.

```
Contig ID
                   14398 2.R1040
5'-most EST
                   LIB3170-020-Q1-J1-G3
Seq. No.
                   8838
                   14398 3.R1040
Contig ID
                   jex700903540.hl
5'-most EST
Seq. No.
                   8839
                   14409 1.R1040
Contig ID
                   eep70\overline{0}867225.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2649424
BLAST score
                   143
                   7.0e-09
E value
Match length
                   100
% identity
NCBI Description
                   (AE001023) A. fulgidus predicted coding region AF1178
                   [Archaeoglobus fulgidus]
Seq. No.
                   8840
Contig ID
                   14410 1.R1040
5'-most EST
                   jC-qmle01810041c03a1
Seq. No.
Contig ID
                   14414 1.R1040
5'-most EST.
                   LIB3107-005-Q1-K1-G11
Seq. No.
                   8842
Contiq ID
                   14419 1.R1040
5'-most EST
                   fde700872835.h1
Method
                   BLASTX
NCBI GI
                   q585322
BLAST score
                   231
E value
                   5.0e-19
Match length
                   84
% identity
NCBI Description
                   INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE)
                   (PPASE) >gi 539751 pir A45153 inorganic pyrophosphatase
                   (EC 3.6.1.1) - bovine
Seq. No.
                   8843
                   14419 3.R1040
Contig ID
5'-most EST
                   ssr700556335.hl
Seq. No.
                   8844
                   14425 1.R1040
Contig ID
5'-most EST
                   LIB3040-002-Q1-E1-H3
                   8845
Seq. No.
Contig ID
                   14427 1.R1040
5'-most EST
                   LIB30\overline{4}0-002-Q1-E1-H7
                   8846
Seq. No.
                   14432 1.R1040
Contig ID
                   LIB3040-003-Q1-E1-A2
5'-most EST
Method
                   BLASTX
```

q4325354

NCBI GI

```
BLAST score
                  244
E value
                  7.0e-25
                  96
Match length
% identity
NCBI Description
                  (AF128395) contains similarity to retrovirus-related
                  polyproteins and to CCHC zinc finger protein (Pfam:
                  PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]
                  8847
Seq. No.
Contig ID
                  14434 1.R1040
5'-most EST
                  LIB3040-002-Q1-E1-E7
Seq. No.
                  8848
                  14437 1.R1040
Contig ID
5'-most EST
                  LIB3170-020-Q1-J1-F8
Seq. No.
                  8849
                  14447 1.R1040
Contig ID
5'-most EST
                  LIB3040-002-Q1-E1-G11
                  8850
Seq. No.
                  14450 1.R1040
Contig ID
                  LIB3040-002-Q1-E1-C6
5'-most EST
Method
                  BLASTX
                  q2947062
NCBI GI
BLAST score
                  248
                  7.0e-21
E value
                  168
Match length
% identity
                  42
NCBI Description
                  (AC002521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  8851
                  14457 1.R1040
Contig ID
5'-most EST
                  LIB3170-079-01-K1-D10
Method
                  BLASTX
NCBI GI
                  q2134723
BLAST score
                  275
                  1.0e-23
E value
                  191
Match length
% identity
                  AlkB homolog protein ABH - human >gi 1237210 emb CAA63047
NCBI Description
                  (X91992) alkB homolog protein [Homo sapiens]
                  >gi_1588535_prf__2208455A ABH gene [Homo sapiens]
                  8852
Seq. No.
Contig ID
                  14458 1.R1040
5'-most EST
                  LIB3040-002-Q1-E1-D8
                  BLASTX
Method
NCBI GI
                  q466044
BLAST score
                  153
E value
                  3.0e-15
Match length
                  146
% identity
                  35
                  HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III
NCBI Description
                  >qi 630780 pir S44909 ZK686.4 protein - Caenorhabditis
                  elegans >gi 304346 (L17337) coded for by C. elegans cDNAs
```

GenBank: M88869 and T01933; putative [Caenorhabditis

```
elegans]
Seq. No.
                   8853
                   14463 1.R1040
Contig ID
                   uC-gmronoir013f02b1
5'-most EST
                   BLASTX
Method
                   q3024652
NCBI GI
                   195
BLAST score
                   1.0e-14
E value
                   155
Match length
% identity
                   36
                   SORCIN >gi_1655733 (U39069) sorcin [Schistosoma japonicum]
NCBI Description
                   8854
Seq. No.
                   14463 3.R1040
Contig ID
5'-most EST
                   leu701144523.h1
                   8855
Seq. No.
                   14467 1.R1040
Contig ID
                   LIB3040-002-Q1-E1-B10
5'-most EST
                   8856
Seq. No.
Contig ID
                   14469 1.R1040
5'-most EST
                   jC-gmro02910034b12a1
Method
                   BLASTN
NCBI GI
                   g3819163
BLAST score
                   586
E value
                   0.0e + 00
Match length
                   638
                   98
% identity
                   Glycine max cctd gene
NCBI Description
                   8857
Seq. No.
Contig ID
                   14476 1.R1040
5'-most EST
                   LIB3040-002-Q1-E1-B8
Method
                   BLASTX
NCBI GI
                   q3024666
BLAST score
                   196
E value
                   4.0e-15
                   90
Match length
% identity
                   46
                   STRICTOSIDINE SYNTHASE 1/2 PRECURSOR >gi 1754983 (U43713)
NCBI Description
                   strictosidine synthase [Arabidopsis thaliana] >qi 1754985
                   (U43945) strictosidine synthase [Arabidopsis thaliana]
                   8858
Seq. No.
                   14481 1.R1040
Contig ID
5'-most EST
                   r1r70\overline{0}901879.h1
                   8859
Seq. No.
Contig ID
                   14481 2.R1040
5'-most EST
                   sat701002952.hl
                   8860
Seq. No.
                   14483 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220077f06a1
```

BLASTX

Method

NCBI Description

```
NCBI GI
                    g2804280
BLAST score
                    497
 E value
                    3.0e-50
Match length
                    133
                    66
 % identity
 NCBI Description
                    (AB003687) 6-4 photolyase [Arabidopsis thaliana]
                    >gi_3929918_dbj_BAA34711_ (AB017331) 6-4 photolyase
                    [Arabidopsis thaliana]
                    8861
 Seq. No.
                    14492 1.R1040
 Contig ID
                    LIB3138-002-Q1-N1-E2
 5'-most EST
Method
                    BLASTN
 NCBI GI
                    g2924257
                    191
 BLAST score
                    1.0e-102
 E value
Match length
                    739
 % identity
                    86
NCBI Description
                    Tobacco chloroplast genome DNA
                    8862
 Seq. No.
                    14492 2.R1040
 Contig ID
 5'-most EST
                    LIB3109-001-Q1-K1-A6
                    BLASTN
Method
NCBI GI
                    g2924257
                                                         4°= --
 BLAST score
                    82
                    7.0e-38
 E value
                    375
Match length
                    85
 % identity
                   Tobacco chloroplast genome DNA
 NCBI Description
                    8863
 Seq. No.
                    14497_1.R1040
Contig ID
                    LIB3040-002-Q1-E1-A3
 5'-most EST
                    BLASTX
Method
NCBI GI
                    g3327269
BLAST score
                    172
                    3.0e-12
 E value
Match length
                    99
                    49
 % identity
NCBI Description
                    (AB015999) PKn1 [Ipomoea nil]
 Seq. No.
                    8864
                    14509 1.R1040
 Contig ID
                    LIB3170-018-Q1-J1-E4
 5'-most EST
Seq. No.
                    8865
                    14512_1.R1040
Contig ID
 5'-most EST
                    zsq70\overline{1}119070.h1
Method
                    BLASTX
NCBI GI
                    g4567312
BLAST score
                    325
E value
                    1.0e-29
Match length
                    221
 % identity
                    44
```

(AC005956) hypothetical protein [Arabidopsis thaliana]

NCBI GI

```
Seq. No.
                  8866
Contig ID
                  14512 2.R1040
5'-most EST
                  LIB3051-090-Q1-K1-D3
Seq. No.
                  8867
Contig ID
                  14516 1.R1040
5'-most EST
                  LIB3087-010-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  q2181184
BLAST score
                  672
E value
                  1.0e-70
Match length
                  180
% identity
                  72
NCBI Description
                  (Y13577) JR3 protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                  14524 1.R1040
5'-most EST
                  LIB3040-001-Q1-E1-C7
Seq. No.
Contig ID
                  14526 1.R1040
                  LIB3170-013-Q1-J1-E9
5'-most EST
Seq. No.
Contig ID
                  14526 2.R1040
5'-most EST
                  LIB3170-019-Q1-J1-E10
                  8871
Seq. No.
Contig ID
                  14528 1.R1040
5'-most EST
                  LIB3040-001-Q1-E1-D7
                  8872
Seq. No.
Contig ID
                  14534 2.R1040
5'-most EST
                  LIB3040-001-01-E1-E2
                  8873
Seq. No.
Contig ID
                  14538 1.R1040
5'-most EST
                  uC-gmropic064c03b1
Method
                  BLASTX
NCBI GI
                  g2492825
BLAST score
                  615
E value
                  2.0e-63
Match length
                  364
                  38
% identity
NCBI Description
                  N-CARBAMYL-L-AMINO ACID AMIDOHYDROLASE
                  >gi 538915 pir JN0885 N-carbamyl-L-amino acid
                  amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus
                  (strain NS1122A) >gi 460895 bbs 141971 (S67784)
                  N-carbamyl-L-amino acid amidohydrolase [Bacillus
                  stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus
                  stearothermophilus]
Seq. No.
                  8874
                  14538 2.R1040
Contig ID
5'-most EST
                  asn701134260.hl
Method
                  BLASTX
                  g3249039
```

5'-most EST

```
BLAST score
                   250
E value
                   4.0e-21
Match length
                   132
% identity
                   (AF071221) N-carbamyl-L-amino acid amidohydrolase
NCBI Description
                   [Arthrobacter aurescens]
Seq. No.
                   8875
                   14539 1.R1040
Contig ID
                   kmv700739010.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4531443
BLAST score
                   954
                   1.0e-103
E value
Match length
                   264
                   73
% identity
NCBI Description
                   (AC006224) putative 50s ribosomal protein L3 [Arabidopsis
                   thaliana]
                   8876
Seq. No.
Contig ID
                   14539 2.R1040
5'-most EST
                   LIB3049-051-Q1-E1-H5
                   BLASTX
Method
NCBI GI
                   g4531443
BLAST score
                   383
                   5.0e-37
E value
                   127
Match length
% identity
                   (AC006224) putative 50s ribosomal protein L3 [Arabidopsis
NCBI Description
                   thaliana]
                   8877
Seq. No.
Contig ID
                   14540 1.R1040
5'-most EST
                   LIB3049-047-Q1-E1-B2
Seq. No.
Contig ID
                   14540 2.R1040
5'-most EST
                   leu70\overline{1}157315.h1
Seq. No.
                   8879
                   14553 1.R1040
Contig ID
5'-most EST
                   LIB3073-004-Q1-K1-H7
                   BLASTN
Method
NCBI GI
                   g11570
BLAST score
                   139
                   3.0e-72
E value
Match length
                   155
% identity
                   Soybean chloroplast DNA for ribosomal protein L20
NCBI Description
                   8880
Seq. No.
Contig ID
                   14586 1.R1040
5'-most EST
                   LIB3170-078-Q1-J1-A2
                   8881
Seq. No.
Contig ID
                   14605 1.R1040
```

LIB3040-024-Q1-E1-C1

```
Method
                   BLASTN
NCBI GI
                   g1139584
BLAST score
                   189
                   1.0e-102
E value
Match length
                   341
                   89
% identity
NCBI Description
                   Lupinus albus tRNA nucleotidyltransferase (CCA1) mRNA,
                   complete cds
                   8882
Seq. No.
                   14608 1.R1040
Contig ID
5'-most EST
                   LIB3072-018-Q1-E1-B1
Method
                   BLASTX
NCBI GI
                   g3551257
BLAST score
                   536
E value
                   1.0e-54
Match length
                   178
% identity
                   32
NCBI Description
                   (AB012708) 98b [Daucus carota]
                   8883
Seq. No.
                   14608 2.R1040
Contig ID
5'-most EST
                   leu701146919.hl
Method
                   BLASTX
NCBI GI
                   g3551257
BLAST score
                   438
E value
                   2.0e-43
Match length
                   107
% identity
                   29
                   (AB012708) 98b [Daucus carota]
NCBI Description
Seq. No.
                   8884
                   14615 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220125f02a1
                   8885
Seq. No.
                   14622 1.R1040
Contig ID
5'-most EST
                   LIB3040-028-Q1-E1-H3
Seq. No.
                   8886
Contig ID
                   14626 1.R1040
5'-most EST
                  LIB3040-029-Q1-E1-G9
                   8887
Seq. No.
Contig ID
                   14629 1.R1040
5'-most EST
                   uC-gmronoir060d08b1
Method
                   BLASTX
NCBI GI
                   g4467130
BLAST score
                   383
                   1.0e-36
E value
Match length
                   130
% identity
NCBI Description
                   (AL035538) glycosyltransferase like protein [Arabidopsis
                   thaliana]
```

14647 1.R1040

Seq. No. Contig ID

NCBI Description

```
5'-most EST
                  LIB3040-038-Q1-E1-H2
                  8889
Seq. No.
                  14671 1.R1040
Contig ID
5'-most EST
                  LIB3170-015-Q1-J1-D1
                   8890
Seq. No.
Contig ID
                  14675 1.R1040
                  LIB3040-050-Q1-E1-D12
5'-most EST
                   8891
Seq. No.
                   14692 1.R1040
Contig ID
5'-most EST
                  LIB3139-061-P1-N1-F11
                   8892
Seq. No.
                   14692 2.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy029f10b1
Seq. No.
                   8893
Contig ID
                   14696 1.R1040
                   leu701156412.h1
5'-most EST
                   BLASTN
Method
                   g11576
NCBI GI
BLAST score
                   634
E value
                   0.0e + 00
                   689
Match length
                   98
% identity
                   Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
NCBI Description
                   NADH dehydrogenase and ORF
                   8894
Seq. No.
Contig ID
                   14696 3.R1040
                   hyd700726585.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   q11576
                   83
BLAST score.
                   5.0e-39
E value
                   209
Match length
                   99
% identity
NCBI Description
                   Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val,
                   NADH dehydrogenase and ORF
                   8895
Seq. No.
                   14702 1.R1040
Contig ID
5'-most EST
                   LIB3170-018-Q1-K1-C11
                   8896
Seq. No.
                   14708 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400029d10a1
                   BLASTX
Method
NCBI GI
                   q3540204
BLAST score
                   328
E value
                   2.0e-30
Match length
                   114
% identity
                   52
```

(AC004260) Hypothetical protein [Arabidopsis thaliana]

```
8897
Seq. No.
Contig ID
                   14708 2.R1040
 5'-most EST
                   LIB3138-065-Q1-N1-G9
                   BLASTX
Method
NCBI GI
                   q3540204
BLAST score
                   312
                   9.0e-29
E value
Match length
                   76
                   71
 % identity
NCBI Description
                   (AC004260) Hypothetical protein [Arabidopsis thaliana]
                   8898
Seq. No.
Contig ID
                   14710 1.R1040
 5'-most EST
                   jC-qmro02910005f04d1
                   8899
Seq. No.
Contig ID
                   14711 1.R1040
5'-most EST
                   LIB3049-056-Q1-E1-H1
Method
                   BLASTX
NCBI GI
                   q2498490
BLAST score
                   458
                   3.0e-93
E value
Match length
                   320
 % identity
                   54
                   VIRAL INTEGRATION SITE PROTEIN INT-6 >qi 1854579 (L35556)
NCBI Description
                   Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse
                   Int-6 [Homo sapiens] >gi 2351382 (U54562) eIF3-p48 [Homo
                   sapiens] >gi 2688818 (U8\overline{5}947) Int-6 [Homo sapiens]
                   >gi 2695701 (U94175) mammary tumor-associated protein INT6
                   [Homo sapiens] >gi 4503521 ref NP 001559.1 pEIF3S6 murine
                   mammary tumor integration site 6 (oncogene homolog)
Seq. No.
                   8900
Contig ID
                   14713 1.R1040
 5'-most EST
                   uC-qmropic004e10b1
Method
                   BLASTX
NCBI GI
                   q2815493
BLAST score
                   1296
                   1.0e-143
E value
Match length
                   376
                   62
% identity
NCBI Description
                   SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
                   (CP-MI) >gi 1731988 emb CAA70816 (Y09603) serine
                   carboxypeptidase I, CP-MI [Hordeum vulgare]
Seq. No.
                   8901
Contig ID
                   14713 2.R1040
5'-most EST
                   LIB3049-056-Q1-E1-H11
Method
                   BLASTX
NCBI GI
                   q2815493
BLAST score
                   666
E value
                   8.0e-70
Match length
                   174
% identity
                   SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
NCBI Description
                   (CP-MI) >gi 1731988 emb CAA70816 (Y09603) serine
```

carboxypeptidase I, CP-MI [Hordeum vulgare]

5'-most EST

Method

```
Seq. No.
                   8902
                   14714 1.R1040
Contig ID
5'-most EST
                   LIB3049-056-Q1-E1-H12
Method
                  BLASTX
NCBI GI
                   g2673908
BLAST score
                   202
E value
                   1.0e-15
Match length
                   110
% identity
                   (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   8903
Seq. No.
                   14714 2.R1040
Contig ID
5'-most EST
                   fua701043419.hl
                   BLASTX
Method
NCBI GI
                   q2673908
BLAST score
                   373
E value
                   2.0e-35
Match length
                   217
                   47
% identity
                   (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   14717 1.R1040
Contig ID
5'-most EST
                   asn701131988.hl
                   BLASTX
Method
                   q2244920
NCBI GI
BLAST score
                   581
E value
                   7.0e-60
                   177
Match length
% identity
                   (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8905
                   14731 1.R1040
Contig ID
5'-most EST
                   LIB3049-056-Q1-E1-F7
                   8906
Seq. No.
Contig ID
                   14734 1.R1040
                   leu70\overline{1}146805.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1711512
BLAST score
                   537
                   6.0e-55
E value
Match length
                   127
                   76
% identity
                   SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)
NCBI Description
                   >gi 1076577 pir S51598 signal recognition particle 54K
                   protein - tomato (cv. UC82-B) >gi 556902 emb CAA84288
                   (Z34527) 54-kD signal recognition particle (SRP) specific
                   protein [Lycopersicon esculentum]
Seq. No.
                   8907
Contiq ID
                   14734 2.R1040
```

zhf700953055.hl

BLASTX

```
g1711512
NCBI GI
                    443
BLAST score
                    5.0e-44
E value
                   97
Match length
                    92
% identity
                   SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)
NCBI Description
                   >gi_1076577_pir__S51598 signal recognition particle 54K
protein - tomato (cv. UC82-B) >gi_556902_emb_CAA84288__
                    (Z34527) 54-kD signal recognition particle (SRP) specific
                    protein [Lycopersicon esculentum]
                    8908
Seq. No.
                    14739 1.R1040
Contig ID
                    LIB30\overline{4}9-056-Q1-E1-E9
5'-most EST
                    BLASTX
Method
                    g3980377
NCBI GI
                    302
BLAST score
                    3.0e-27
E value
                    83
Match length
                    69
% identity
                    (AC004561) unknown protein [Arabidopsis thaliana]
NCBI Description
                    8909
Seq. No.
                    14746_1.R1040
Contig ID
                    seb700651468.hl
5'-most EST
                    BLASTX
Method
                    g3128186
NCBI GI
BLAST score
                    347
E value
                    2.0e-32
                    183
Match length
                    52
% identity
                    (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    8910
                    14746 2.R1040
Contig ID
                    LIB3138-029-Q1-N1-H5
5'-most EST
                    8911
Seq. No.
Contig ID
                    14747 1.R1040
                    LIB3049-056-Q1-E1-D9
5'-most EST
                    8912
Seq. No.
                    14755 1.R1040
Contig ID
                    fde700876676.h1
5'-most EST
                    BLASTX
Method
                    g2827536
NCBI GI
                    192
BLAST score
                    1.0e-14
E value
Match length
                    60
% identity
                    (AL021633) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    8913
Seq. No.
                    14762 1.R1040
Contig ID
                    LIB3170-039-Q1-K2-H3
5'-most EST
```

Seq. No.

% identity

```
Contig ID
                  14762 2.R1040
                  LIB3109-002-Q1-K3-G1
5'-most EST
                  8915
Seq. No.
                  14778 1.R1040
Contig ID
                  LIB3049-056-Q1-E1-A11
5'-most EST
                  8916
Seq. No.
                  14779 1.R1040
Contig ID
                  LIB3049-056-Q1-E1-A12
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4531444
                  1632
BLAST score
                  0.0e+00
E value
Match length
                   465
% identity
                   (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  8917
Seq. No.
                  14779 2.R1040
Contig ID
                   dpv701097679.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4531444
BLAST score
                   261
                   2.0e-22
E value
Match length
                   62
                   76
% identity
                   (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8918
                   14780 1.R1040
Contig ID
                   LIB3049-056-Q1-E1-A2
5'-most EST
Seq. No.
                   8919
                   14780 2.R1040
Contig ID
                   dkc700968064.h1
5'-most EST
                   8920
Seq. No.
Contig ID
                   14782 1.R1040
5'-most EST
                   LIB3049-056-Q1-E1-A4
Method
                   BLASTX
                   g4432835
NCBI GI
                   289
BLAST score
                   7.0e-26
E value
                   88
Match length
% identity
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   8921
Seq. No.
                   14782 2.R1040
Contig ID
                   LIB3049-042-Q1-E1-A4
5'-most EST
                   BLASTX
Method
                   g4432835
NCBI GI
                   241
BLAST score
                   2.0e-20
E value
                   76
Match length
                   54
```

```
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
                  8922
Seq. No.
                  14785 1.R1040
Contig ID
                  LIB3109-011-Q1-K1-A9
5'-most EST
                  BLASTX
Method
                  q4539452
NCBI GI
BLAST score
                  1172
                  1.0e-129
E value
Match length
                  289
                  71
% identity
                  (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                  [Arabidopsis thaliana]
                  8923
Seq. No.
Contig ID
                  14795 1.R1040
                  asn701139392.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  q455949
BLAST score
                  39
                  2.0e-12
E value
                  39
Match length
                  100
% identity
                  18S rRNA {3' region} [Glycine max=soybeans, var. Pella 86,
NCBI Description
                  leaves, rRNA Partial, 111 nt]
                  8924
Seq. No.
                  14795 2.R1040
Contig ID
5'-most EST
                  LIB3073-001-Q1-K1-H4
                  8925
Seq. No.
                  14796 1.R1040
Contig ID
                  awf700837919.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g100226
BLAST score
                  167
                  2.0e-11
E value
Match length
                  76
                  43
% identity
                  hypothetical protein - tomato >gi 19275_emb CAA78112
NCBI Description
                   (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi_445619_prf__1909366A Leu zipper protein
                   [Lycopersicon esculentum]
Seq. No.
                  8926
                  14796 3.R1040
Contig ID
                   fde700874185.hl
5'-most EST
                  8927
Seq. No.
Contig ID
                   14800 1.R1040
                   zzp700830261.hl
5'-most EST
                  8928
Seq. No.
                  14807 1.R1040
Contig ID
                  LIB3170-038-Q1-K1-G2
5'-most EST
Method
                  BLASTX
```

q3033377

NCBI GI

A see Section 1

```
103
; BLAST score
                    1.0e-09
 E value
 Match length
                    119
 % identity
                    34
                    (AC004238) putative berberine bridge enzyme [Arabidopsis
 NCBI Description
                    thaliana]
                    8929
 Seq. No.
 Contig ID
                    14808 1.R1040
                    LIB3170-039-Q1-K2-H2
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    q4544386
 BLAST score
                    685
 E value
                    3.0e-72
 Match length
                    157
                    79
 % identity
                    (AC007047) putative cell division control protein
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    8930
                    14809 2.R1040
 Contig ID
 5'-most EST
                    zhf700961825.h1
 Method
                    BLASTX
 NCBI GI
                    g3047104
 BLAST score
                    565
                    3.0e-58
 E value
 Match length
                    157
                    70
 % identity
                    (AF058919) No definition line found [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    8931
 Contig ID
                    14810 1.R1040
                    LIB3049-055-Q1-E1-E5
 5'-most EST
 Seq. No.
                    8932
                    14818 1.R1040
 Contig ID
 5'-most EST
                    LIB3049-055-Q1-E1-F4
 Seq. No.
                    8933
 Contig ID
                    14820 1.R1040
                    ssr700555180.h1
 5'-most EST
                    8934
 Seq. No.
                    14821 1.R1040
 Contig ID
                    LIB3049-055-Q1-E1-F7
 5'-most EST
 Method
                    BLASTX
                    q3915463
 NCBI GI
 BLAST score
                    225
                    5.0e-23
 E value
 Match length
                    136
 % identity
                    46
                    HYPOTHETICAL 33.1 KD PROTEIN SLR1592
 NCBI Description
                    >gi_1652063 dbj BAA16988 (D90902) hypothetical protein
                    [Synechocystis sp.]
                    8935
 Seq. No.
```

14822 1.R1040

Contig ID

```
LIB3170-040-Q1-K1-B3
5'-most EST
Seq. No.
                  8936
Contig ID
                   14824 1.R1040
                   k11701209491.h1
5'-most EST
Method
                  BLASTX
                  g2598575
NCBI GI
                   293
BLAST score
                   3.0e-26
E value
                  120
Match length
                   47
% identity
NCBI Description
                   (Y15293) MtN21 [Medicago truncatula]
Seq. No.
                  8937
Contig ID
                  14829 1.R1040
5'-most EST
                  leu701148315.h1
Seq. No.
                  8938
                   14831 1.R1040
Contig ID
5'-most EST
                  LIB3051-036-Q1-K1-G8
Method
                  BLASTX
NCBI GI
                  g2832700
BLAST score
                  229
E value
                   2.0e-47
Match length
                  152
% identity
NCBI Description
                   (AL021713) unknown protein [Arabidopsis thaliana]
Seq. No.
                  8939
Contig ID
                   14832 1.R1040
5'-most EST
                  LIB3049-012-Q1-E1-D1
Method
                  BLASTX
                  g3297808
NCBI GI
BLAST score
                  248
                   4.0e-21
E value
                  97
Match length
                  52
% identity
                   (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   8940
Contig ID
                   14834 1.R1040
5'-most EST
                  LIB3049-055-Q1-E1-D6
Seq. No.
                  8941
Contig ID
                  14847 1.R1040
5'-most EST
                  LIB3049-055-Q1-E1-B3
                  8942
Seq. No.
                  14848 1.R1040
Contig ID
                  k11701211013.h1
5'-most EST
                  8943
Seq. No.
                  14850 1.R1040
Contig ID
                  LIB3170-037-Q1-K1-H2
5'-most EST
                  8944
Seq. No.
```

14851 1.R1040

Contig ID

Contig ID

5'-most EST

```
5'-most EST
                  LIB3170-039-Q1-K2-A2
                                                 \gamma
Method
                  BLASTX
NCBI GI
                   g3860263
BLAST score
                   358
                   9.0e - 34
E value
                   111
Match length
% identity
                   59
                   (AC005824) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                   thaliana]
                   8945
Seq. No.
                   14853 1.R1040
Contig ID
                   LIB3049-055-Q1-E1-B9
5'-most EST
                   BLASTX
Method
                   g2208946
NCBI GI
BLAST score
                   451
                   4.0e-45
E value
Match length
                   102
% identity
                   86
                   (Y10116) signal recognition particle subunit 14
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   8946
Contig ID
                   14854 1.R1040
                   LIB3170-023-Q1-K1-F7
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4508073
BLAST score
                   411
E value
                   3.0e-40
Match length
                   123
                   65
% identity
                   (AC005882) 43220 [Arabidopsis thaliana]
NCBI Description
                   8947
Seq. No.
                   14860 1.R1040
Contig ID
5'-most EST
                   LIB3049-054-Q1-E1-H3
                   8948
Seq. No.
Contig ID
                   14862 1.R1040
5'-most EST
                   g5058294
Seq. No.
                   8949
Contig ID
                   14863 1.R1040
                   LIB3170-009-Q2-J1-E12
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4220462
BLAST score
                   526
                   1.0e-53
E value
Match length
                   110
% identity
                   (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)
NCBI Description
                   gene from Arabidopsis thaliana containing Homeobox PF 00046
                   and bZIP PF_00170 domains. [Arabidopsis thaliana]
                   8950
Seq. No.
```

14865 1.R1040

LIB3049-051-Q1-E1-E9

5'-most EST

```
BLASTX
Method
NCBI GI
                  q4455800
BLAST score
                   404
E value
                  8.0e-39
Match length
                  145
                  55
% identity
                  (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                  8951
Seq. No.
                   14865 2.R1040
Contig ID
                   jC-gmro02800031g07a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1729891
BLAST score
                   184
                   1.0e-13
E value
                   108
Match length
% identity
                   35
NCBI Description
                  TEGT PROTEIN (TESTIS ENHANCED GENE TRANSCRIPT)
                  >gi_2136254_pir__I38334 TEGT (testis enhanced gene
                   transcript) - human >gi_458545 emb CAA53472 (X75861) TEGT
                   [Homo sapiens] >gi 4507\overline{4}33 ref NP 003208.1 pTEGT testis
                   enhanced gene transcript
Seq. No.
                   8952
                   14869 1.R1040
Contig ID
                   LIB3049-055-Q1-E1-A11
5'-most EST
Seq. No.
Contig ID
                   14869 2.R1040
5'-most EST
                   LIB3109-018-Q1-K1-A8
                   BLASTX
Method
                   q3047102
NCBI GI
BLAST score
                   187
                   5.0e-14
E value
Match length
                   86
% identity
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                   8954
Seq. No.
Contig ID
                   14872 1.R1040
5'-most EST
                   g5126928
                   8955
Seq. No.
                   14873 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220097c01a1
Method
                   BLASTN
NCBI GI
                   g2275194
BLAST score
                   226
                   1.0e-124
E value
Match length
                   662
                   84
% identity
                   Arabidopsis thaliana chromosome II BAC T08I13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   8956
Seq. No.
Contig ID
                   14882 1.R1040
```

LIB3051-058-Q1-K2-F4

```
Method
                  BLASTX
NCBI GI
                  g2708624
BLAST score
                  1543
                  1.0e-172
E value
Match length
                  358
                  76
% identity
                  (AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]
NCBI Description
                  8957
Seq. No.
                  14888 1.R1040
Contig ID
                  LIB3170-039-Q1-K2-E1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2160173
BLAST score
                  179
                  5.0e-13
E value
Match length
                  78
% identity
                   46
                   (AC000132) Similar to N. tabacum salt-inducible protein
NCBI Description
                   (gb U08285). [Arabidopsis thaliana]
Seq. No.
                  8958
Contig ID
                  14891 1.R1040
5'-most EST
                  jC-gmst02400073a05a1
Method
                  BLASTX
NCBI GI
                  q4432823
BLAST score
                   433
                   2.0e-42
E value
                   240
Match length
% identity
                   45
                   (AC006593) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   14910 1.R1040
5'-most EST
                   k11701205175.h1
Method
                   BLASTX
NCBI GI
                   g1172874
BLAST score
                   210
E value
                   2.0e-16
Match length
                   149
% identity
NCBI Description
                   DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
                   >gi 479589 pir S34823 dehydration-induced protein RD22 -
                  Arabidopsis thaliana >gi 391608 dbj BAA01546 (D10703) rd22
                   [Arabidopsis thaliana] >gi 447134 prf 1913421A rd22 gene
                   [Arabidopsis thaliana]
                   8960
Seq. No.
                   14912 2.R1040
Contig ID
                   LIB3049-054-Q1-E1-B7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2252838
BLAST score
                   159
E value
                   2.0e-10
Match length
                   155
% identity
                   27
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
```

```
8961
Seq. No.
Contig ID
                  14915 1.R1040
                  gsv701055256.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2244850
BLAST score
                   257
                   5.0e-22
E value
Match length
                  111
                   52
% identity
                  (297337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   8962
Seq. No.
Contig ID
                   14915 2.R1040
5'-most EST
                   kl1701212335.h1
                  BLASTX
Method
NCBI GI
                  g2244850
BLAST score
                   188
                   4.0e-14
E value
Match length
                  85
% identity
                  (297337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   8963
Seq. No.
Contig ID
                   14917 1.R1040
5'-most EST
                  LIB3049-054-Q1-E1-C12
Method
                  BLASTN
                  q3449331
NCBI GI
                   33
BLAST score
E value
                  8.0e-09
Match length
                  73
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNC17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   8964
                   14924 1.R1040
Contig ID
                   fde700877065.h1
5'-most EST
Method
                  BLASTX
                  q4191779
NCBI GI
BLAST score
                   404
                   1.0e-39
E value
Match length
                  100
% identity
                  74
NCBI Description
                  (AC005917) putative recA protein [Arabidopsis thaliana]
Seq. No.
                   8965
Contig ID
                   14925 1.R1040
5'-most EST
                  LIB3049-008-Q1-E1-G12
                  BLASTX
Method
NCBI GI
                  g2618723
BLAST score
                   387
E value
                   6.0e-37
Match length
                  173
% identity
NCBI Description
                   (U49073) IAA17 [Arabidopsis thaliana] >gi 2921756
                   (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana]
```

>gi_4389514_gb_AAB70451_ (AC000104) Identical to

Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis thaliana]

Seq. No. 8966

Contig ID 14926_1.R1040 5'-most EST ssr700555756.h1

Seq. No. 8967

Contig ID 14926 2.R1040

5'-most EST uC-gmflminsoy078f07b1

Seq. No. 8968

Contig ID 14926 3.R1040

5'-most EST LIB3170-035-Q1-K1-F10

Seq. No. 8969

Contig ID 14931 1.R1040

5'-most EST LIB3049-046-Q1-E1-H4

Seq. No. 8970

Contig ID 14932_1.R1040

5'-most EST LIB3170-033-Q1-K1-F12

Seq. No. 8971

Contig ID 14945 1.R1040

5'-most EST LIB3170-034-Q1-K1-H2

Method BLASTN
NCBI GI g1420886
BLAST score 124
E value 5.0e-63

Match length 302 % identity 86

NCBI Description Phaseolus vulgaris non-specific lipid transfer-like protein

mRNA, complete cds

Seq. No. 8972

Contig ID 14947 1.R1040

5'-most EST LIB3093-038-Q1-K1-A6

Method BLASTX
NCBI GI g1352267
BLAST score 405
E value 2.0e-39
Match length 147
% identity 56

NCBI Description DEOXYHYPUSINE SYNTHASE >gi_994715 (L39068) deoxyhypusine

synthase [Homo sapiens] >gi_1710220 (U79262) deoxyhypusine

synthase [Homo sapiens] >gi_3021398_emb_CAA04940_
(AJ001701) deoxyhypusine synthase [Homo sapiens]

>gi 4503325 ref NP 001921.1 pDHPS deoxyhypusine synthase

Seq. No. 8973

Contig ID 14948_1.R1040 5'-most EST trc700567438.h1

Seq. No. 8974

Contig ID 14949 1.R1040

```
5'-most EST
                    LIB3049-010-Q1-E1-H5
 Method
                    BLASTX
                    g3643609
 NCBI GI
 BLAST score
                    541
                    5.0e-55
 E value
 Match length
                    158
 % identity
                    70
                    (AC005395) putative Cys3His zinc finger protein
 NCBI Description
                    [Arabidopsis thaliana]
                    8975
 Seq. No.
                    14949 2.R1040
 Contig ID
 5'-most EST
                    g4395984
 Method
                    BLASTX
                    g3687237
 NCBI GI
 BLAST score
                    163
 E value
                    4.0e-11
 Match length
                    57
 % identity
                    67
                    (AC005169) putative Cys3His zinc-finger protein
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    8976
 Contig ID
                    14951 1.R1040
 5'-most EST
                    LIB3049-053-Q1-E1-G10
                    8977
 Seq. No.
 Contig ID
                    14953 1.R1040
 5'-most EST
                    LIB3170-034-Q1-K1-H10
                    8978
 Seq. No.
                    14955 1.R1040
 Contig ID
                    LIB3049-053-Q1-E1-G3
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g2464914
 BLAST score
                    501
 E value
                    1.0e-50
 Match length
                    146
                    70
 % identity
                    (Z99708) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    8979
                    14955 2.R1040
 Contig ID
5'-most EST
                    LIB3107-033-Q1-K1-G12
 Method
                    BLASTX
 NCBI GI
                    q2464914
 BLAST score
                    195
                    5.0e-15
 E value
                    71
 Match length
 % identity
                    (Z99708) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    8980
 Seq. No.
                    14960 1.R1040
 Contig ID
                    LIB3139-007-P1-N1-A7
 5'-most EST
 Method
                    BLASTX
```

q1488043

NCBI GI

```
BLAST score
                  1846
                  0.0e+00
E value
Match length
                  438
% identity
                  80
                  (U63784) PAPS-reductase-like protein [Catharanthus roseus]
NCBI Description
                  8981
Seq. No.
                  14960 2.R1040
Contig ID
                  gsv70\overline{1}047450.h1
5'-most EST
Method
                  BLASTX
                  g1488043
NCBI GI
BLAST score
                  210
                  7.0e-17
E value
                  100
Match length
                  49
% identity
                  (U63784) PAPS-reductase-like protein [Catharanthus roseus]
NCBI Description
                  8982
Seq. No.
                  14960 3.R1040
Contig ID
                  k11701202445.h1
5'-most EST
                  8983
Seq. No.
Contig ID
                  14963 1.R1040
                  seb700653658.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g731520
BLAST score
                  196
E value
                  8.0e-15
Match length
                  80
% identity
                  CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15
NCBI Description
                  >gi 1077711 pir S50644 cytochrome oxidase assembly factor
                  COX15 - yeast (Saccharomyces cerevisiae) >gi 603381
                   (U18917) Cox15p: Cytochrom oxidase assembly factor
                  [Saccharomyces cerevisiae] >gi_603947 (L38643) cytochrome
                  oxidase assembly factor [Saccharomyces cerevisiae]
Seq. No.
                  8984
Contig ID
                  14963 2.R1040
5'-most EST
                  fC-gmse700754560a2
Seq. No.
                  8985
Contig ID
                  14964 1.R1040
                  LIB3051-009-Q1-E1-C9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2245030
BLAST score
                  306
                  3.0e-27
E value
                  207
Match length
% identity
                   (Z97341) apetala2 domain TINY homolog [Arabidopsis
NCBI Description
                  thaliana]
                  8986
Seq. No.
```

14965 1.R1040

LIB3049-053-Q1-E1-E1

Contig ID 5'-most EST

5'-most EST

```
8987
Seq. No.
Contig ID
                   14970 1.R1040
5'-most EST
                   LIB3170-033-Q1-J1-E12
Seq. No.
                   8988
                   14971 1.R1040
Contig ID
                   uaw700666538.hl
5'-most EST
Method
                   BLASTX
                   q3776578
NCBI GI
                   206
BLAST score
                   3.0e-16
E value
Match length
                   80
                   49
% identity
                   (ACO05388) ESTs gb F13915 and gb F13916 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
Seq. No.
                   8989
Contig ID
                   14975 1.R1040
5'-most EST
                   awf700838186.hl
                   8990
Seq. No.
                   14977 1.R1040
Contig ID
5'-most EST
                   r1r70\overline{0}901579.h1
Method
                   BLASTX
NCBI GI
                   q2459431
BLAST score
                   164
                   6.0e-11
E value
                   97
Match length
% identity
                   47
                   (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                   8991
Seq. No.
Contig ID
                   14979 1.R1040
5'-most EST
                   fde700874980.h1
                   8992
Seq. No.
Contig ID
                   14982 1.R1040
5'-most EST
                   LIB3049-053-Q1-E1-B9
Seq. No.
                   8993
Contig ID
                   14986 1.R1040
5'-most EST
                   LIB3074-029-Q1-K1-D5
Seq. No.
                   8994
Contig ID
                   14988 1.R1040
5'-most EST
                   LIB3049-053-Q1-E1-C4
Method
                   BLASTX
NCBI GI
                   g3688171
BLAST score
                   373
E value
                   1.0e-35
Match length
                   168
% identity
                   (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                   8995
Seq. No.
                   14992 1.R1040
Contig ID
```

LIB3093-045-Q1-K1-E7

```
Method
                  BLASTX
NCBI GI
                  q3150406
BLAST score
                  685
E value
                  6.0e-72
Match length
                  317
                  44
% identity
NCBI Description
                  (AC004165) putative indole-3-acetate
                  beta-qlucosyltransferase [Arabidopsis thaliana]
                  8996
Seq. No.
                  14993 1.R1040
Contig ID
5'-most EST
                  LIB3049-053-Q1-E1-D11
Method
                  BLASTX
NCBI GI
                  q4039152
BLAST score
                  182
E value
                  3.0e-13
Match length
                  53
% identity
NCBI Description
                  (AF104221) low temperature and salt responsive protein.
                  LTI6B [Arabidopsis thaliana] >qi 4325219 qb AAD17303
                  (AF122006) hydrophobic protein [Arabidopsis thaliana]
                  8997
Seq. No.
                  14993 2.R1040
Contig ID
                  taw700657926.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4039152
BLAST score
                  182
E value
                  3.0e-13
Match length
                  53
                  64
% identity
                  (AF104221) low temperature and salt responsive protein
NCBI Description
                  LTI6B [Arabidopsis thaliana] >qi 4325219 qb AAD17303
                  (AF122006) hydrophobic protein [Arabidopsis thaliana]
                  8998
Seq. No.
Contig ID
                  14997 1.R1040
5'-most EST
                  txt700731851.hl
Seq. No.
                  8999
Contig ID
                  14997 2.R1040
5'-most EST
                  pxt700945886.h1
                  9000
Seq. No.
Contig ID
                  14998 1.R1040
5'-most EST
                  eep700866824.h1
Method
                  BLASTX
NCBI GI
                  q4160280
BLAST score
                  245
E value
                  2.0e-20
Match length
                  165
% identity
NCBI Description
                  (AJ006224) purple acid phosphatase [Ipomoea batatas]
                  9001
Seq. No.
```

14999 1.R1040

jC-qmf102220141d07a1

Contig ID 5'-most EST

NCBI Description

```
Method
                    BLASTX
NCBI GI
                    g3785997
BLAST score
                    622
                    9.0e-65
E value
Match length
                    200
% identity
                    (AC005499) putative annexin [Arabidopsis thaliana]
NCBI Description
                    9002
Seq. No.
                    15000 1.R1040
Contig ID
5'-most EST
                    uC-gmronoir053e10b1
Seq. No.
                    9003
                    15000 2.R1040
Contig ID
5'-most EST
                    dpv701103624.h1
Seq. No.
                    9004
                    15002 1.R1040
Contig ID
5'-most EST
                    uC-gmflminsoy091h05b1
Method
                    BLASTN
NCBI GI
                    g3746902
                    286
BLAST score
E value
                    1.0e-159
Match length
                    517
                    89
% identity
                    Pisum sativum signal recognition particle 54 kDa subunit
NCBI Description
                    precursor (Ffc) mRNA, nuclear gene encoding chloroplast
                    protein, partial cds
Seq. No.
                    9005
                    15004 1.R1040
Contig ID
5'-most EST
                    LIB3049-053-Q1-E1-A6
                    9006
Seq. No.
                    15007 1.R1040
Contig ID
5'-most EST
                    LIB3049-040-Q1-E1-G11
Method
                    BLASTX
                    g1076387
NCBI GI
BLAST score
                    789
E value
                    3.0e-84
                    181
Match length
% identity
                   protein kinase homolog - Arabidopsis thaliana
>gi_717180_emb_CAA55866_ (X79279) protein kinase homologous
NCBI Description
                    to shaggy and \overline{g}lycogen \overline{s}ynthase kinase-3 [Arabidopsis
                    thaliana]
                    9007
Seq. No.
Contig ID
                    15007 2.R1040
5'-most EST
                    fC-gmle700872092d2
Method
                    BLASTN
NCBI GI
                    q1504062
BLAST score
                    241
E value
                    1.0e-132
Match length
                    703
% identity
```

A.thaliana mRNA for shaggy-like kinase kappa

```
9008
Seq. No.
                   15007 3.R1040
Contig ID
5'-most EST
                   LIB3049-053-Q1-E1-A9
Method
                   BLASTX
                   g1076387
NCBI GI
                   187
BLAST score
E value
                   2.0e-18
                   70
Match length
% identity
                   73
                   protein kinase homolog - Arabidopsis thaliana
NCBI Description
                   >gi 717180 emb CAA55866 (X79279) protein kinase homologous
                   to shaggy and glycogen synthase kinase-3 [Arabidopsis
                   thaliana]
                   9009
Seq. No.
Contig ID
                   15007 4.R1040
5'-most EST
                   LIB3109-012-Q1-K1-E6
Seq. No.
                   9010
                   15008 1.R1040
Contig ID
5'-most EST
                   seb70\overline{0}652702.h1
                   9011
Seq. No.
                   15008 2.R1040
Contig ID
                   seb70\overline{0}652769.h1
5'-most EST
                   9012
Seq. No.
Contig ID
                   15008 3.R1040
5'-most EST
                   epx70\overline{1}106574.h1
                   9013
Seq. No.
                   15013 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400009b04a1
Seq. No.
                   9014
                   15023 1.R1040
Contig ID
5'-most EST
                   uaw700664606.hl
                   BLASTX
Method
NCBI GI
                   g1255951
BLAST score
                   1406
E value
                   1.0e-156
                   363
Match length
% identity
                   (X96932) PS60 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   9015
Contig ID
                   15027 1.R1040
5'-most EST
                   LIB3138-071-P1-N1-B7
                   BLASTX
Method
NCBI GI
                   q3892056
BLAST score
                   568
                   3.0e-58
E value
Match length
                   126
% identity
                   87
```

NCBI Description (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

BLAST score

289

```
9016
Seq. No.
Contig ID
                   15033 1.R1040
                   LIB3109-038-Q1-K1-D6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2832435
BLAST score
                   205
                   3.0e-16
E value
Match length
                   102
                   42
% identity
                   (AJ223042) noisette [Drosophila melanogaster]
NCBI Description
                   9017
Seq. No.
Contig ID
                   15035 1.R1040
5'-most EST
                   LIB3074-025-Q1-E1-B9
Method
                   BLASTX
NCBI GI
                   g4530585
BLAST score
                   373
                   1.0e-35
E value
Match length
                   87
% identity
                   76
                   (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
                   9018
Seq. No.
Contig ID
                   15035 2.R1040
5'-most EST
                   LIB3049-045-Q1-E1-D12
Method
                   BLASTX
                   g4530585
NCBI GI
BLAST score
                   276
E value
                   3.0e-25
Match length
                   78
% identity
                   76
                   (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
                   9019
Seq. No.
Contig ID
                   15036 1.R1040
                   LIB30\overline{4}9-052-Q1-E1-E9
5'-most EST
                   9020
Seq. No.
                   15037 1.R1040
Contig ID
5'-most EST
                   LIB3049-012-Q1-E1-C12
Method
                   BLASTX
NCBI GI
                   q3183088
BLAST score
                   291
                   5.0e-26
E value
                   101
Match length
% identity
                   53
                   PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                   (LTP) >gi 629658 pir S47084 lipid transfer like protein -
                   cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer
                   like protein [Vigna unguiculata]
                   9021
Seq. No.
Contig ID
                   15037 2.R1040
5'-most EST
                   LIB3049-047-Q1-E1-A5
Method
                   BLASTX
NCBI GI
                   q3183088
```

NCBI GI

```
E value
                  6.0e-26
                  98
Match length
% identity
                  51
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                  (LTP) >gi 629658 pir S47084 lipid transfer like protein -
                  cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
                  like protein [Vigna unguiculata]
                  9022
Seq. No.
                  15039 1.R1040
Contig ID
                  ncj700982409.hl
5'-most EST
Method
                  BLASTX
                  g3860257
NCBI GI
BLAST score
                  266
E value
                  1.0e-22
Match length
                  136
% identity
                  43
NCBI Description
                  (AC005824) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  15039 2.R1040
Contig ID
5'-most EST
                  zzp700834617.h1
Seq. No.
Contig ID
                  15040 1.R1040
5'-most EST
                  LIB3072-046-Q1-K1-C12
                  BLASTX
Method
NCBI GI
                  q1085952
BLAST score
                  204
E value
                  4.0e-16
Match length
                  106
% identity
NCBI Description
                  hypothetical protein S1 - Phalaris coerulescens
                  >gi 556831 emb CAA57519 (X81991) S1 [Phalaris
                  coerulescens] >gi 1103489 emb CAA63108 (X92351)
                  self-incompatibility mutant protein [Phalaris coerulescens]
Seq. No.
Contig ID
                  15042 1.R1040
5'-most EST
                  LIB3109-029-Q1-K1-C9
                  BLASTX
Method
NCBI GI
                  q3122287
BLAST score
                  146
E value
                  9.0e-09
Match length
                  152
% identity
                  PUTATIVE BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE
NCBI Description
                  (TRANSAMINASE B) (BCAT) >gi 2127785 pir G64425
                  branched-chain amino acid aminotransferase - Methanococcus
                  jannaschii >gi 1591667 (U67543) branched-chain amino acid
                  aminotransferase (ilvE) [Methanococcus jannaschii]
Seq. No.
                  9026
Contig ID
                  15043 1.R1040
5'-most EST
                  jC-gmle01810067h04a1
Method
                  BLASTX
```

q1432058

```
BLAST score
                   696
E value
                   7.0e-82
Match length
                   280
% identity
                   57
                   (U58540) WRKY2 [Petroselinum crispum]
NCBI Description
                   9027
Seq. No.
Contig ID
                   15044 1.R1040
                   jC-qmst02400030c02a1
5'-most EST
                   BLASTX
Method
                   g2702272
NCBI GI
BLAST score
                   475
E value
                   4.0e-56
Match length
                   236
                   29
% identity
NCBI Description
                   (AC003033) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   15046 1.R1040
5'-most EST
                   uC-qmrominsoy271h03b1
                   BLASTX
Method
NCBI GI
                   q3878134
BLAST score
                   213
E value
                   7.0e-17
                   61
Match length
% identity
                   (Z68218) K01H12.1 [Caenorhabditis elegans]
NCBI Description
Seq. No.
                   9029
Contig ID
                   15046 2.R1040
                   LIB3049-052-Q1-E1-E11
5'-most EST
                   BLASTX
Method
NCBI GI
                   a3878134
BLAST score
                   213
E value
                   4.0e-17
Match length
                   61
                   59
% identity
                   (Z68218) K01H12.1 [Caenorhabditis elegans]
NCBI Description
Seq. No.
Contig ID
                   15051 1.R1040
5'-most EST
                   sat701013119.hl
                   9031
Seq. No.
Contig ID
                   15051 2.R1040
5'-most EST
                   LIB3072-002-Q1-K1-D12
                   9032
Seq. No.
Contig ID
                   15053 1.R1040
5'-most EST
                   g5342522
Method
                   BLASTX
NCBI GI
                   q3204108
BLAST score
                   606
E value
                   8.0e-63
Match length
                   163
% identity
NCBI Description
                   (AJ006764) putative deoxycytidylate deaminase [Cicer
```

ATT.

arietinum] Seq. No. 9033 Contig ID 15053 2.R1040 LIB3049-052-Q1-E1-D1 5'-most EST Method BLASTX NCBI GI g3204108 247 BLAST score 4.0e-21 E value 69 Match length 64 % identity NCBI Description (AJ006764) putative deoxycytidylate deaminase [Cicer arietinum] Seq. No. 9034 Contig ID 15053 3.R1040 LIB3050-008-Q1-E1-F5 5'-most EST 9035 Seq. No. 15054 1.R1040 Contig ID LIB3139-038-P1-N1-G6 5'-most EST BLASTX Method NCBI GI q3355471 BLAST score 218 E value 3.0e-17 96 Match length 43 % identity NCBI Description (AC004218) putative lysophospholipase [Arabidopsis thaliana] 9036 Seq. No. 15058 1.R1040 Contig ID 5'-most EST LIB3073-004-Q1-K1-E12 Seq. No. 9037 Contig ID 15059 1.R1040 5'-most EST : LIB3170-035-Q1-K1-A10 Seq. No. 9038 Contig ID 15069 1.R1040 5'-most EST LIB3049-052-Q1-E1-A7 Method BLASTX NCBI GI q2244989 BLAST score 421 \dot{z} E value 3.0e-41Match length 121 68 % identity (Z97340) strong similarity to naringenin 3-dioxygenase NCBI Description [Arabidopsis thaliana] 9039 Seq. No. 15076 1.R1040 Contig ID 5'-most EST LIB3049-052-Q1-E1-B4 Method BLASTX g3763920 NCBI GI BLAST score 311

. . . .

1.0e-28

E value

```
Match length
                  133
% identity
                  (AC004450) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  9040
                  15079 1.R1040
Contig ID
5'-most EST
                  kl1701210864.hl
Method
                  BLASTX
                  q2642158
NCBI GI
BLAST score
                  568
                  4.0e-58
E value
Match length
                  271
% identity
                  46
                   (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  9041
Seq. No.
                  15082 1.R1040
Contig ID
5'-most EST
                  LIB3049-052-Q1-E1-C12
Method
                  BLASTX
NCBI GI
                  q267131
BLAST score
                  554
                   3.0e-56
E value
                   286
Match length
% identity
                  NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN)
NCBI Description
                  >gi 423120_pir__A46174 RNA-binding protein TIAR - human
                  >gi 189310 (M96954) nucleolysin TIAR [Homo sapiens]
                   >qi 4507499 ref NP 003243.1 pTIAL1 TIA1 cytotoxic
                   granule-associated RNA-binding protein-like
                   9042
Seq. No.
                   15082 2.R1040
Contia ID
5'-most EST
                   jC-qmst02400015f11d1
Seq. No.
                   9043
                   15083 1.R1040
Contig ID
                   LIB3055-011-Q1-N1-H4
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2496789
BLAST score
                   1250
                   1.0e-138
E value
Match length
                   381
                   64
% identity
                   1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP
NCBI Description
                   REDUCTOISOMERASE) >gi_1001556_dbj_BAA10183 (D64000)
                   hypothetical protein [Synechocystis sp.]
                   9044
Seq. No.
                   15083 2.R1040
Contig ID
5'-most EST
                   seb700652689.h1
Method
                   BLASTX
NCBI GI
                   g2496789
BLAST score
                   557
                   7.0e-57
E value
Match length
                   162
% identity
                   1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP
NCBI Description
```

Contig ID

```
Seq. No.
Contig ID
                  15083 3.R1040
                  uC-gmropic046g01b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2496789
                  199
BLAST score
                  3.0e-15
E value
                  73
Match length
                  55
% identity
                  1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP
NCBI Description
                  REDUCTOISOMERASE) >gi 1001556 dbj BAA10183 (D64000)
                  hypothetical protein [Synechocystis sp.]
                   9046
Seq. No.
                   15083 4.R1040
Contig ID
5'-most EST
                  LIB3139-023-P1-N1-G8
Method
                  BLASTN
                  q2656029
NCBI GI
                   47
BLAST score
                   3.0e-17
E value
Match length
                  127
                  84
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQB2
Seq. No.
                   9047
Contig ID
                   15086 1.R1040
                   fC-gmse7000751793r1
5'-most EST
                   9048
Seq. No.
                   15089 1.R1040
Contig ID
5'-most EST
                   LIB3049-051-Q1-E1-H12
Method
                   BLASTX
                   q1213629
NCBI GI
                   149
BLAST score
                   1.0e-09
E value
Match length
                   99
% identity
                   41
NCBI Description
                   (X95991) pectinesterase [Prunus persica]
Seq. No.
                   9049
                   15090 1.R1040
Contig ID
5'-most EST
                   LIB3170-025-Q1-K1-A11
                   BLASTX
Method
                   q1420887
NCBI GI
BLAST score
                   184
                   2.0e-13
E value
Match length
                   75
% identity
                   (U34334) non-specific lipid transfer-like protein
NCBI Description
                   [Phaseolus vulgaris]
                   9050
Seq. No.
```

REDUCTOISOMERASE) >gi 1001556 dbj BAA10183 (D64000)

hypothetical protein [Synechocystis sp.]

15094 1.R1040

5'-most EST

```
5'-most EST
                  LIB3049-051-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  g1346478
BLAST score
                   237
E value
                   4.0e-20
                   76
Match length
                   58
% identity
NCBI Description
                  MAJOR ALLERGEN MAL D 1 (MAL D I) >gi 747852 emb CAA58646
                   (X83672) Mal d 1 [Malus domestica]
                   9051
Seq. No.
                   15101 1.R1040
Contig ID
5'-most EST
                  LIB3074-004-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                   g3702962
BLAST score
                   553
E value
                   1.0e-56
Match length
                   110
% identity
                   95
                   (AF079484) rac GTP binding protein Arac7 [Arabidopsis
NCBI Description
                  thaliana]
                   9052
Seq. No.
Contig ID
                   15102 1.R1040
                  LIB3049-052-Q1-E1-A2
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4309969
BLAST score
                   386
E value
                   4.0e-37
Match length
                   128
% identity
                   58
NCBI Description
                   (AC002983) putative phosphoglyceride transfer protein
                   [Arabidopsis thaliana]
Seq. No.
                   9053.
                   15104 1.R1040
Contig ID
                  LIB3049-052-Q1-E1-A4
5'-most EST
                   9054
Seq. No.
Contig ID
                   15104 3.R1040
5'-most EST
                   trc700561613.hl
                   9055
Seq. No.
                   15104 4.R1040
Contiq ID
                  sat701002972.h1
5'-most EST
                   9056
Seq. No.
                   15107 1.R1040
Contiq ID
5'-most EST
                  jC-gmro02910026b02a1
Seq. No.
                   9057
                   15115 1.R1040
Contig ID
5'-most EST
                  trc700565473.hl
Seq. No.
                   9058
                   15115 2.R1040
Contig ID
```

 $qsv70\overline{1}050017.h1$

```
9059
Seq. No.
                  15116 1.R1040
Contig ID
5'-most EST
                  LIB3049-051-Q1-E1-G11
                  9060
Seq. No.
                  15117 1.R1040
Contig ID
5'-most EST
                  LIB3170-032-Q1-K1-E12
                  9061
Seq. No.
                  15122 1.R1040
Contig ID
                  epx70\overline{1}104947.h1
5'-most EST
                  BLASTX
Method
                  q3695023
NCBI GI
                  149
BLAST score
                  1.0e-09
E value
Match length
                  46
% identity
                  (AF055850) unknown [Arabidopsis thaliana]
NCBI Description
                  9062
Seq. No.
                  15127 1.R1040
Contig ID
                  LIB3072-051-Q1-E1-G1
5'-most EST
                   9063
Seq. No.
                  15127 2.R1040
Contig ID
                  LIB3072-043-Q1-K1-E10
5'-most EST
                   9064
Seq. No.
Contig ID
                   15132 1.R1040
5'-most EST
                  pxt700945365.hl
                  BLASTX
Method
                  g1706319
NCBI GI
                   1231
BLAST score
                   1.0e-135
E value
Match length
                   393
                   58
% identity
                  HISTIDINE DECARBOXYLASE (HDC) (TOM92)
NCBI Description
                   >gi_481829_pir__S39554 histidine decarboxylase (EC
                   4.1.1.22) - tomato >gi 416534 emb CAA50719 (X71900)
                 histidine decarboxylase [Lycopersicon esculentum]
                   9065
Seq. No.
                   15132 2.R1040
Contig ID
                   leu701149945.hl
5'-most EST
                   9066
Seq. No.
                   15135 1.R1040
Contig ID
                   g4396421
5'-most EST
                   9067
Seq. No.
                   15141 1.R1040
Contig ID
                   LIB3109-028-Q1-K1-H9
5'-most EST
                   BLASTN
Method
NCBI GI
                   g3821780
                   33
BLAST score
E value
                   7.0e-09
```

NCBI GI

```
Match length
                  37
% identity
                  97
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  9068
                  15141 2.R1040
Contig ID
5'-most EST
                  LIB3049-051-Q1-E1-D12
Method
                  BLASTX
NCBI GI
                  q3036796
BLAST score
                  480
                   4.0e-48
E value
Match length
                  106
% identity
                  86
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3805858_emb_CAA21478_ (AL031986) putative protein
                   [Arabidopsis thaliana]
                   9069
Seq. No.
Contig ID
                  15147 1.R1040
5'-most EST
                  LIB3049-051-Q1-E1-B9
                   9070
Seq. No.
                  15147 2.R1040
Contig ID
                  uC-gmropic031d03b1
5'-most EST
                  9071
Seq. No.
                  15147 3.R1040
Contig ID
                  LIB3170-051-Q1-K1-H5
5'-most EST
Seq. No.
                   9072
                  15148 1.R1040
Contig ID
5'-most EST
                  LIB3049-051-Q1-E1-C1
                   9073
Seq. No.
Contig ID
                   15159 1.R1040
5'-most EST
                  LIB3109-015-Q1-K1-G1
                   9074
Seq. No.
                   15166 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy173d03b1
                   BLASTX
Method
NCBI GI
                   q3036807
BLAST score
                   482
                   3.0e-48
E value
                   225
Match length
% identity
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                   9075
Seq. No.
Contig ID
                   15167 1.R1040
5'-most EST
                   LIB3170-035-Q1-K1-H8
                   9076
Seq. No.
Contig ID
                   15168 1.R1040
5'-most EST
                   uC-gmropic019a03b1
                   BLASTX
Method
```

q2194132

```
939
BLAST score
E value
                  1.0e-101
Match length
                  468
% identity
                  49
                  (AC002062) No definition line found [Arabidopsis thaliana]
NCBI Description
                   9077
Seq. No.
                   15169 1.R1040
Contig ID
                  LIB3049-051-Q1-E1-A2
5'-most EST
                   9078
Seq. No.
                   15170 1.R1040
Contig ID
                   LIB3049-051-Q1-E1-A3
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3075399
BLAST score
                   145
E value
                   4.0e-09
                   80
Match length
% identity
                   44
                   (AC004484) SF16-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   15175 1.R1040
Contig ID
5'-most EST
                   LIB3167-019-P1-K1-C7
                   BLASTX
Method
                   q481384
NCBI GI
                   158
BLAST score
                   1.0e-10
E value
Match length
                   72
% identity
                   outer envelope protein omp24, chloroplast - spinach
NCBI Description
                   >gi_1076265_pir__S46542 chloroplast outer envelope 24 kD
                   protein - spinach >gi 414200 emb CAA53243 (X75563)
                   chloroplast outer envelope 24 kD protein (omp24) [Spinacia
                   oleracea]
                   9080
Seq. No.
                   15175 2.R1040
Contig ID
                   LIB3050-007-Q1-E1-C4
5'-most EST
                   9081
Seq. No.
Contig ID
                   15179 1.R1040
5'-most EST
                   LIB3170-033-Q1-K1-C9
                   9082
Seq. No.
                   15185 1.R1040
Contig ID
                   awf70\overline{0}841540.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4006893
BLAST score
                   533
E value
                   2.0e-54
Match length
                   126
                   76
% identity
                   (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
NCBI Description
```

9083

15185 2.R1040

Seq. No.

Contig ID

```
5'-most EST
                   k11701211190.h1
                                              , J.
Method
                   BLASTX
                   q4006893
NCBI GI
BLAST score
                   273
                   2.0e-24
E value
                   67
Match length
                   66
% identity
                   (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
NCBI Description
                   9084
Seq. No.
                   15187 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy030f07b1
Method
                   BLASTX
                   q4512687
NCBI GI
BLAST score
                   664
                   1.0e-69
E value
Match length
                   163
% identity
                   (AC006931) floral homeotic protein AGL5 [Arabidopsis
NCBI Description
                   thalianal
                   9085
Seq. No.
                   15194 1.R1040
Contig ID
5'-most EST
                   kl1701206523.h1
                   BLASTX
Method
                   q1871577
NCBI GI
                   468
BLAST score
                   1.0e-46
E value
Match length
                   193
% identity
                   (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                   9086
Seq. No.
                   15198 1.R1040
Contig ID
5'-most EST
                   LIB3049-024-Q1-E1-A3
                   BLASTX
Method
                   q2290528
NCBI GI
BLAST score
                   1143
                   0.0e + 00
E value
Match length
                   344
                   92
% identity
                   (U94746) ATAN11 [Arabidopsis thaliana]
NCBI Description
                   9087
Seq. No.
Contig ID
                   15198 2.R1040
5'-most EST
                   q4303493
                   BLASTX
Method ·
NCBI GI
                   g2290532
BLAST score
                   829
E value
                   6.0e-89
Match length
                   183
% identity
NCBI Description
                   (U94748) AN11 [Petunia x hybrida]
                   9088
Seq. No.
Contig ID
                   15203 1.R1040
5'-most EST
                   gsv701051022.hl
```

Seq. No.

9095

```
BLASTX
 Method
 NCBI GI
                    g3929368
 BLAST score
                    717
                    1.0e-75
 E value
                    186
 Match length
                    75
 % identity
                    PRE-MRNA SPLICING FACTOR SF2 (SR1 PROTEIN) >gi 2443472
 NCBI Description
                    (AF001035) ASF/SF2 homolog [Arabidopsis thaliana]
Seq. No.
 Contig ID
                    15205 1.R1040
                    LIB3170-035-Q1-K1-E8
 5'-most EST
                    BLASTX
 Method
                    g3695392
 NCBI GI
                    628
 BLAST score
                    5.0e-65
 E value
 Match length
                    186
 % identity
                    (AF096371) No definition line found [Arabidopsis thaliana]
 NCBI Description
                    9090
 Seq. No.
                    15211 1.R1040
 Contig ID
                    asn701134725.h2
 5'-most EST
                    BLASTX
 Method
                    g629881
 NCBI GI
                    207
 BLAST score
                    5.0e-16
 E value
                    120
 Match length
                    49
  % identity
                    myosin-related protein - slime mold (Physarum polycephalum)
 NCBI Description
                    >gi 511053 emb CAA79924 (Z21878) myosin-related protein
                     [Physarum polycephalum]
                    9091
  Seq. No.
                    15211 2.R1040
  Contig ID
                    jC-gmle01810089g09a1
  5'-most EST
  Seq. No.
                    15216 1.R1040
  Contig ID
  5'-most EST
                    hyd700725833.hl
                     9093
  Seq. No.
                    15216 2.R1040
  Contig ID
                     sat70\overline{1}013479.h1
  5'-most EST
                    BLASTX
  Method
                     g452593
  NCBI GI
                     336
  BLAST score
                     3.0e-82
  E value
                     266
  Match length
  % identity
  NCBI Description
                     (D21814) ORF [Lilium longiflorum]
                     9094
  Seq. No.
  Contig ID
                     15218 1.R1040
  5'-most EST
                     LIB3094-030-Q1-K1-G6
```

....

NCBI Description

```
Contig ID
                   15218 2.R1040
5'-most EST
                   LIB3051-040-Q1-K1-G5
                   9096
Seq. No.
                   15218 3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy063b02b1
                   9097
Seq. No.
                   15223 1.R1040
Contig ID
5'-most EST
                   g5342402
                   BLASTX
Method
                   g4103342
NCBI GI
                   658
BLAST score
                   5.0e-69
E value
Match length
                   142
% identity
                   91
                   (AF022377) agamous-like putative transcription factor
NCBI Description
                   [Cucumis sativus]
                   9098
Seq. No.
                   15223 2.R1040
Contig ID
                   ek170\overline{0}968115.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3646325
                   58
BLAST score
                   4.0e-24
E value
                   145
Match length
% identity
                   86
NCBI Description
                   Malus domestica mRNA for MADS-box protein, MADS10
                   9099
Seq. No.
                   15226 1.R1040
Contig ID
                   epx70\overline{1}106881.h1
5'-most EST
Method
                   BLASTN
                   g3695062
NCBI GI
BLAST score
                   124
E value
                   3.0e-63
                   258
Match length
% identity
                   87
NCBI Description
                   Lotus japonicus rac GTPase activating protein 3 mRNA,
                   partial cds
                   9100
Seq. No.
                   15236 1.R1040
Contig ID
5'-most EST
                   LIB3049-050-Q1-E1-D1
                   9101
Seq. No.
                   15236 2.R1040
Contig ID
                   LIB30\overline{5}1-018-Q1-E1-H10
5'-most EST
Method
                   BLASTX
                   q3702323
NCBI GI
BLAST score
                   691
E value
                   1.0e-72
Match length
                   264
                   57
% identity
                  (AC005397) unknown protein [Arabidopsis thaliana]
```

Seq. No.

9109

```
9102
Seq. No.
Contig ID
                   15237 1.R1040
5'-most EST
                   LIB3109-010-Q1-K1-C5
Seq. No.
                   9103
                   15238 1.R1040
Contig ID
5'-most EST
                   LIB3170-034-Q1-K1-A8
                   9104
Seq. No.
                   15239 1.R1040
Contig ID
5'-most EST
                   LIB3170-035-Q1-K1-B8
Seq. No.
                   9105
                   15248 1.R1040
Contig ID
5'-most EST
                   LIB3049-050-Q1-E1-A12
Method
                   BLASTX
NCBI GI
                   q3063451
BLAST score
                   451
E value
                   9.0e-45
                   194
Match length
% identity
                   48
NCBI Description
                   (AC003981) F22013.13 [Arabidopsis thaliana]
                   9106
Seq. No.
                   15251 1.R1040
Contig ID
                   LIB30\overline{4}9-050-Q1-E1-A6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4406775
BLAST score
                   363
E value
                   1.0e-60
                   358
Match length
% identity
NCBI Description
                   (AC006836) unknown protein [Arabidopsis thaliana]
Seq. No.
                   9107
                   15253 1.R1040
Contig ID
5'-most EST
                   LIB3056-001-Q1-B1-G5
Method
                   BLASTX
                   g3132470
NCBI GI
BLAST score
                   269
                   1.0e-23
E value
Match length
                   86
% identity
                   57
                   (AC003096) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9108
Contig ID
                   15255 1.R1040
5'-most EST
                   leu701148356.h1
                   BLASTX
Method
NCBI GI
                   g3269297
BLAST score
                   207
                   6.0e-16
E value
Match length
                   83
% identity
NCBI Description
                   (AL030978) putative protein [Arabidopsis thaliana]
```

...

```
15255 2.R1040
Contig ID
5'-most EST
                  uaw700661087.hl
                  BLASTX
Method
NCBI GI
                  q3269297
BLAST score
                   220
                   6.0e-18
E value
                  82
Match length
% identity
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   9110
Seq. No.
                   15259 1.R1040
Contig ID
5'-most EST
                   LIB3170-033-Q1-K1-E8
                   9111
Seq. No.
                   15261 1.R1040
Contig ID
5'-most EST
                   LIB3107-058-Q1-K1-C3
                   BLASTX
Method
NCBI GI
                   q3850583
BLAST score
                   393
                   6.0e-38
E value
                   107
Match length
% identity
                   71
NCBI Description
                   (AC005278) Contains similarity to transcription initiation
                   factor IIE, alpha subunit gb X63468 from Homo sapiens.
                   [Arabidopsis thaliana]
                   9112
Seq. No.
Contig ID
                   15265 1.R1040
5'-most EST
                   LIB3056-006-Q1-N1-H5
                   BLASTX
Method
                   q1755162
NCBI GI
BLAST score
                   715
                   2.0e-75
E value
Match length
                   212
% identity
                   (U75192) germin-like protein [Arabidopsis thaliana]
NCBI Description
                   9113
Seq. No.
Contig ID
                   15265 2.R1040
5'-most EST
                   LIB3170-034-Q1-K1-H7
Method
                   BLASTX
NCBI GI
                   q1070358
BLAST score
                   297
                   8.0e-27
E value
Match length
                   88
                   68
% identity
                   (X93171) oxalate oxidase-like protein or germin-like
NCBI Description
                   protein [Hordeum vulgare]
                   9114
Seq. No.
Contig ID
                   15265 4.R1040
5'-most EST
                   pcp700994150.hl
Method
                   BLASTX
                   g2129594
NCBI GI
BLAST score
                   223
```

2.0e-18

E value

5'-most EST

```
Match length
                   70
% identity
                   60
                  germin type 2 - Arabidopsis thaliana
NCBI Description
                   >gi 1107491 emb CAA63023 (X91957) germin type2
                   [Arabidopsis thaliana]
                   9115
Seq. No.
                   15266 1.R1040
Contig ID
                   jC-qmst02400053e08d1
5'-most EST
                   9116
Seq. No.
                   15270 1.R1040
Contig ID
                   LIB3072-057-Q1-K1-F6
5'-most EST
                   BLASTX
Method
                   q3786009
NCBI GI
                   218
BLAST score
E value
                   2.0e-17
                   81
Match length
% identity
                   57
                  (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
                   9117
Seq. No.
                   15272 1.R1040
Contig ID
5'-most EST
                   LIB3107-033-Q1-K1-C1
                   BLASTN
Method
                   g2224730
NCBI GI
                   256
BLAST score
                   1.0e-141
E value
Match length
                   556
                   89
% identity
                   Vigna radiata mRNA for Aux22d, complete cds
NCBI Description
                   9118
Seq. No.
                   15272 2.R1040
Contig ID
5'-most EST
                   kl1701212274.hl
                   BLASTN
Method
                   g2224730
NCBI GI
                   83
BLAST score
                   6.0e-39
E value
Match length
                   159
                   88
% identity
                   Vigna radiata mRNA for Aux22d, complete cds
NCBI Description
Seq. No.
                   15274 1.R1040
Contig ID
5'-most EST
                   gsv701044983.hl
                   BLASTX
Method
                   g1703574
NCBI GI
BLAST score
                   470
                   7.0e-47
E value
Match length
                   185
% identity
                   (U80437) C43E11.9 [Caenorhabditis elegans]
NCBI Description
Seq. No.
                   9120
                   15281 1.R1040
Contig ID
```

LIB3050-027-Q1-E1-H2

Match length

472

```
BLASTX
Method
NCBI GI
                   g2598597
                   249
BLAST score
                   5.0e-21
E value
Match length
                   101
                   50
% identity
                  (Y15371) MtN5 [Medicago truncatula]
NCBI Description
                   9121
Seq. No.
                   15281 2.R1040
Contig ID
5'-most EST
                   LIB3050-006-Q1-E1-F5
                   BLASTX
Method
NCBI GI
                   q2598597
BLAST score
                   315
                   9.0e-29
E value
                   101
Match length
% identity
                   58
NCBI Description
                   (Y15371) MtN5 [Medicago truncatula]
Seq. No.
                   9122
                   15281 3.R1040
Contig ID
5'-most EST
                   q5688\overline{2}80
                   BLASTX
Method
NCBI GI
                   g2598597
BLAST score
                   296
                   1.0e-26
E value
                   102
Match length
                   59
% identity
NCBI Description
                  (Y15371) MtN5 [Medicago truncatula]
                   9123
Seq. No.
                   15281 5.R1040
Contig ID
                   LIB3107-022-01-K1-G6
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2598597
BLAST score
                   159
                   8.0e-11
E value
Match length
                   44
                   66
% identity
NCBI Description
                   (Y15371) MtN5 [Medicago truncatula]
Seq. No.
Contig ID
                   15281 6.R1040
5'-most EST
                   uC-gmropic033g05b1
Seq. No.
                   9125
Contig ID
                   15284 1.R1040
5'-most EST
                   LIB3049-049-Q1-E1-F10
Seq. No.
                   9126
Contig ID
                   15285 1.R1040
5'-most EST
                   kl1701208201.h1
Method
                   BLASTN
NCBI GI
                   g1420935
BLAST score
                   243
E value
                   1.0e-134
```

.**4**)

```
% identity
NCBI Description Vigna unguiculata aspartic proteinase mRNA, complete cds
Seq. No.
Contig ID
                  15291 1.R1040
                  LIB3170-035-Q1-K1-G7
5'-most EST
Seq. No.
                  15296 1.R1040
Contig ID
                  LIB3093-051-Q1-K1-E12
5'-most EST
                  BLASTX
Method
                  g2160183
NCBI GI
BLAST score
                  431
                  3.0e-42
E value
                  134
Match length
% identity
                  67
                  (AC000132) Identical to A. thaliana U2 SnRNP-specific A'
NCBI Description
                  protein (gb_X69137). ESTs gb_ATTS0705, gb_ATTS0339 come
                  from this gene. [Arabidopsis thaliana]
                  9129
Seq. No.
                  15300 1.R1040
Contig ID
                  taw700654794.hl
5'-most EST
                  BLASTX
Method
                  q2459442
NCBI GI
                  360
BLAST score
                  1.0e-33
E value
                  223
Match length
                  43
% identity
                   (AC002332) putative DNA-binding protein PD1 [Arabidopsis
NCBI Description
                  thaliana]
                  9130
Seq. No.
                  15301 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir037e10b1
                  BLASTX
Method
                  g2281633
NCBI GI
BLAST score
                  473
                   6.0e-47
E value
Match length
                  184
                  57
% identity
                   (AF003097) AP2 domain containing protein RAP2.4
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   9131
Contig ID
                   15301 2.R1040
5'-most EST
                  g5058437
                  BLASTX
Method
NCBI GI
                  g2281633
BLAST score
                   428
                   2.0e-50
E value
Match length
                   180
% identity
                   64
                   (AF003097) AP2 domain containing protein RAP2.4
NCBI Description
                   [Arabidopsis thaliana]
```

9132

Seq. No.

```
15301 3.R1040
Contig ID
                   gsv701052436.hl
5'-most EST
                   9133
Seq. No.
                   15317 1.R1040
Contiq ID
                   LIB3049-049-Q1-E1-A6
5'-most EST
                   9134
Seq. No.
                   15318 1.R1040
Contig ID
                   LIB3049-049-Q1-E1-A7
5'-most EST
                   BLASTX
Method
                   g1730109
NCBI GI
                   382
BLAST score
                   5.0e-37
E value
                   99
Match length
% identity
                   LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
NCBI Description
                   HYDROXYLASE) >gi 499022_emb_CAA53580_ (X75966)
                   leucoanthocyanidin dioxygenase [Vitis vinifera]
                   9135
Seq. No.
                   15325 1.R1040
Contig ID
                   LIB31\overline{7}0-036-Q1-K1-E7
5'-most EST
                   9136
Seq. No.
                   15328 1.R1040
Contig ID
                   LIB30\overline{9}3-036-Q1-K1-D8
5'-most EST
Seq. No.
                   9137
                   15329 1.R1040
Contig ID
                   LIB3092-014-Q1-K1-C10
5'-most EST
                   BLASTX
Method
                   q3434971
NCBI GI
BLAST score
                   307
                   2.0e-27
E value
Match length
                   187
                   45
% identity
                   (AB008105) ethylene responsive element binding factor 3
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   9138
                   15329 2.R1040
Contig ID
                   LIB3049-049-Q1-E1-B9
5'-most EST
Method
                   BLASTX
                   g3434971
NCBI GI
                   237
BLAST score
                   1.0e-19
E value
                   67
Match length
                   69
% identity
                    (AB008105) ethylene responsive element binding factor 3
NCBI Description
                    [Arabidopsis thaliana]
                   9139
Seq. No.
                   15331 1.R1040
Contig ID
                   ssr700559243.hl
5'-most EST
```

<u>.</u>

9140

Seq. No.

% identity

56

```
15331 2.R1040
Contig ID
5'-most EST
                   vzy700752955.hl
                   9141
Seq. No.
Contig ID
                   15335 1.R1040
                   awf70\overline{0}838743.h1
5'-most EST
Method
                  BLASTX
                   g4490339
NCBI GI
                   190
BLAST score
                   1.0e-13
E value
                   325
Match length
% identity
                   27
                  (AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
                   9142
Seq. No.
                   15335 2.R1040 -
Contig ID
5'-most EST
                   crh700851218.hl
Seq. No.
                   9143
                   15335 3.R1040
Contig ID
5'-most EST
                   6HC - 01 - Q1 - E1 - H2
                   9144
Seq. No.
Contig ID
                   15335 4.R1040
5'-most EST
                   crh700850801.h1
                   BLASTX
Method
NCBI GI
                   g4490339
BLAST score
                   148
                   2.0e-09
E value
Match length
                   80
% identity
                   41
                  (AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
                   9145
Seq. No.
Contig ID
                   15335 5.R1040
5'-most EST
                   txt700732387.h1
                   9146
Seq. No.
Contig ID
                   15337 1.R1040
5'-most EST
                  LIB3093-042-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                   g1922242
BLAST score
                   175
E value
                   2.0e-12
Match length
                   70
% identity
NCBI Description
                  (Y10084) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   9147
                   15337 2.R1040
Contig ID
5'-most EST
                   zsg701123968.hl
Method
                   BLASTX
                   g1922242
NCBI GI
BLAST score
                   210
E value
                   1.0e-16
                   70
Match length
```

```
NCBI Description
                 (Y10084) hypothetical protein [Arabidopsis thaliana].
                   9148
Seq. No.
                  15337 3.R1040
Contig ID
5'-most EST
                  LIB3049-048-Q1-E1-H11
                   9149
Seq. No.
Contig ID
                  15339 1.R1040
5'-most EST
                   jC-qmle01810046c08a1
                  BLASTX
Method
NCBI GI
                  g1730502
BLAST score
                   255
E value
                   9.0e-22
Match length
                   160
                   38
% identity
                  TRANSMEMBRANE PROTEIN PFT27 >gi 110903 pir A31351 probable
NCBI Description
                   transmembrane protein FT27 - mouse >gi_535682 (M23568)
                   transmembrane protein [Mus musculus]
Seq. No.
                   15342 1.R1040
Contig ID
5'-most EST
                   LIB3109-036-Q1-K1-F2
                   BLASTN
Method
NCBI GI
                   q3335331
BLAST score
                   41
                   2.0e-13
E value
                   189
Match length
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   15345 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800040f08a1
Method
                   BLASTX
NCBI GI
                   g1297187
BLAST score
                   373
                   3.0e-35
E value
Match length
                   170
% identity
                   (U53501) similar to protein encoded by GenBank Accession
NCBI Description
                   Number U41815, nucleoporin 98 [Arabidopsis thaliana]
                   9152
Seq. No.
Contig ID
                   15346 1.R1040
5'-most EST
                   LIB3170-027-Q2-K1-G11
                   BLASTX
Method
NCBI GI
                   g3914667
BLAST score
                   451
E value
                   1.0e-44
                   136
Match length
                   72
% identity
                   50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_2459427 (AC002332) putative chloroplast 50S ribosomal
```

No. 9153

Seq. No.

protein L28 [Arabidopsis thaliana]

5'-most EST

```
15347 1.R1040 😹
Contig ID
5'-most EST
                   jC-gmro02910035b06d1
Seq. No.
                   9154
                   15348 1.R1040
Contig ID
                   LIB3170-033-Q1-K1-B7
5'-most EST
Seq. No.
                   9155
                   15349 1.R1040
Contig ID
                   LIB3072-061-Q1-K1-B1
5'-most EST
                   9156
Seq. No.
Contig ID
                   15353 1.R1040
                   LIB3049-048-Q1-E1-G9
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2708484
BLAST score
                   559
                   1.0e-57
E value
Match length
                   117
                   85
% identity
                  (U79557) IAA24 [Arabidopsis thaliana]
NCBI Description
                   9157
Seq. No.
Contig ID
                   15358 1.R1040
5'-most EST
                   LIB30\overline{4}9-048-Q1-E1-F7
                   9158
Seq. No.
                   15360 1.R1040
Contig ID
5'-most EST
                   LIB3170-034-Q1-K1-D6
Method
                   BLASTX
                   q2827555
NCBI GI
BLAST score
                   421
                   2.0e-41
E value
                   139
Match length
% identity
                   44
                   (AL021635) Translation factor EF-1 alpha - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   9159
Seq. No.
Contig ID
                   15361 1.R1040
                   ncj700975258.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3641837
BLAST score
                   809
                   1.0e-86
E value
Match length
                   243
                   70
% identity
                   (AL023094) Nonclathrin coat protein gamma - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   9160
Seq. No.
                   15363 1.R1040
Contig ID
5'-most EST
                   LIB3049-048-Q1-E1-G12
                   9161
Seq. No.
Contig ID
                   15364 1.R1040
```

LIB3049-048-Q1-E1-G2

```
Seq. No.
                   9162
                   15367 1.R1040
Contig ID
5'-most EST
                   uC-gmropic075g06b1
Method
                   BLASTX
                   g3063457
NCBI GI
BLAST score
                   298
E value
                   5.0e-27
Match length
                   113
% identity
NCBI Description
                  (AC003981) F22013.19 [Arabidopsis thaliana]
Seq. No.
                   9163
                   15367 2.R1040
Contig ID
5'-most EST
                   jsh70\overline{1}064577.h1
                   BLASTX
Method
NCBI GI
                   g3063457
BLAST score
                   165
                   2.0e-11
E value
Match length
                   99
% identity
                   39
                  (AC003981) F22013.19 [Arabidopsis thaliana]
NCBI Description
                   9164
Seq. No.
                   15368 1.R1040
Contig ID
5'-most EST
                   fua701041455.hl
                   BLASTX
Method
                   g3551954
NCBI GI
BLAST score
                   607
E value
                   9.0e-63
                   245
Match length
% identity
                   (AF082030) senescence-associated protein 5 [Hemerocallis
NCBI Description
                   hybrid cultivar]
                   9165
Seq. No.
Contig ID
                   15374 1.R1040
5'-most EST
                   LIB3049-048-Q1-E1-E1
Seq. No.
                   9166
Contig ID
                   15375 1.R1040
5'-most EST
                   LIB3049-048-Q1-E1-E10
Seq. No.
Contig ID
                   15377 1.R1040
5'-most EST
                   LIB3053-011-01-N1-A4
Seq. No.
                   9168
Contig ID
                   15380 1.R1040
5'-most EST
                   LIB3049-011-Q1-E1-B5
Method
                   BLASTX
NCBI GI
                   q3860274
BLAST score
                   338
E value
                   4.0e-31
Match length
                   160
% identity
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
```

```
protein [Arabidopsis thaliana]
Seq. No.
                  15380 2.R1040
Contig ID
                  wrq700787816.h2
5'-most EST
                  9170
Seq. No.
                  15380 8.R1040
Contig ID
                  LIB3049-030-Q1-E1-A4
5'-most EST
                  9171
Seq. No.
                  15388 1.R1040
Contig ID
                  jex70\overline{0}909190.h1
5'-most EST
                  BLASTX
Method
                  q2583108
NCBI GI
BLAST score
                  177
                  1.0e-12
E value
Match length
                  52
% identity
                  (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
                  9172
Seq. No.
                  15395 1.R1040
Contig ID
                  LIB3170-036-Q1-K1-H6
5'-most EST
                  BLASTX
Method
                  q4544407
NCBI GI
                   356
BLAST score
                   1.0e-33
E value
Match length
                   96
                   61
% identity
                  (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   15397 1.R1040
Contig ID
                   LIB3049-048-Q1-E1-D10
5'-most EST
                   BLASTX.
Method
                   q3914467
NCBI GI
BLAST score
                   579
E value
                   8.0e-60
                   145
Match length
% identity
                   79
                   26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                   >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana
                   tabacum]
                   9174
Seq. No.
                   15399 1.R1040
Contig ID
                   LIB3170-034-Q1-K1-B6
5'-most EST
                   9175
Seq. No.
                   15401 1.R1040
Contig ID
                   LIB3049-048-Q1-E1-B4
5'-most EST
```

>gi 4314397 gb_AAD15607_ (AC006232) putative zinc finger

9176

15402 1.R1040

uC-gmronoir051g02b1

Seq. No.

Contig ID

5'-most EST

```
BLASTX
Method
NCBI GI
                  q4220474
BLAST score
                  1493
E value
                  1.0e-166
Match length
                  487
% identity
NCBI Description
                  (AC006069) putative myosin heavy chain [Arabidopsis
                  thaliana]
                  9177
Seq. No.
                  15402 2.R1040
Contig ID
5'-most EST
                  jC-gmro02800023b09d1
Seq. No.
                  15404 1.R1040
Contig ID
5'-most EST
                  LIB3170-036-Q1-K2-C6
                   9179
Seq. No.
Contig ID
                  15408 1.R1040
5'-most EST
                  LIB3139-072-P1-N1-D6
Seq. No.
                   9180
                  15414 1.R1040
Contig ID
5'-most EST
                  LIB3170-036-Q1-K2-F6
                  BLASTX
Method
                   g2315451
NCBI GI
BLAST score
                   291
                   7.0e-26
E value
Match length
                   224
% identity
                   (AF016448) No definition line found [Caenorhabditis
NCBI Description
                  elegans]
                   9181
Seq. No.
Contig ID
                   15417 1.R1040
5'-most EST
                   vwf700675916.hl
                   BLASTN
Method
                   q12387
NCBI GI
                   34
BLAST score
E value
                   2.0e-09
                   69
Match length
% identity
                  Vicia faba chloroplast tRNA-Leu, tRNA-Phe, tRNA-His, ORFX,
NCBI Description
                   NADH-deydrogenase genes & partial sequence ORFx & psbA
                   genes
                   9182
Seq. No.
Contig ID
                   15420 1.R1040
5'-most EST
                   LIB3049-047-Q1-E1-G12
Seq. No.
                   9183
                   15425 1.R1040
Contig ID
5'-most EST
                   LIB3170-035-Q1-K1-H5
Seq. No.
                   9184
Contig ID
                   15426 1.R1040
```

vwf700677929.h1

5'-most EST

NCBI GI

```
Method
                  BLASTX
NCBI GI
                  g3236240
BLAST score
                   947
E value
                  1.0e-102
Match length
                   428
% identity
                   (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                 9185
Seq. No.
Contig ID
                   15426 2.R1040
5'-most EST
                   uC-gmropic041f01b1
                  BLASTX
Method
NCBI GI
                  q4099833
BLAST score
                   227
                   3.0e-18
E value
                  70
Match length
% identity
                   61
                   (U90265) bifunctional nuclease [Zinnia elegans]
NCBI Description
Seq. No.
                   9186
Contig ID
                  15426 3.R1040
5'-most EST
                  leu701155823.h1
Method
                  BLASTX
NCBI GI
                  g3236240
BLAST score
                   1071
                  1.0e-117
E value
                  292
Match length
% identity
                  72
NCBI Description
                   (AC004684) unknown protein [Arabidopsis thaliana]
                   9187
Seq. No.
                  15426 4.R1040
Contig ID
                  LIB3051-050-Q1-K1-B10
5'-most EST
Method
                  BLASTX
                  g3236240
NCBI GI
BLAST score
                   373
E value
                  1.0e-35
                  77
Match length
                   91
% identity
NCBI Description
                   (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                   9188
Contig ID
                  15426 5.R1040
5'-most EST
                  zlv700807524.h1
                  BLASTX
Method
NCBI GI
                  g3236240
BLAST score
                   604
E value
                  1.0e-74
Match length
                  175
% identity
NCBI Description
                   (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                  9189
Contig ID
                  15426 9.R1040
5'-most EST
                  LIB3051-019-Q1-E1-C6
Method
                  BLASTX
```

q3236240

Seq. No.

9197

```
BLAST score
                  213
                  2.0e-22
E value
Match length
                  77
                  71
% identity
NCBI Description
                  (AC004684) unknown protein [Arabidopsis thaliana]
                  9190
Seq. No.
                  15436 1.R1040
Contig ID
                  LIB3049-044-Q1-E1-E1
5'-most EST
                  9191
Seq. No.
                  15436 2.R1040
Contig ID
5'-most EST
                  LIB31\overline{0}9-022-Q1-K1-E12
                  9192
Seq. No.
                  15439 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy011d09b1
Seq. No.
                  9193
Contig ID
                  15441 1.R1040
5'-most EST
                  LIB3073-006-Q1-K1-F10
                  9194
Seq. No.
                  15443 1.R1040
Contig ID
5'-most EST
                  LIB3049-047-Q1-E1-F1
                  9195
Seq. No.
                  15445 1.R1040
Contig ID
                  LIB3051-003-Q1-E1-F12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2129541
                  1586
BLAST score
E value
                  1.0e-177
                  474
Match length
                   67
% identity
                  ATPK19 protein - Arabidopsis thaliana >gi_914079_bbs_160872
NCBI Description
                  ATPK19=ribosomal-protein S6 kinase homolog [Arabidopsis
                  thaliana, Peptide, 471 aa] >gi_867995_dbj_BAA07661
                   (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis
                  thaliana]
                  9196
Seq. No.
Contig ID
                  15445 3.R1040
5'-most EST
                   jC-gmle01810020b07d1
                  BLASTX
Method
NCBI GI
                  q2129541
BLAST score
                  219
                  9.0e-18
E value
Match length
                  63
% identity
                  ATPK19 protein - Arabidopsis thaliana >gi 914079 bbs 160872
NCBI Description
                  ATPK19=ribosomal-protein S6 kinase homolog [Arabidopsis
                  thaliana, Peptide, 471 aa] >gi_867995_dbj_BAA07661
                   (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis
                  thaliana]
```

Contig ID

```
Contig ID
                  15449 1.R1040
5'-most EST
                  LIB3049-047-Q1-E1-F7
                  BLASTX
Method
                  g1731146
NCBI GI
BLAST score
                  406
                  3.0e-39
E value
Match length
                  186
% identity
                  45
                  HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III
NCBI Description
                  >qi 3881615 emb CAA87435 (Z47358) similar to YJU2 protein
                  [Caenorhabditis elegans]
Seq. No.
                  9198
                  15449 2.R1040
Contig ID
                  sat701011550.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1731146
BLAST score
                  209
E value
                  8.0e-17
                  54
Match length
                  69
% identity
                  HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III
NCBI Description
                  >gi 3881615 emb CAA87435 (Z47358) similar to YJU2 protein
                  [Caenorhabditis elegans]
                  9199
Seq. No.
                  15451 1.R1040
Contig ID
5'-most EST
                  leu701156291.hl
Seq. No.
                  9200
                  15451 2.R1040
Contig ID
5'-most EST
                  LIB3049-047-Q1-E1-G1
Method
                  BLASTX
                  a4406775
NCBI GI
BLAST score
                  429
E value
                  1.0e-41
                  379
Match length
% identity
                  (AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
                  9201
Seq. No.
Contig ID
                  15454 1.R1040
                  LIB3139-004-P1-N1-E1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4127781
BLAST score
                  352
                  4.0e-33
E value
Match length
                  130
% identity
                  (AJ012588) Notchless protein [Drosophila melanogaster]
NCBI Description
                  9202
Seq. No.
Contig ID
                  15454 2.R1040
5'-most EST
                  uC-gmflminsoy007g09b1
                  9203
Seq. No.
```

15455_1.R1040

```
5'-most EST
                  LIB3170-033-Q1-K1-F5
                  9204
Seq. No.
                  15456 1.R1040
Contig ID
5'-most EST
                  LIB3087-002-Q1-K1-A7
                  BLASTX
Method
                  q3600051
NCBI GI
BLAST score
                  185
                  2.0e-13
E value
Match length
                  44
                  77
% identity
                  (AF080120) contains similarity to the single-strand binding
NCBI Description
                  proteins family (Pfam: SSB.hmm, score: 24.02) [Arabidopsis
                  thaliana]
                  9205
Seq. No.
Contig ID
                  15463 1.R1040
5'-most EST
                  LIB3049-047-Q1-E1-D11
Method
                  BLASTX
                  q4138581
NCBI GI
BLAST score
                  275
                  2.0e-24
E value
                  131
Match length
% identity
                   (X98474) mitochondrial energy transfer protein [Solanum
NCBI Description
                  tuberosum]
                   9206
Seq. No.
Contig ID
                   15466 1.R1040
5'-most EST
                  LIB3092-011-Q1-K1-C5
                  BLASTN
Method
                  g3985934
NCBI GI
                  53
BLAST score
                   8.0e-21
E value
Match length
                   279
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MJE7, complete sequence [Arabidopsis thaliana]
                   9207
Seq. No.
Contig ID
                   15467 1.R1040
5'-most EST
                   LIB3049-047-Q1-E1-D5
                   9208
Seq. No.
Contig ID
                   15476 1.R1040
5'-most EST
                   LIB3170-033-Q1-K1-E5
                   BLASTX
Method
                   g1168251
NCBI GI
BLAST score
                   416
                   9.0e-41
E value
Match length
                   95
                   79
% identity
                   PROBABLE CYSTEINE PROTEINASE A494 PRECURSOR
NCBI Description
                   >gi_1076384_pir__S46535 probable cysteine proteinase (EC
                   3.4.22.-) (clone A1494) - Arabidopsis thaliana (fragment)
                   >qi 516865 emb CAA52403 (X74359) putative thiol protease
```

[Arabidopsis thaliana]

BLAST score

616

```
9209
Seq. No.
                  15477 1.R1040
Contig ID
                  LIB3170-036-Q1-K2-F5
5'-most EST
                   BLASTX
Method
                  g4006904
NCBI GI
                   278
BLAST score
                   1.0e-24
E value
                   103
Match length
% identity .
                  (Z99708) putative MADS-box protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9210
                   15483 1.R1040
Contig ID
5'-most EST
                   LIB3049-047-Q1-E1-B7
Seq. No.
                   9211
                   15483 2.R1040
Contig ID.
                   zzp70\overline{0}835537.h1
5'-most EST
                   9212
Seq. No.
                   15484 1.R1040
Contig ID
                   LIB3051-039-Q1-K1-B12
5'-most EST
                   9213
Seq. No.
                   15484 2.R1040
Contig ID
                   bth700847209.h1
5'-most EST
Seq. No.
                   9214
Contig ID
                   15485 1.R1040
                   LIB3049-047-Q1-E1-B9
5'-most EST
                   9215
Seq. No.
                   15485 2.R1040
Contig ID
5'-most EST
                   bth700845065.h1
                   9216
Seq. No.
                   15486 1.R1040
Contig ID
                   LIB3049-047-Q1-E1-C1
5'-most EST
Method
                   BLASTX
                   g3859591
NCBI GI
BLAST score
                   202
                   2.0e-15
E value
Match length
                   104
                   40
% identity
                   (AF104919) No definition line found [Arabidopsis thaliana]
NCBI Description
                   9217
Seq. No.
Contig ID
                   15489 1.R1040
5'-most EST
                   zpv700763607.hl
                   9218
Seq. No.
Contig ID
                   15492 1.R1040
5'-most EST
                   q5126671
Method
                   BLASTX
NCBI GI
                   q4538978
```

```
E value
                   8.0e-64
Match length
                   163
                   72
% identity
                   (AL049487) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9219
Seq. No.
                   15499 1.R1040
Contig ID
                   hyd700725239.h1
5'-most EST
                   BLASTX
Method
                   g2911047
NCBI GI
                   400
BLAST score
                   8.0e-39
E value
                   112
Match length
                   73
% identity
                   (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   9220
Seq. No.
Contig ID
                   15500 1.R1040
                   LIB3109-022-Q1-K1-C2
5'-most EST
                   9221
Seq. No.
                   15500 2.R1040
Contig ID
5'-most EST
                   LIB3051-104-Q1-K1-C6
                   9222
Seq. No.
                   15500 3.R1040
Contig ID
                   fC-gm\overline{f}1700907636a1
5'-most EST
Seq. No.
                   9223
Contig ID
                   15507 1.R1040
                   LIB3049-046-Q1-E1-F5
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4335725
BLAST score
                   236
                   8.0e-20
E value
Match length
                   85
% identity
                   (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9224
Contig ID
                   15513 1.R1040
                   LIB31\overline{3}8-090-P1-N1-A6
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2827699
BLAST score
                   447
E value
                   6.0e-44
Match length
                   278
% identity
                   (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   9225
Seq. No.
                   15515 1.R1040
Contig ID
5'-most EST
                   LIB3170-033-Q1-K1-A5
Seq. No.
                   9226
Contig ID
                   15516 1.R1040
```

LIB3049-046-Q1-E1-G4

```
Seq. No.
                  9227
                  15518 1.R1040
Contig ID
                  LIB3049-046-Q1-E1-G7
5'-most EST
Method
                  BLASTN
                  q3421089
NCBI GI
BLAST score
                  270
E value
                  1.0e-150
Match length
                  654
                  85
% identity
NCBI Description
                  Arabidopsis thaliana 20S proteasome subunit PAE2 (PAE2)
                  mRNA, complete cds
                  9228
Seq. No.
Contig ID
                  15518 2.R1040
5'-most EST
                  LIB3170-052-Q1-J1-F7
Seq. No.
                  9229
Contig ID
                  15518 3.R1040
5'-most EST
                  LIB3051-029-Q1-K1-B3
Method
                  BLASTN
                  q3421089
NCBI GI
                  125
BLAST score
E value
                  8.0e-64
                  333
Match length
% identity
                  Arabidopsis thaliana 20S proteasome subunit PAE2 (PAE2)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  9230
Contig ID
                  15518 4.R1040
5'-most EST
                  fua701039082.h1
                  BLASTX
Method
                  q3421090
NCBI GI
BLAST score
                  224
                  3.0e-36
E value
                  101
Match length
% identity
NCBI Description
                  (AF043525) 20S proteasome subunit PAE2 [Arabidopsis
                  thaliana]
Seq. No.
                  9231
Contig ID
                  15523 1.R1040
5'-most EST
                  uC-gmflminsoy018c06b1
Method
                  BLASTX
NCBI GI
                  q2129559
BLAST score
                  754
                  3.0e-80
E value
Match length
                  181
% identity
NCBI Description
                  cellulase homolog OR16pep - Arabidopsis thaliana
                  >gi 1022807 (U37702) cellulase [Arabidopsis thaliana]
                  >gi 3493633 (AF074092) cellulase [Arabidopsis thaliana]
                  >gi 3598956 (AF074375) cellulase [Arabidopsis thaliana]
```

[Arabidopsis thaliana]

>gi 3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN

Method

BLASTX

```
9232
Seq. No.
                  15523 2.R1040
Contig ID
5'-most EST
                  pmv700890951.hl
                  BLASTX
Method
                  q2129559
NCBI GI
                  162
BLAST score
                  1.0e-20
E value
                  70
Match length
                  79
% identity
                  cellulase homolog OR16pep - Arabidopsis thaliana
NCBI Description
                  >gi 1022807 (U37702) cellulase [Arabidopsis thaliana]
                  >qi 3493633 (AF074092) cellulase [Arabidopsis thaliana]
                  >qi 3598956 (AF074375) cellulase [Arabidopsis thaliana]
                  >qi 3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                   [Arabidopsis thaliana]
                  9233
Seq. No.
                  15525 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy063d10b1
                   9234
Seq. No.
                  15526 1.R1040
Contig ID
                   jC-qmf102220143d02d1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q421948
BLAST score
                   666
                   9.0e-70
E value
                   191
Match length
                   64
% identity
                  UDP rhamnose--anthocyanidin-3-glucoside
NCBI Description
                   rhamnosyltransferase - garden petunia
                   9235
Seq. No.
                   15527 1.R1040
Contig ID
5'-most EST
                   pmv700890051.hl
                   9236
Seq. No.
                   15528 1.R1040
Contig ID
                   LIB3049-046-Q1-E1-E12
5'-most EST
                   BLASTX
Method
                   g3600033
NCBI GI
BLAST score
                   570
                   7.0e-59
E value
Match length
                   149
                   71
% identity
                   (AF080119) contains similarity to the N terminal domain of
NCBI Description
                   the El protein (Pfam: El_N.hmm, score: 12.36) [Arabidopsis
                   thaliana]
                   9237
Seq. No.
Contig ID
                   15529 1.R1040
5'-most EST
                   LIB3170-035-Q1-K1-D4
                   9238
Seq. No.
Contig ID
                   15535 1.R1040
5'-most EST
                   zhf700952064.h1
```

```
NCBI GI
                  g1946367
BLAST score
                  215
                  6.0e-17
E value
Match length
                  65
                  62
% identity
                  (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  15535 2.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy040a03b1
                  BLASTX
Method
                  q1946367
NCBI GI
BLAST score
                  611
                  2.0e-63
E value
                  164
Match length
                  70
% identity
NCBI Description
                  (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                  9240
                  15537 1.R1040
Contig ID
                  jC-gmro02910061h09a1
5'-most EST
                  BLASTX
Method
                  q3724328
NCBI GI
BLAST score
                  144
                  1.0e-08
E value
                  160
Match length
                  27
% identity
                  (AB013095) heme-binding protein [Mus musculus]
NCBI Description
                  9241
Seq. No.
                  15541 1.R1040
Contig ID
5'-most EST
                  LIB3049-046-Q1-E1-C3
                  9242
Seq. No.
Contig ID
                  15541 2.R1040
5'-most EST
                  LIB3072-061-Q1-K1-A2
                   9243
Seq. No.
                  15542 1.R1040
Contig ID
                  pcp700993990.h1
5'-most EST
Seq. No.
                   9244
                  15546 1.R1040
Contig ID
5'-most EST
                  LIB3170-028-Q1-K1-B12
Seq. No.
                   9245
Contig ID
                  15546 2.R1040
5'-most EST
                  leu701147556.h1
                   9246
Seq. No.
Contig ID
                   15550 1.R1040
5'-most EST
                  LIB3170-034-Q1-K1-B4
Seq. No.
                   9247
Contig ID
                   15550 2.R1040
```

LIB3138-097-Q1-N1-F10

```
9248
Seq. No.
Contig ID
                   15551 1.R1040
5'-most EST
                   LIB3049-046-Q1-E1-B9
                   BLASTX
Method
NCBI GI
                   q1706311
                   376
BLAST score
                   5.0e-36
E value
Match length
                   189
                   43
% identity
                   PROBABLE ATP-DEPENDENT RNA HELICASE DBP1 (HELICASE CA1)
NCBI Description
                   >gi 2132404 pir S62003 probable ATP-dependent RNA helicase
                   DBPI - yeast (Saccharomyces cerevisiae) >gi_1163095
                   (U43503) Dbp1p, Lph8p [Saccharomyces cerevisiae]
                   9249
Seq. No.
                   15557 1.R1040
Contig ID
5'-most EST
                   zsq701119272.hl
Seq. No.
                   9250
Contig ID
                   15560 1.R1040
                   LIB3170-033-Q1-K1-D4
5'-most EST
                   BLASTX
Method
                   q1076715
NCBI GI
BLAST score
                   239
E value
                   9.0e-20
                   82
Match length
% identity
                   50
                   abscisic acid-induced protein HVA22 - barley >gi 404589
NCBI Description
                   (L19119) A22 [Hordeum vulgare]
                   9251
Seq. No.
Contig ID
                   15561 1.R1040
                   fua701043583.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2252631
                   263
BLAST score
                   7.0e-23
E value
                   83
Match length
                   63
% identity
NCBI Description
                   (U95973) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   9252
                   15561 2.R1040
Contig ID
5'-most EST
                   trc700561886.hl
Seq. No.
                   9253
                   15565 1.R1040
Contig ID
5'-most EST
                   LIB3049-046-Q1-E1-B3
                   BLASTX
Method
NCBI GI
                   g2288985
BLAST score
                   216
                   3.0e-17
E value
Match length
                   94
% identity
                   (AC002335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

9254

Seq. No.

```
15566 1.R1040
Contig ID
5'-most EST
                  LIB3049-046-Q1-E1-B4
                  9255
Seq. No.
Contig ID
                  15572 1.R1040
                  hrw701060691.hl
5'-most EST
Seq. No.
                  9256
                  15579 1.R1040
Contig ID
5'-most EST
                  LIB3170-033-Q1-K1-A4
Seq. No.
                  9257
Contig ID
                  15583 1.R1040
5'-most EST
                  LIB3170-036-Q1-K1-B4
                  9258
Seq. No.
Contig ID
                  15587 1.R1040
5'-most EST
                  LIB3049-046-Q1-E1-A2
Method
                  BLASTN
                  g2959438
NCBI GI
BLAST score
                  79
                  2.0e-36
E value
Match length
                  229
% identity
                  Glycine max gene for phosphoenolpyruvate carboxylase, 5'
NCBI Description
                  untranslated region, partial cds
                  9259
Seq. No.
Contig ID
                  15594 1.R1040
5'-most EST
                  uC-gmrominsoy298f01b1
Method
                  BLASTX
                  q1246823
NCBI GI
                  1426
BLAST score
                  1.0e-158
E value
Match length
                  349
% identity
                  (X89865) unknown [Phoenix dactylifera]
NCBI Description
                  9260
Seq. No.
Contig ID
                  15594 2.R1040
5'-most EST
                  uC-gmflminsoy084e03b1
Method
                  BLASTX
                  g1246823
NCBI GI
BLAST score
                  170
                  4.0e-12
E value
Match length
                  49
                  69
% identity
                  (X89865) unknown [Phoenix dactylifera]
NCBI Description
                  9261
Seq. No.
Contig ID
                  15595 1.R1040
5'-most EST
                  LIB3170-034-Q1-K1-G3
Seq. No.
                  9262
                  15597 1.R1040
Contig ID
```

LIB3170-036-Q1-K1-A4

```
Seq. No.
                   9263
Contig ID
                   15598 1.R1040
5'-most EST
                   uC-gmrominsoy060e11b1
Method
                   BLASTX
NCBI GI
                   q4469026
BLAST score
                   294
E value
                   2.0e-26
Match length
                   106
% identity
                   60
NCBI Description
                   (AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   9264
Contig ID
                   15598 2.R1040
5'-most EST
                   pcp700991182.h1
Method
                   BLASTX
NCBI GI
                   q4469026
BLAST score
                   185
E value
                   9.0e-14
Match length
                   70
% identity
NCBI Description
                   (AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   9265
Contig ID
                   15605 1.R1040
5'-most EST
                   smc700747914.hl
Seq. No.
                   9266
Contig ID
                   15605 2.R1040
5'-most EST
                   kl1701206351.h1
Seq. No.
                   9267
Contig ID
                   15610 1.R1040
5'-most EST
                   LIB3170-034-Q1-K1-F8
                   9268
Seq. No.
Contig ID
                   15612 1.R1040
5'-most EST
                   crh700852730.h1
Method
                   BLASTX
NCBI GI
                   g4263707
BLAST score
                   819
E value
                   1.0e-110
Match length
                   307
% identity
                   64
NCBI Description
                   (AC006223) putative 70kD heat shock protein [Arabidopsis]
                   thaliana]
                   9269
Seq. No.
                   15613 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir0001c11a1
Method
                   BLASTX
NCBI GI
                   g4337044
BLAST score
                   319
E value
                   2.0e-29
Match length
                  90
% identity
                   69
NCBI Description
                   (AF124161) molybdopterin synthase sulphurylase [Nicotiana
```

plumbaginifolia]

E value

```
9270
Seq. No.
Contig ID
                   15613 2.R1040
5'-most EST
                   LIB3049-045-Q1-E1-E4
Method
                   BLASTX
NCBI GI
                   g4337044
BLAST score
                   297
                   5.0e-27
E value
Match length
                   86
% identity
                   (AF124161) molybdopterin synthase sulphurylase [Nicotiana
NCBI Description
                   plumbaginifolia]
Seq. No.
                   9271
Contig ID
                   15614 1.R1040
5'-most EST
                   LIB3170-036-Q1-J1-F11
Seq. No.
                   9272
Contig ID
                   15615 1.R1040
5'-most EST
                   LIB3109-014-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   g2982243
BLAST score
                   475
E value
                   3.0e-47
Match length
                   158
% identity
NCBI Description
                   (AF051204) hypothetical protein [Picea mariana]
Seq. No.
                   9273
Contig ID
                   15615 2.R1040
5'-most EST
                   LIB3107-029-Q1-K1-E11
                   BLASTX
Method
NCBI GI
                   g2982243
BLAST score
                   187
E value
                   7.0e-14
Match length
                   69
                   54
% identity
NCBI Description
                   (AF051204) hypothetical protein [Picea mariana]
Seq. No.
                   9274
Contig ID
                   15615 4.R1040
5'-most EST
                   LIB3109-055-Q1-K1-F5
                   BLASTX
Method
NCBI GI
                   g2982243
BLAST score
                   196
E value
                   4.0e-15
Match length
                   93
% identity
NCBI Description
                   (AF051204) hypothetical protein [Picea mariana]
Seq. No.
                   9275
Contig ID
                   15617 1.R1040
5'-most EST
                   LIB3094-011-Q1-K1-E3
Method
                   BLASTN
NCBI GI
                   g21045
BLAST score
                   214
```

1.0e-116

```
691
Match length
                   61
% identity
                  P.vulgaris mRNA for prolin-rich protein (PvPRP1)
NCBI Description
                  9276
Seq. No.
                  15617 2.R1040
Contig ID
                   asn70\overline{1}135096.h1
5'-most EST
                  BLASTN
Method
                   g21045
NCBI GI
                   35
BLAST score
                   3.0e-10
E value
                   93
Match length
                   90
% identity
                  P.vulgaris mRNA for prolin-rich protein (PvPRP1)
NCBI Description
Seq. No.
                   9277
                   15620 1.R1040
Contig ID
                   rca700998350.hl
5'-most EST
                   BLASTX
Method
                   q4191782
NCBI GI
BLAST score
                   548
                   2.0e-56
E value
Match length
                   124
% identity
                   (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
NCBI Description
                   9278
Seq. No.
Contig ID
                   15621 1.R1040
5'-most EST
                   LIB3072-053-Q1-E1-D8
                   9279
Seq. No.
                   15623 1.R1040
Contig ID
                   wrg700791003.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3461884
BLAST score
                   340
                   1.0e-31
E value
                   95
Match length
                   72
% identity
                   (AB006082) phosphoribosyl-ATP pyrophosphohydrolase
NCBI Description
                   [Arabidopsis thaliana] >gi 3461886_dbj_BAA32529_ (AB006083)
                   phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis
                   thaliana]
                   9280
Seq. No.
                   15626 1.R1040
Contig ID
                   LIB3170-087-Q1-K1-C5
5'-most EST
Method
                   BLASTX
                   g2706450
NCBI GI
BLAST score
                   903
                   2.0e-97
E value
Match length
                   216
% identity
                   81
                   (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                   pyrophosphatase [Solanum tuberosum]
```

9281

Seq. No.

% identity

```
15626_2.R1040
Contig ID
                   1eu70\overline{1}146961.h1
5'-most EST
                   BLASTX
Method
                   g3695383
NCBI GI
                   581
BLAST score
                   6.0e-60
E value
                   124
Match length
                   86
% identity
                   (AF096370) similar to inorganic pyrophosphatase (Pfam:
NCBI Description
                   PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis
                   thaliana]
                   9282
Seq. No.
                   15626 3.R1040
Contig ID
                   uC-gmrominsoy208e01b1
5'-most EST
                   BLASTX
Method
                   g2706450
NCBI GI
                   322
BLAST score
                   1.0e-29
E value
                   75
Match length
                   79
% identity
                   (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                   pyrophosphatase [Solanum tuberosum]
                   9283
Seq. No.
                   15626 4.R1040
Contig ID
                   jC-gmro02800028b03d1
5'-most EST
Method
                   BLASTX
                   q2706450
NCBI GI
                   257
BLAST score
                   4.0e-22
E value
                   59
Match length
                   85
% identity
                   (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                   pyrophosphatase [Solanum tuberosum]
                   9284
Seq. No.
                   15626 5.R1040
Contig ID
                   LIB3107-052-Q1-K1-E6
5'-most EST
Method
                   BLASTX
                   g2706450
NCBI GI
                   305
BLAST score
                   9.0e-28
E value
                   85
Match length
% identity
                   71
                   (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                   pyrophosphatase [Solanum tuberosum]
                   9285
Seq. No.
                   15626 6.R1040
Contig ID
                   kl1701207561.hl
5'-most EST
                   BLASTX
Method
                   g3695383
NCBI GI
                   328
BLAST score
                   2.0e-30
E value
                   70
Match length
                   86
```

```
(AF096370) similar to inorganic pyrophosphatase (Pfam:
NCBI Description
                   PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis
                  thaliana]
                  9286
Seq. No.
                  15627 1.R1040
Contig ID
                   jC-gmro02800032f02a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3775999
BLAST score
                  472
                  6.0e-47
E value
Match length
                  102
                  86
% identity
                  (AJ010463) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  9287
Seq. No.
                  15632 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810091a04d1
                  BLASTX
Method
                  g3702321
NCBI GI
BLAST score
                  541
E value
                  3.0e-55
                  114
Match length
                  88
% identity
                   (AC005397) putative TGF-beta receptor interacting protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  9288
                  15632 2.R1040
Contig ID
                   jC-gmro02910046d09d1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3702321
BLAST score
                  453
                  3.0e-45
E value
                  91
Match length
                  93
% identity
                   (AC005397) putative TGF-beta receptor interacting protein
NCBI Description
                   [Arabidopsis thaliana]
                  9289
Seq. No.
                  15635 1.R1040
Contig ID
5'-most EST
                  leu70\overline{1}145544.h1
                  BLASTX
Method
NCBI GI
                  q3063698
BLAST score
                  551
                  2.0e-56
E value
                  179
Match length
% identity
NCBI Description
                   (AL022537) putative protein [Arabidopsis thaliana]
                  9290
Seq. No.
                  15642 1.R1040
Contig ID
```

5'-most EST LIB3049-045-Q1-E1-A3

Seq. No.

Contig ID 15645 1.R1040

5'-most EST LIB3138-073-P1-N1-C9

9291

1654

1.

```
9292
Seq. No.
                   15648 1.R1040
Contig ID
5'-most EST
                   LIB3170-036-Q1-K2-H3
                   9293
Seq. No.
                   15648 3.R1040
Contig ID
                   bth700846272.h1
5'-most EST
                   9294
Seq. No.
                   15649 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910016h09a1
                   9295
Seq. No.
                   15650 1.R1040
Contig ID
5'-most EST
                   LIB3170-034-Q1-K1-B3
                   BLASTX
Method
                   g3876622
NCBI GI
                   243
BLAST score
                   2.0e-20
E value
                   96
Match length
                   45
% identity
                   (Z81523) Similarity to Yeast SOH-1 protein (SW:P38633)
NCBI Description
                   [Caenorhabditis elegans]
                   9296
Seq. No.
                   15652 1.R1040
Contig ID
5'-most EST
                   LIB3049-040-Q1-E1-B1
                   9297
Seq. No.
                   15654 1.R1040
Contig ID
                   LIB3170-035-Q1-K1-A3
5'-most EST
                   9298
Seq. No.
                   15659 1.R1040
Contig ID
                   leu70\overline{1}150418.h1
5'-most EST
                   BLASTX
Method
                   g2982698
NCBI GI
BLAST score
                   290
                   2.0e-25
E value
                   208
Match length
% identity
                   (AB006153) tFZR1 [Oncorhynchus mykiss]
NCBI Description
                   9299
Seq. No.
                   15661 1.R1040
Contig ID
                   LIB3170-036-Q1-K2-E3
5'-most EST
                   9300
Seq. No.
                   15662_1.R1040
Contig ID
5'-most EST
                   LIB3049-044-Q1-E1-G8
                   BLASTX
Method
                   g3341443
NCBI GI
                   333
BLAST score
                   4.0e-31
E value
                   120
Match length
```

.....

55

% identity

100

```
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                  9301
Seq. No.
                   15665 1.R1040
Contig ID
5'-most EST
                   LIB3049-044-Q1-E1-H11
                   9302
Seq. No.
                   15667 1.R1040
Contig ID
5'-most EST
                   dpv70\overline{1}097441.h1
Method
                   BLASTX
                   g3668089
NCBI GI
                   840
BLAST score
                   6.0e-90
E value
Match length
                   298
% identity
                   52
                   (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9303
                   15667 2.R1040
Contig ID
5'-most EST
                   ncj700982585.h1
Method
                   BLASTX
                   g3668089
NCBI GI
BLAST score
                   162
                   4.0e-11
E value
                   55
Match length
% identity
                   51
                   (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9304
                   15672 1.R1040
Contig ID
                   uC-gmropic096g06b1
5'-most EST
Method
                   BLASTX
                   g2832632
NCBI GI
BLAST score
                   616
                   6.0e-64
E value
Match length
                   191
% identity
                   68
                   (AL021711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9305
Seq. No.
Contig ID
                   15673 1.R1040
5'-most EST
                   ckk700605877.h2
                   9306
Seq. No.
Contig ID
                   15678 1.R1040
5'-most EST
                   LIB3049-044-Q1-E1-F11
Method
                   BLASTX
                   g3560243
NCBI GI
BLAST score
                   169
E value
                   8.0e-12
Match length
                   74
% identity
NCBI Description
                   (AL031532) putative hydrolase [Schizosaccharomyces pombe]
                   9307
Seq. No.
                   15678 2.R1040
Contig ID
```

LIB3106-035-Q1-K1-G12

.

```
BLASTX
Method-
                   q3560243
NCBI GI
BLAST score
                   192
                   3.0e-14
E value
Match length
                   99
                   56
% identity
                   (AL031532) putative hydrolase [Schizosaccharomyces pombe]
NCBI Description
                   9308
Seq. No.
                   15679 1.R1040
Contig ID
                   LIB3170-036-Q1-K1-D3
5'-most EST
                   BLASTX
Method
                   g3319357
NCBI GI
BLAST score
                   191
                   2.0e-14
E value
                   67
Match length
                   57
% identity
                   (AF077407) contains similarity to phosphoenolpyruvate
NCBI Description
                   synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
                   9309
Seq. No.
                   15685_1.R1040
Contig ID
5'-most EST
                   gsv701049807.hl
Method
                   BLASTX
                   g3687224
NCBI GI
BLAST score
                   378
                   4.0e-36
E value
Match length
                   126
% identity
                   59
                   (AC005169) putative N-acetyl-gamma-glutamyl-phosphate
NCBI Description
                   reductase [Arabidopsis thaliana]
                   9310
Seq. No.
Contig ID
                   15685 2.R1040
                   LIB3109-017-Q1-K2-F7
5'-most EST
Method
                   BLASTX
                   g3687224
NCBI GI
                   208
BLAST score
E value
                   2.0e-16
Match length
                   71
% identity
                   58
                   (AC005169) putative N-acetyl-gamma-glutamyl-phosphate
NCBI Description
                   reductase [Arabidopsis thaliana]
Seq. No.
                   9311
                   15689 1.R1040
Contig ID
                   LIB3170-033-Q1-J1-E3
5'-most EST
                   9312
Seq. No.
Contig ID
                   15690 1.R1040
                   LIB3049-008-Q1-E1-B4
5'-most EST
Method
                   BLASTN
                   g4164411
NCBI GI
                   34
BLAST score
                   2.0e-09
E value
Match length
                   38
```

97

% identity

```
NCBI Description Pisum sativum mitochondrial rpl5, rps14 and cob genes
                  9313
Seq. No.
                  15692 1.R1040
Contig ID
5'-most EST
                  kl1701202946.hl
                  BLASTX
Method
                  g3063695
NCBI GI
BLAST score
                  321
E value
                  2.0e-29
Match length
                  109
% identity
                  62
                  (AL022537) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  9314
Contig ID
                  15701 1.R1040
                  LIB3049-044-Q1-E1-E12
5'-most EST
Method
                  BLASTX
                  g2346988
NCBI GI
BLAST score
                  174
                  3.0e-12
E value
                  98
Match length
                  25
% identity
                  (AB006606) ZPT4-4 [Petunia x hybrida]
NCBI Description
                  9315
Seq. No.
                  15704 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy318b03b1
Method
                  BLASTN
                  g11303
NCBI GI
                   637
BLAST score
                  0.0e + 00
E value
Match length
                  725
                  97
% identity
                  G.max chloroplast mRNA for ndhK polypeptide and orf 158/159
NCBI Description
                  9316
Seq. No.
                  15704 2.R1040
Contig ID
5'-most EST
                  LIB3109-031-Q1-K1-E4
Method
                  BLASTN
                  g881440
NCBI GI
                   232
BLAST score
                   1.0e-127
E value
                   328
Match length
                   93
% identity
                  Lupinus luteus NADH-plastoquinone oxidoreductase (ndhC)
NCBI Description
                   gene, chloroplast gene encoding chloroplast protein,
                   complete cds
                   9317
Seq. No.
                   15706_1.R1040
Contig ID
                  hrw701058184.h1
5'-most EST
                   BLASTX
Method
                   g3320120
NCBI GI
                   162
BLAST score
                   6.0e-11
E value
                   65
Match length
```

48

% identity



NCBI Description (U66669) 3-hydroxyisobutyryl-coenzyme A hydrolase [Homo sapiens]

Seq. No. 9318

Contig ID 15711_1.R1040 5'-most EST hyd700728580.h1

Method BLASTX
NCBI GI g3935166
BLAST score 205
E value 6.0e-16
Match length 141
% identity 38

NCBI Description (AC004557) F17L21.9 [Arabidopsis thaliana]

Seq. No. 9319

Contig ID 15712_1.R1040

5'-most EST LIB3106-022-Q1-K1-B9

Method BLASTX
NCBI GI g2500116
BLAST score 1786
E value 0.0e+00
Match length 402
% identity 87

NCBI Description GLUTATHIONE REDUCTASE, CYTOSOLIC (GR) (GRASE) (GOR2)

>gi_1370285_emb_CAA66924_ (X98274) glutathione reductase

[Pisum sativum]

Seq. No. 9320

Contig ID 15712_3.R1040 5'-most EST nsy700645585.h1

Seq. No. 9321

Contig ID 15715_1.R1040 5'-most EST kl1701214315.h1

Seq. No. 9322

Contig ID 15716_1.R1040

5'-most EST LIB3049-044-Q1-E1-C2

Seq. No. 9323

Contig ID 15720_1.R1040

5'-most EST LIB3170-035-Q1-K1-E2

Method BLASTX
NCBI GI g2988398
BLAST score 160
E value 1.0e-10
Match length 108
% identity 37

NCBI Description (AC004381) Unknown gene product [Homo sapiens]

Seq. No. 9324

Contig ID 15720_2.R1040

5'-most EST LIB3049-033-Q1-E1-C11

Seq. No. 9325

Contig ID 15720_3.R1040

5'-most EST LIB3106-065-P1-K1-E4

```
9326
Seq. No.
                  15721 1.R1040
Contig ID
                  LIB3049-044-Q1-E1-C8
5'-most EST
                  BLASTX
Method
                  g3297808
NCBI GI
BLAST score
                  210
E value
                  2.0e-33
                  136
Match length
% identity
                  51
                  (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
                  9327
Seq. No.
                  15727 1.R1040
Contig ID
                  LIB3049-044-Q1-E1-A3
5'-most EST
                  9328
Seq. No.
                  15738 1.R1040
Contig ID
                  sat701004184.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4263711
BLAST score
                  658
E value
                   9.0e-69
Match length
                  250
                   52
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   9329
Seq. No.
                  15738 2.R1040
Contig ID
5'-most EST
                  LIB3092-037-Q1-K1-B3
Method
                  BLASTX
                   g4263711
NCBI GI
                   285
BLAST score
                   2.0e-25
E value
Match length
                   121
                   47
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   9330
Seq. No.
                   15740 1.R1040
Contig ID
                   LIB3049-044-Q1-E1-B6
5'-most EST
                   BLASTX
Method
NCBI GI
                   g128378
BLAST score
                   205
                   3.0e-16
E value
Match length
                  -76
                   50
% identity
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN A (NS-LTP A)
                   (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)
                   >gi_82031_pir__S07142 nonspecific lipid transfer protein -
                   castor bean >gi 224909 prf 1204170A protein, nonspecific
                   lipid transfer [Ricinus communis]
                   9331
Seq. No.
```

15742 1.R1040

Contig ID

```
dkc700968011.h1
5'-most EST
                   BLASTX
Method
                   g2245138
NCBI GI
                   858
BLAST score
                   4.0e-92
E value
                   258
Match length
                   70
% identity
                   (297344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9332
Seq. No.
                   15742 2.R1040
Contig ID
                   jC-gmst02400025c09a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2245138
BLAST score
                   374
E value
                   8.0e-36
Match length
                   121
                   64
% identity
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9333
Seq. No.
Contig ID
                   15749 1.R1040
5'-most EST
                   LIB3049-043-Q1-E1-H1
                   9334
Seq. No.
                   15754 1.R1040
Contig ID
                   wvk700682131.hl
5'-most EST
                   BLASTX
Method
                   q3668080
NCBI GI
BLAST score
                   912
                   2.0e-98
E value
Match length
                   289
                   67
% identity
                   (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   9335
Seq. No.
Contig ID
                   15754 2.R1040
5'-most EST
                   LIB3106-063-Q1-K1-C9
                   9336
Seq. No.
Contig ID
                   15757 1.R1040
                   LIB3170-035-Q1-K1-D2
5'-most EST
                   9337
Seq. No.
                   15759 1.R1040
Contig ID
                   LIB30\overline{9}3-044-Q1-K1-F3
5'-most EST
                   BLASTX
Method
                   g4091117
NCBI GI
BLAST score
                   535
                   2.0e-54
E value
                   171
Match length
% identity
                   (AF047428) nucleic acid binding protein [Oryza sativa]
NCBI Description
                   9338
Seq. No.
```

15759 2.R1040

LIB3049-043-Q1-E1-G2

Contig ID

5'-most EST

```
Method
                   BLASTX
                   g166410
NCBI GI
BLAST score
                   219
                   6.0e-18
E value
Match length
                   48
                   85
% identity
                   (L07291) Alfin-1 [Medicago sativa]
NCBI Description
                   9339
Seq. No.
                   15761 1.R1040
Contig ID
                   LIB3170-036-Q1-K1-H2
5'-most EST
Method
                   BLASTX
                   g3201554
NCBI GI
BLAST score
                   767
E value
                   1.0e-81
Match length
                   219
% identity
                   68
NCBI Description
                   (AJ006501) beta-D-glucosidase [Tropaeolum majus]
Seq. No.
                   9340
Contig ID
                   15763 1.R1040
5'-most EST
                   jC-gmst02400001d02a1
Method
                   BLASTX
NCBI GI
                   g2190007
BLAST score
                   623
E value
                   2.0e-65
Match length
                   307
                   43
% identity
NCBI Description
                   (AB004109) phosphatidylserine synthase II [Cricetulus
                   griseus]
                   9341
Seq. No.
Contig ID
                   15764 1.R1040
5'-most EST
                   LIB3170-036-Q1-K1-B2
Seq. No.
                   9342
Contig ID
                   15769 1.R1040
5'-most EST
                   jsh701063734.hl
Method
                   BLASTX
NCBI GI
                   q1076670
BLAST score
                   483
E value
                   1.0e-48
Match length
                   99
% identity
NCBI Description
                   NADH dehydrogenase (EC 1.6.99.3) - potato
                   >gi 668985 emb CAA59062 (X84319) NADH dehydrogenase
                   [Solanum tuberosum]
                   9343
Seq. No.
Contig ID
                   15770 1.R1040
5'-most EST
                   uC-gmrominsoy246d02b1
Method
                   BLASTX
NCBI GI
                   g2059326
BLAST score
                   181
E value
                   4.0e-13
Match length
                   109
```

35

% identity

```
(D67067) thymic epithelial cell surface antigen [Mus
NCBI Description
                  musculus]
                  9344
Seq. No.
                  15770 2.R1040
Contig ID
5'-most EST
                  LIB3056-007-Q1-N1-F9
                  9345
Seq. No.
                  15771 1.R1040
Contig ID
5'-most EST
                  kmv700739716.h1
Seq. No.
                  9346
Contig ID
                  15775 1.R1040
                  LIB3170-036-Q1-K2-D2
5'-most EST
                  BLASTX
Method
                  q4467126
NCBI GI
BLAST score
                  393
                  8.0e-38
E value
Match length
                  175
% identity
                  46
                   (AL035538) guanine nucleotide-exchange protein-like
NCBI Description
                   [Arabidopsis thaliana]
                  9347
Seq. No.
                  15777 1.R1040
Contig ID
                  LIB3049-043-Q1-E1-G11
5'-most EST
Method
                  BLASTX
                  g4335745
NCBI GI
BLAST score
                   583
E value
                   8.0e-60
                   311
Match length
                   42
% identity
                   (AC006284) putative hydrolase (contains an
NCBI Description
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
                   9348
Seq. No.
                   15781 1.R1040
Contig ID
5'-most EST
                  LIB3074-040-Q1-K1-A7
                   9349
Seq. No.
Contig ID
                   15781 3.R1040
5'-most EST
                   gsv701054002.hl
                   9350
Seq. No.
Contig ID
                   15782 1.R1040
5'-most EST
                   vwf700674333.hl
                   BLASTX
Method
NCBI GI
                   g1922242
BLAST score
                   272
                   9.0e-24
E value
Match length
                   67
% identity
                   (Y10084) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

9351

15792 1.R1040

Seq. No.

Contig ID

```
5'-most EST
                  LIB3049-043-Q1-E1-E12
                   9352
Seq. No.
                  15795 1.R1040
Contig ID
                  LIB3138-054-Q1-N1-C2
5'-most EST
                  BLASTX
Method
                   q2980762
NCBI GI
BLAST score
                   160
                   8.0e-11
E value
Match length
                   68
                   46
% identity
                   (AL022198) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   15799 1.R1040
Contig ID
                   LIB3049-043-Q1-E1-B4
5'-most EST
Method
                   BLASTX
                   q3540181
NCBI GI
BLAST score
                   521
                   7.0e-53
E value
                   227
Match length
% identity
                   (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   9354
Seq. No.
                   15807 1.R1040
Contig ID
5'-most EST
                   LIB3049-043-Q1-E1-C3
Seq. No.
                   9355
Contig ID
                   15808 1.R1040
5'-most EST
                   LIB3170-034-Q1-K1-E1
                   9356
Seq. No.
                   15812 1.R1040
Contig ID
5'-most EST
                   LIB3049-043-Q1-E1-C7
                   9357
Seq. No.
                   15817 1.R1040
Contig ID
5'-most EST
                   LIB3049-042-Q1-E1-H6
                   9358
Seq. No.
Contig ID
                   15819 1.R1040
                   jC-gmf102220093d01a1
5'-most EST
Seq. No.
                   9359
Contig ID
                   15820 1.R1040
                   LIB3049-042-Q1-E1-H9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g133872
BLAST score
                   445
E value
                   4.0e-44
Match length
                   115
                   73
% identity
                   30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
NCBI Description
                   >gi 282838 pir S26494 ribosomal protein S1, chloroplast -
                   spinach >gi_322404_pir__A44121 small subunit ribosomal
```

protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_

× 100

(X66135) ribosomal protein S1 [Spinacia oleracea]
>gi_170143 (M82923) chloroplast ribosomal protein S1
[Spinacia oleracea]

```
9360
Seq. No.
                   15827 1.R1040
Contig ID
                   LIB3139-041-P1-N1-B4
5'-most EST
                   9361
Seq. No.
                   15840 1.R1040
Contig ID
                   LIB3049-042-Q1-E1-G4
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3738289
BLAST score
                   416
                   1.0e-40
E value
                   116
Match length
                   69
% identity
                   (AC005309) Not56-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   15849 1.R1040
Contig ID
                   LIB3049-042-Q1-E1-E2
5'-most EST
                   9363
Seq. No.
                   15857 1.R1040
Contig ID
                   LIB3049-042-Q1-E1-F10
5'-most EST
                   BLASTX
Method
                   q3894191
NCBI GI
BLAST score
                   194
E value
                   8.0e-15
                   102
Match length
% identity
                   (AC005662) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9364
                   15858 1.R1040
Contig ID
                   LIB30\overline{4}9-042-Q1-E1-F11
5'-most EST
                   9365
Seq. No.
Contig ID
                   15872 1.R1040
5'-most EST
                   LIB3139-004-P1-N1-D1
                   9366
Seq. No.
                   15873 1.R1040
Contig ID
                   LIB3170-030-Q1-K1-F12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2832629
BLAST score
                   321
                   8.0e-30
E value
Match length
                   127
% identity
                    46
                    (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis
NCBI Description
                    thaliana]
```

9367

15875 1.R1040

uC-gmflminsoy031a04b1

Seq. No.

Contig ID

5'-most EST

```
BLASTX
Method
NCBI GI
                   q3309086
                   1046
BLAST score
E value
                   1.0e-114
Match length
                   226
                   90
% identity
                   (AF076253) calcineurin B-like protein 3 [Arabidopsis
NCBI Description
                   thaliana]
                   9368
Seq. No.
Contig ID
                   15875 2.R1040
5'-most EST
                   LIB3049-042-Q1-E1-D7
Method
                   BLASTX
NCBI GI
                   g3309084
BLAST score
                   158
                   1.0e-10
E value
Match length
                   48
% identity
NCBI Description
                   (AF076252) calcineurin B-like protein 2 [Arabidopsis
                   thaliana]
                   9369
Seq. No.
                   15881 1.R1040
Contig ID
5'-most EST
                   leu701150201.h1
Method
                   BLASTX
                   g4097547
NCBI GI
BLAST score
                   549
E value
                   4.0e-56
Match length
                   167
% identity
                   66
                   (U64906) ATFP3 [Arabidopsis thaliana]
NCBI Description
                   9370
Seq. No.
                   15881 2.R1040
Contig ID
5'-most EST
                   LIB3072-057-Q1-K1-H7
Method
                   BLASTX
NCBI GI
                   q4097547
BLAST score
                   291
                   4.0e-26
E value
Match length
                   66
                   41
% identity
NCBI Description
                   (U64906) ATFP3 [Arabidopsis thaliana]
                   9371
Seq. No.
Contig ID
                   15881 3.R1040
5'-most EST
                   LIB3170-083-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                   g4097547
BLAST score
                   214
E value
                   3.0e-17
Match length
                   53
% identity
NCBI Description
                   (U64906) ATFP3 [Arabidopsis thaliana]
                   9372
Seq. No.
                   15891 1.R1040
Contig ID
```

asn701136815.hl

E value

3.0e-43

```
BLASTX
Method
                  g2505874
NCBI GI
BLAST score
                  1051
                  1.0e-119
E value
                  250
Match length
% identity
                  (Y12776) putative kinase [Arabidopsis thaliana]
NCBI Description
                   9373
Seq. No.
                  15894 1.R1040
Contig ID
                  LIB3073-014-Q1-K1-E8
5'-most EST
Seq. No.
                   9374
                   15894 2.R1040
Contig ID
                   jsh701067288.hl
5'-most EST
                   9375
Seq. No.
                   15894 3.R1040
Contig ID
5'-most EST
                  LIB3073-013-Q1-K1-E8
                   9376
Seq. No.
                   15894 4.R1040
Contig ID
                   jC-gmst02400008a10a1
5'-most EST
                   9377
Seq. No.
                   15894 5.R1040
Contig ID
                   seb70\overline{0}651282.h1
5'-most EST
                   9378
Seq. No.
Contig ID
                   15898 1.R1040
5'-most EST
                   pxt700944642.hl
                   BLASTX
Method
NCBI GI
                   g3540197
BLAST score
                   211
                   1.0e-16
E value
Match length
                   72
                   56
% identity
                  (AC004260) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   9379
Seq. No.
                   15900 1.R1040
Contig ID
5'-most EST
                   LIB3170-024-Q1-K1-E1
Method
                   BLASTX
                   q4336747
NCBI GI
                   416
BLAST score
                   2.0e-40
E value
Match length
                   281
% identity
                   (AF104924) unconventional myosin heavy chain [Zea mays]
NCBI Description
Seq. No.
                   9380
                   15901 1.R1040
Contig ID
                   LIB3049-041-Q1-E1-H5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2245128
BLAST score
                   438
```

Method

NCBI GI

BLASTN q3046856

```
Match length
                   126
                   65
% identity
                   (297344) peroxidase [Arabidopsis thaliana]
NCBI Description
                   9381
Seq. No.
                   15902 1.R1040
Contig ID
                   hyd700727214.h1
5'-most EST
                   9382
Seq. No.
                   15902 2.R1040
Contig ID
                   zsg701120876.hl
5'-most EST
Method
                   BLASTX
                   g2351846
NCBI GI
                   269
BLAST score
E value
                   2.0e-23
Match length
                   111
                   52
% identity
                   (U93050) poly(A) binding protein II [Mus musculus]
NCBI Description
                   9383
Seq. No.
                   15910 1.R1040
Contig ID
                   uC-gmropic044c11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4415942
BLAST score
                   240
                   2.0e-35
E value
Match length
                   161
% identity
                   53
                   (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9384
Seq. No.
                   15910 2.R1040
Contig ID
                   LIB3139-050-P1-N1-B6
5'-most EST
Method
                   BLASTX
                   g4415942
NCBI GI
BLAST score
                   226
                   3.0e-18
E value
Match length
                   118
% identity
                   39
                   (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9385
Seq. No.
                   15913 1.R1040
Contig ID
                   k1170\overline{1}211472.h1
5'-most EST
Method
                   BLASTX
                   g4432855
NCBI GI
BLAST score
                   1127
                   1.0e-123
E value
Match length
                   339
% identity
                   (AC006300) unknown protein [Arabidopsis thaliana]
NCBI Description
                   9386
Seq. No.
                   15915 1.R1040
Contig ID
                   LIB3170-041-Q1-K1-B3
5'-most EST
```

```
BLAST score
                   57
                   4.0e-23
E value
Match length
                   141
% identity
                   86
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXI22, complete sequence [Arabidopsis thaliana]
                   9387
Seq. No.
                   15917 1.R1040
Contig ID
                   LIB3049-040-Q1-E1-H6
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1362078
                   578
BLAST score
                   2.0e-59
E value
Match length
                   216
% identity
                   60
                   endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
NCBI Description
                   - common nasturtium >qi 311835 emb CAA48324 (X68254)
                   cellulase [Tropaeolum majus]
                   9388
Seq. No.
                   15921 1.R1040
Contig ID
5'-most EST
                   LIB3138-023-Q1-N1-G4
Method
                   BLASTX
NCBI GI
                   g2920839
BLAST score
                   337
E value
                   2.0e-31
Match length
                   129
% identity
                   51
NCBI Description
                   (U95136) Os-FIERG2 gene product [Oryza sativa]
Seq. No.
                   9389
Contig ID
                   15924 1.R1040
5'-most EST
                   LIB3093-024-Q1-K1-A6
Method
                   BLASTX
NCBI GI
                   g3063709
BLAST score
                   358
E value
                   5.0e-34
Match length
                   135
% identity
NCBI Description
                   (AL022537) putative protein [Arabidopsis thaliana]
                   9390 -
Seq. No.
Contig ID
                   15926 1.R1040
5'-most EST
                   LIB3170-022-Q1-K1-E6
Method
                  BLASTN
                   g3985958
NCBI GI
BLAST score
                   41
E value
                   2.0e-13
Match length
                  290
% identity
                  82
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MZN1, complete sequence [Arabidopsis thaliana]
                   9391
Seq. No.
Contig ID
                   15926 3.R1040
```

LIB3170-032-Q1-K1-E4

```
Method
                  BLASTN
NCBI GI
                  g3985958
BLAST score
                  33
                  5.0e-09
E value
                  182
Match length
                  82
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MZN1, complete sequence [Arabidopsis thaliana]
                  9392
Seq. No.
                  15931 1.R1040
Contig ID
5'-most EST
                  LIB3049-041-Q1-E1-G9
Method
                  BLASTX
NCBI GI
                  g3914156
BLAST score
                  357
                   6.0e-34
E value
                  94
Match length
                  70
% identity
                  NUCLEOLAR PROTEIN AT BAND 60B >qi 2661227 (AF017230)
NCBI Description
                  nucleolar protein at band 60B [Drosophila melanogaster]
                  >gi 4322557 gb AAD16092 (AF089837) minifly protein
                  [Drosophila melanogaster]
Seq. No.
                  9393
Contig ID
                  15939 1.R1040
5'-most EST
                  LIB3073-013-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q4559358
BLAST score
                  422
E value
                  2.0e-41
Match length
                  100
% identity
                   (AC006585) putative steroid binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  9394
Seq. No.
Contig ID
                  15939 2.R1040
5'-most EST
                  LIB3049-041-Q1-E1-E11
Method
                  BLASTX
NCBI GI
                  g4559358
BLAST score
                  398
E value
                  1.0e-38
Match length
                  99
% identity
NCBI Description
                   (AC006585) putative steroid binding protein [Arabidopsis
                  thaliana]
                  9395
Seq. No.
                  15941 1.R1040
Contig ID
5'-most EST
                  gbt700547911.h1
                  9396
Seq. No.
Contig ID
                  15942 1.R1040
5'-most EST
                  LIB3049-041-Q1-E1-E3
Seq. No.
                  9397
```

15950 1.R1040

Contig ID

Match length

106

```
5'-most EST
                   taw700656026.h1
Method
                   BLASTX
NCBI GI
                   q2244822
BLAST score
                   235
E value
                   2.0e-19
Match length
                   63
                   70
% identity
NCBI Description
                   (Z97336) RNA polymerase II fifth largest subunit homolog
                   [Arabidopsis thaliana]
                   9398
Seq. No.
Contig ID
                   15952 1.R1040
5'-most EST
                   LIB3049-016-Q1-E1-C3
Method
                   BLASTX
NCBI GI
                   g2896687
BLAST score
                   165
E value
                   2.0e-11
Match length
                   87
% identity
                   48
                   (AL021897) hypothetical protein Rv1050 [Mycobacterium
NCBI Description
                   tuberculosis]
                   9399
Seq. No.
Contig ID
                   15952 2.R1040
5'-most EST
                   fde700876935.h1
                   9400
Seq. No.
                   15953 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910005e12d1
Method
                   BLASTX
NCBI GI
                   q3033400
BLAST score
                   245
                   4.0e-20
E value
Match length
                   104
% identity
                   50
                   (AC004238) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   9401
Contig ID
                   15955 1.R1040
5'-most EST
                   fua701038882.hl
Method
                   BLASTX
NCBI GI
                   g2827699
BLAST score
                   422
                   3.0e-41
E value
Match length
                   206
                   52
% identity
NCBI Description
                   (AL021684) predicted protein [Arabidopsis thaliana]
                   9402
Seq. No.
Contig ID
                   15955 2.R1040
5'-most EST
                   crh70\overline{0}853141.h1
Method
                   BLASTX
NCBI GI
                   q2827699
BLAST score
                   120
E value
                   7.0e-14
```

Seq. No.

Contig ID

5'-most EST

9412

15994 1.R1040

LIB3049-040-Q1-E1-G12

```
% identity
                  52
NCBI Description
                  (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                  9403
                  15957 1.R1040
Contig ID
                  zhf700951979.hl
5'-most EST
Seq. No.
                  9404
                  15966 1.R1040
Contig ID
5'-most EST
                  LIB3049-041-Q1-E1-C5
Seq. No.
                  9405
Contig ID
                  15971 1.R1040
5'-most EST
                  g4294765
                  9406
Seq. No.
Contig ID
                  15972 1.R1040
5'-most EST
                  LIB3072-061-01-K1-H6
Seq. No.
Contig ID
                  15974 1.R1040
5'-most EST
                  LIB3049-040-Q1-E1-H7
Seq. No.
                  9408
                  15976 1.R1040
Contig ID
5'-most EST
                  gsv701052356.hl
Method
                  BLASTX
                  g1170606
NCBI GI
BLAST score
                  673
E value
                  1.0e-70
Match length
                  188
                  70
% identity
                  ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3),
                  chloroplast - maize >gi 3114421 pdb 1ZAK A Chain A,
                  Adenylate Kinase From Maize In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
                  >qi 3114422 pdb 1ZAK B Chain B, Adenylate Kinase From Maize
                  In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
Seq. No.
                  9409
Contig ID
                  15986 1.R1040
5'-most EST
                  LIB3049-041-01-E1-B10
Seq. No.
                  9410
Contig ID
                  15991 1.R1040
5'-most EST
                  LIB3107-012-Q1-K1-G6
Seq. No.
                  9411
Contig ID
                  15991 2.R1040
5'-most EST
                  LIB3049-040-Q1-E1-G1
```

Contig ID 5'-most EST

```
9413
Seq. No.
Contig ID
                  15995 1.R1040
                  nsy700645633.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3868852
BLAST score
                  268
                   1.0e-149
E value
Match length
                  588
                  88
% identity
                  Vigna radiata ARG8 mRNA for GPI-anchored protein, complete
NCBI Description
Seq. No.
                   9414
Contig ID
                   15995 2.R1040
5'-most EST
                   ssr700557224.hl
Seq. No.
                   9415
                   15995 3.R1040
Contig ID
5'-most EST
                   LIB3049-040-Q1-E1-G2
                   BLASTN
Method
NCBI GI
                   q3868852
BLAST score
                   103
                   1.0e-50
E value
Match length
                   333
                   84
% identity
                  Vigna radiata ARG8 mRNA for GPI-anchored protein, complete
NCBI Description
Seq. No.
                   9416
Contig ID
                   15995 4.R1040
                   LIB3093-018-Q1-K1-H7
5'-most EST
                   BLASTN
Method
NCBI GI
                   q3868852
BLAST score
                   155
E value
                   1.0e-81
                   293
Match length
                   89
% identity
                   Vigna radiata ARG8 mRNA for GPI-anchored protein, complete
NCBI Description
                   9417
Seq. No.
Contig ID
                   15996 1.R1040
                   ncj700988212.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2655037
BLAST score
                   274
E value
                   4.0e-36
Match length
                   261
                   35
% identity
                   (AF019952) tumor suppressing STF cDNA 1 [Homo sapiens]
NCBI Description
                   >gi 4507703 ref NP 003301.1 pTSSC1 tumor suppressing
                   subtransferable candidate
Seq. No.
                   9418
                   15997 1.R1040
```

uxk700671968.hl

```
Seq. No.
                   9419
                   15997 2.R1040
Contig ID
5'-most EST
                   LIB3049-040-Q1-E1-G4
                   9420
Seq. No.
                   16005 1.R1040
Contig ID
                   LIB3170-030-Q1-K1-D11
5'-most EST
                   9421
Seq. No.
                   16007 1.R1040
Contig ID
                   LIB3049-008-Q1-E1-B7
5'-most EST
Method
                   BLASTX
                   q4309700
NCBI GI
                   257
BLAST score
E value
                   5.0e-22
Match length
                   94
                   53
% identity
NCBI Description
                   (AC006266) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   9422
                   16009 1.R1040
Contig ID
                   LIB30\overline{5}6-013-Q1-N1-G8
5'-most EST
Seq. No.
                   9423
                   16009 2.R1040
Contig ID
5'-most EST
                   LIB3049-040-Q1-E1-E2
Seq. No.
                   9424
Contig ID
                   16009 3.R1040
                   LIB3138-019-Q1-N1-D1
5'-most EST
Seq. No.
                   9425
Contig ID
                   16013 1.R1040
5'-most EST
                   LIB3074-040-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   q3283057
BLAST score
                   237
E value
                   1.0e-19
Match length
                   87
% identity
NCBI Description
                   (AF054617) one helix protein [Arabidopsis thaliana]
                   9426
Seq. No.
                   16016 1.R1040
Contig ID
5'-most EST
                   zzp700834673.h1
                   9427
Seq. No.
                   16017 1.R1040
Contig ID
5'-most EST
                   LIB3049-040-Q1-E1-F12
                   9428
Seq. No.
                   16021 1.R1040
Contig ID
5'-most EST
                   LIB3049-040-Q1-E1-F5
                   9429
Seq. No.
Contig ID
                   16025 1.R1040
5'-most EST
                   LIB3049-040-Q1-E1-C6
```

```
Method
                   BLASTX
NCBI GI
                   g3068713
BLAST score
                   243
                   1.0e-20
E value
Match length
                   67
                   75
% identity
NCBI Description
                   (AF049236) unknown [Arabidopsis thaliana]
                   9430
Seq. No.
                   16029 1.R1040
Contig ID
                   LIB3049-040-Q1-E1-D2
5'-most EST
Method
                   BLASTX
                   g4559351
NCBI GI
BLAST score
                   176
E value
                   1.0e-12
Match length
                   45
% identity
                   71
NCBI Description
                   (AC006585) hypothetical protein [Arabidopsis thaliana]
                   9431
Seq. No.
                   16029 2.R1040
Contig ID
5'-most EST
                   uaw700663387.h1
Method
                   BLASTX
NCBI GI
                   q4101574
BLAST score
                   276
E value
                   6.0e-24
Match length
                   187
% identity
NCBI Description
                   (AF004876) 54TMp [Homo sapiens]
Seq. No.
                   9432
Contig ID
                   16029 3.R1040
5'-most EST
                   dpv701099693.h1
Method
                   BLASTN
NCBI GI
                   q4191760
BLAST score
                   33
E value
                   6.0e-09
Match length
                   155
                   81
% identity
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC F17F8,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   9433
Contig ID
                   16042 1.R1040
5'-most EST
                   LIB3049-040-Q1-E1-E11
Method
                   BLASTX
NCBI GI
                   g3157923
BLAST score
                   162
E value
                   2.0e-11
Match length
                   81
% identity
                   44
NCBI Description
                   (AC002131) F12F1.7 [Arabidopsis thaliana]
Seq. No.
                   9434
Contig ID
                   16049 1.R1040
```

LIB3049-040-Q1-E1-B5

Method

```
9435
Seq. No.
                   16060 1.R1040
Contig ID
5'-most EST
                   kmv700738950.h1
Method
                   BLASTX
                   g3445209
NCBI GI
                   1036
BLAST score
                   1.0e-113
E value
Match length
                   368
                   53
% identity
                   (AC004786) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                   thaliana]
                   9436
Seq. No.
Contig ID
                   16063 1.R1040
5'-most EST
                   uC-qmflminsoy047e02b1
Seq. No.
                   9437
                   16063 2.R1040
Contig ID
5'-most EST
                   LIB3049-055-Q1-E1-C10
                   9438
Seq. No.
                   16064 1.R1040
Contig ID
                   bth700844340.hl
5'-most EST
Method
                   BLASTX
                   q1914683
NCBI GI
BLAST score
                   422
                   2.0e-41
E value
                   184
Match length
% identity
                   57
NCBI Description
                   (Y12013) RAD23, isoform I [Daucus carota]
Seq. No.
                   9439
                   16064 2.R1040
Contig ID
5'-most EST
                   LIB3049-039-Q1-E1-H5
Method
                   BLASTX
NCBI GI
                   g1914683
BLAST score
                   251
                   1.0e-21
E value
                   88
Match length
% identity
                   (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
                   9440
Seq. No.
                   16065 1.R1040
Contig ID
5'-most EST
                   LIB3073-017-Q1-K1-E1
Method
                   BLASTX
NCBI GI
                   g2253442
BLAST score
                   221
                   1.0e-17
E value
Match length
                   61
% identity
                   (AF007784) LTCOR11 [Lavatera thuringiaca]
NCBI Description
Seq. No.
                   9441
Contig ID
                   16065 2.R1040
```

LIB3051-041-Q1-K1-B4

BLASTX

Seq. No.

Contig ID

9450

16081 1.R1040

```
NCBI GI
                   g2253442
BLAST score
                   223
E value
                   8.0e-18
Match length
                   61
                   62
% identity
                   (AF007784) LTCOR11 [Lavatera thuringiaca]
NCBI Description
Seq. No.
                   9442
                   16068 1.R1040
Contig ID
                   sat701002941.hl
5'-most EST
Seq. No.
                   9443
                   16069 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir060f12b1
Seq. No.
                   9444
Contig ID
                   16070 1.R1040
5'-most EST
                   zsq701117861.h2
Seq. No.
                   9445
                   16074 1.R1040
Contig ID
5'-most EST
                   LIB3170-030-Q1-K1-D10
Seq. No.
                   9446
Contig ID
                   16075 1.R1040
5'-most EST
                   LIB3170-031-Q1-K1-G10
Seq. No.
                   9447
Contig ID
                   16078 1.R1040
5'-most EST
                   LIB3139-044-P1-N1-D4
Method
                   BLASTX
NCBI GI
                   q4206789
BLAST score
                   835
E value
                   1.0e-89
Match length
                   253
% identity
                   (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   9448
Contig ID
                   16079 1.R1040
5'-most EST
                   LIB3170-035-Q1-K1-E3
Method.
                   BLASTX
NCBI GI
                   q3033395
BLAST score
                   168
                   2.0e-11
E value
Match length
                   60
% identity
                   (AC004238) putative zinc-finger protein [Arabidopsis
NCBI Description
                   thaliana]
                  .9449
Seq. No.
                   16080 1.R1040
Contig ID
5'-most EST
                   LIB3049-039-Q1-E1-F9
```

```
LIB3049-039-Q1-E1-G1
5'-most EST
                  BLASTX
Method
                  g3860255
NCBI GI
                   222 -
BLAST score
                   6.0e-18
E value
                  128
Match length
                   41
% identity
                   (AC005824) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9451
Seq. No.
                   16083 1.R1040
Contig ID
                   gsv701054107.hl
5'-most EST
                   BLASTN
Method
                   g3869074
NCBI GI
                   38
BLAST score
                   1.0e-11
E value
                   50
Match length
                   94
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MMI9, complete sequence [Arabidopsis thaliana]
                   9452
Seq. No.
                   16089 1.R1040
Contig ID
                   LIB3049-039-Q1-E1-G7
5'-most EST
                   9453
Seq. No.
                   16090 1.R1040
Contig ID
                   LIB3049-039-Q1-E1-G9
5'-most EST
                   9454
Seq. No.
                   16093 1.R1040
Contig ID
                   LIB3139-026-P1-N1-H3
5'-most EST
                   BLASTX
Method
                   g1532163
NCBI GI
                   211
BLAST score
                   2.0e-16
E value
                   90
Match length
% identity
                   (U63815) similar to glutaredoxin encoded by GenBank
NCBI Description
                   Accession Number Z49699; localized according to blastn
                   similarity to EST sequences; therefore, the coding span
                   corresponds only to an area of similarity since the
                   initation codon and stop c
                   9455
Seq. No.
                   16093 2.R1040
Contig ID
                   LIB3049-039-Q1-E1-E1
5'-most EST
                   9456
Seq. No.
                   16095 1.R1040
Contig ID
                   LIB3170-029-Q1-K1-G10
5'-most EST
                   9457
Seq. No.
                   16101 1.R1040
Contig ID
                   sat70\overline{1}008810.h1
5'-most EST
                   BLASTX
Method
```

g2191150

NCBI GI

```
BLAST score
                   291
E value
                   4.0e-26
                   91
Match length
% identity
NCBI Description
                   (AF007269) similar to mitochondrial carrier family
                   [Arabidopsis thaliana]
                   9458
Seq. No.
                   16101 2.R1040
Contig ID
5'-most EST
                   txt700734741.hl
                   9459
Seq. No.
Contig ID
                   16109 1.R1040
5'-most EST
                   LIB3049-039-Q1-E1-C4
                   9460
Seq. No.
Contig ID
                   16110 1.R1040
5'-most EST
                   zhf700952664.h1
Seq. No.
                   9461
                   16110 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy118e10b1
                   9462
Seq. No.
                   16111 1.R1040
Contig ID
                   vzy700753767.hl
5'-most EST
                   BLASTX
Method
                   q4006909
NCBI GI
BLAST score
                   346
E value
                   2.0e-32
                   155
Match length
% identity
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9463
                   16111 2.R1040
Contig ID
5'-most EST
                   LIB3049-039-Q1-E1-C6
                   9464
Seq. No.
Contig ID
                   16112 1.R1040
5'-most EST
                   LIB3049-039-Q1-E1-C7
                   9465
Seq. No.
                   16115 1.R1040
Contig ID
                   LIB3049-039-Q1-E1-D1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1078074
BLAST score
                   165
                   3.0e-11
E value
Match length
                   106
% identity
                   42
                   probable membrane protein YLR328w - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi_662140 (U20618) Ylr328wp [Saccharomyces
                   cerevisiae]
```

16118 1.R1040

Seq. No. Contig ID

```
ncj700980834.h1
5'-most EST
                  BLASTX
Method
                  g2978452
NCBI GI
                  333
BLAST score
                  2.0e-30
E value
                  89
Match length
                  71
% identity
                   (AE001274) MCAK; L549.3 [Leishmania major]
NCBI Description
                   9467
Seq. No.
                   16122 1.R1040
Contig ID
                   leu70\overline{1}154824.h1
5'-most EST
                   9468
Seq. No.
                   16122 2.R1040
Contig ID
                   bth700849722.h1
5'-most EST
                   BLASTX
Method
                   g3877951
NCBI GI
                   241
BLAST score
                   3.0e-20
E value
Match length
                   133
                   29
% identity
                   (281555) predicted using Genefinder [Caenorhabditis
NCBI Description
                   elegans]
                   9469
Seq. No.
                   16124 1.R1040
Contig ID
5'-most EST
                   wrg700790632.h2
Method
                   BLASTX
NCBI GI
                   g3201477
BLAST score
                   695
                   6.0e-73
E value
Match length
                   280
% identity
                   (AJ006021) putative PRL1 associated protein [Arabidopsis
NCBI Description
                   thaliana]
                   9470
Seq. No.
Contig ID
                   16125 1.R1040
                   LIB3049-039-Q1-E1-C3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4218126
BLAST score
                   470
                   6.0e-47
E value
Match length
                   165
% identity
                   (AL035353) putative protein [Arabidopsis thaliana]
NCBI Description
                   9471
Seq. No.
Contig ID
                   16128 1.R1040
                   LIB3049-039-Q1-E1-B2
5'-most EST
                   9472
Seq. No.
                   16131 1.R1040
Contig ID
                   LIB3049-039-Q1-E1-B5
5'-most EST
```

Seq. No.

```
Contig ID
                    16132 1.R1040
                    LIB3049-039-Q1-E1-B6
5'-most EST
                    BLASTX
Method
                    g3377509
NCBI GI
                    434
BLAST score
                    9.0e-43
E value
                    96
Match length
                    80
% identity
                    (AF056027) auxin transport protein REH1 [Oryza sativa]
NCBI Description
                    9474
Seq. No.
                    16133 1.R1040
Contig ID
                    LIB3167-077-P1-K2-G7
5'-most EST
                    BLASTX
Method
                    q2191136
NCBI GI
BLAST score
                    431
                    3.0e-42
E value
Match length
                    142
                    57
% identity
                    (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                    coded for by A. thaliana cDNA T46230; coded for by A.
                    thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                    [Arabidopsis thaliana]
                    9475
Seq. No.
                    16135 1.R1040
Contig ID
                    ssr70\overline{0}560864.h1
5'-most EST
                    BLASTX
Method
                    g3152615
NCBI GI
                    219
BLAST score
                    1.0e-17
E value
                    142
Match length
                    40
% identity
                     (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    >gi 3242727 (AC003040) hypothetical protein [Arabidopsis
                    thaliana]
                    9476
Seq. No.
Contig ID
                    16139 1.R1040
                     jC-qmle01810053h07a1
5'-most EST
                    BLASTX
Method
                     q3122638
NCBI GI
                     420
BLAST score
                     4.0e-82
E value
Match length
                     218
% identity
                     PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1
NCBI Description
                     >gi_1076381_pir__S49820 PRL1 protein - Arabidopsis thaliana
                    >gi_577733 emb_CAA58031_ (X82824) PRL1 [Arabidopsis
thaliana] >gi_577735_emb_CAA58032_ (X82825) PRL1
[Arabidopsis thaliana] >gi_2244947_emb_CAB10369.1_ (Z97339)
                     PRL1 protein - Arabidopsis thaliana
                     9477
Seq. No.
                     16144 1.R1040
Contig ID
```

LIB3170-032-Q1-K1-H9

```
9478
Seq. No.
                  16144 2.R1040
Contig ID
                  LIB3072-054-Q1-E1-E9
5'-most EST
                  9479
Seq. No.
                  16145 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy157e03b1
                  BLASTX
Method
                  q2665890
NCBI GI
                  2241
BLAST score
                  0.0e + 00
E value
                  534
Match length
                  81
% identity
                  (AF035944) calcium-dependent protein kinase [Fragaria x
NCBI Description
                  ananassa]
                  9480
Seq. No.
Contig ID
                  16147 1.R1040
5'-most EST
                  LIB3049-034-Q1-E1-F8
Method
                  BLASTX
                  q729538
NCBI GI
BLAST score
                  243
                  3.0e-20
E value
Match length
                  103
                  54
% identity
                  FERREDOXIN-THIOREDOXIN REDUCTASE, VARIABLE CHAIN PRECURSOR
NCBI Description
                   (FTR-V) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT A)
                   (FTR-A) >gi_2144358_pir__RDSPTA ferredoxin--thioredoxin
                  reductase (EC 1.18.-.-) chain A precursor - spinach
                  >gi 474766 emb CAA55480_ (X78880) ferredoxin:thioredoxin
                  reductase [Spinacia oleracea] >gi_861138_emb_CAA54408_
                   (X77163) ferredoxin-thioredoxin reductase SU A [Spinacia
                  oleracea]
                   9481
Seq. No.
Contig ID
                   16147 2.R1040
                   smc70\overline{0}745464.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g1362192
BLAST score
                   195
                   1.0e-14
E value
Match length
                   64
% identity
                   53
                  ferredoxin--thioredoxin reductase (EC 1.18.-.-) variable
NCBI Description
                   chain - maize
                   9482
Seq. No.
                   16148 1.R1040
Contig ID
                   LIB3170-032-Q1-K1-B5
5'-most EST
Seq. No.
                   9483
                   16148 2.R1040
Contig ID
5'-most EST
                   vwf700675339.hl
Seq. No.
                   9484
                   16148 3.R1040
Contig ID
```

txt700733039.hl

Seq. No.

9491

```
9485
Seq. No.
                   16157 1.R1040
Contig ID
                   LIB3055-006-Q1-N1-B11
5'-most EST
                   9486
Seq. No.
                   16158 1.R1040
Contig ID
 5'-most EST
                   LIB3049-038-Q1-E1-G1
                   9487
 Seq. No.
                   16162 1.R1040
Contig ID
                   LIB30\overline{4}9-038-Q1-E1-G2
 5'-most EST
                   BLASTX
Method
                   g1421730
NCBI GI
                   284
 BLAST score
                   2.0e-25
E value
                   74
Match length
 % identity
 NCBI Description
                   (U43082) RF2 [Zea mays]
                   9488
 Seq. No.
                   16163 1.R1040
 Contig ID
                   pmv700891217.h1
 5'-most EST
                   BLASTN
 Method
 NCBI GI
                   g2281081
 BLAST score
                   46
                   1.0e-16
 E value
                   46
 Match length
                   100
 % identity
                   Arabidopsis thaliana chromosome II BAC F18019 genomic
 NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                    9489
 Seq. No.
                    16163 3.R1040
 Contig ID
                   LIB3072-023-Q1-E1-D8
 5'-most EST
Method
                    BLASTN
                   g2281081
NCBI GI
 BLAST score
                    46
                    9.0e-17
 E value
                    46
 Match length
                    100
 % identity
                   Arabidopsis thaliana chromosome II BAC F18019 genomic
 NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
                                              9490
 Seq. No.
                    16165 1.R1040
 Contig ID
                    awf700839728.h1
 5'-most EST
                    BLASTX
 Method
                    g3287683
 NCBI GI
                    778
 BLAST score
                    1.0e-82
 E value
                    337
 Match length
                    15
 % identity
                    (AC003979) Similar to apoptosis protein MA-3 gb_D50465 from
 NCBI Description
                    Mus musculus. [Arabidopsis thaliana]
```

```
16170 1.R1040
Contig ID
                  LIB3170-030-Q1-K1-H9
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2583123
BLAST score
                  450
                  6.0e-45
E value
Match length
                  122
% identity
                  75
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
NCBI Description
                  thaliana]
                                               -- \
                  9492
Seq. No.
                  16171 1.R1040
Contig ID
                  LIB3170-032-Q1-K1-A5
5'-most EST
                  BLASTX
Method
                  q730692
NCBI GI
BLAST score
                  234
                  2.0e-19
E value
Match length
                  122
                   44
% identity
                  RUBISCO-ASSOCIATED PROTEIN >gi_454179 (L28804) putative
NCBI Description
                   [Glycine max] >gi 1090839 prf 2019481A RuBisCO complex
                  protein [Glycine max]
                   9493
Seq. No.
                   16173 1.R1040
Contig ID
                   LIB3109-028-Q1-K1-D6
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4325282
BLAST score
                   362
                   2.0e-47
E value
                   109
Match length
                   86
% identity
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                   >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
                   9494
Seq. No.
Contig ID
                   16176 1.R1040
5'-most EST
                   LIB3170-030-Q1-K1-A9
Seq. No.
                   9495
Contig ID
                   16177 1.R1040
5'-most EST
                   jC-qmst02400065b11a2
Seq. No.
                   9496
                   16177 2.R1040
Contig ID
                   zhf700952970.h1
5'-most EST
                   9497
Seq. No.
                   16180 1.R1040
Contig ID
                   LIB3049-038-Q1-E1-E8
5'-most EST
                   9498
Seq. No.
                   16183 1.R1040
Contig ID
```

LIB3106-092-Q1-K1-F6

Seq. No.

9506

```
9499
Seq. No.
                  16186 1.R1040
Contig ID
                  ssr700553976.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1171577
                   337
BLAST score
                   2.0e-31
E value
Match length
                  166
% identity
                   42
                  (X95343) hypersensitivity-related gene [Nicotiana tabacum]
NCBI Description
Seq. No.
Contig ID
                   16188 1.R1040
                  LIB3170-031-Q1-J1-D9
5'-most EST
Seq. No.
                   16198 1.R1040
Contig ID
                   LIB3049-038-Q1-E1-D1
5'-most EST
Method
                   BLASTN
                   q558628
NCBI GI
                   441
BLAST score
                   0.0e + 00
E value
                   978
Match length
% identity
                  P.vulgaris mRNA for RNP1 chloroplast RNA binding protein
NCBI Description
                   9502
Seq. No.
                   16198 2.R1040
Contig ID
5'-most EST
                   LIB3106-108-Q1-K1-A2
Method
                   BLASTN
                   g558628
NCBI GI
                   71
BLAST score
                   1.0e-31
E value
                   285
Match length
                   87
% identity
                  P.vulgaris mRNA for RNP1 chloroplast RNA binding protein
NCBI Description
                   9503
Seq. No.
                   16200 1.R1040
Contig ID
5'-most EST
                   LIB3170-032-Q1-K1-A4
Seq. No.
                   9504
                   16200 2.R1040
Contig ID
5'-most EST
                   leu701157014.hl
Seq. No.
                   9505
                   16201 1.R1040
Contiq ID
                   LIB3170-077-Q1-K1-F12
5'-most EST
                   BLASTX
Method
NCBI GI
                   g404690
BLAST score
                   1290
E value
                   1.0e-142
Match length
                   484
% identity
                   (L19075) cytochrome P450 [Catharanthus roseus]
NCBI Description
```

```
16201 3.R1040
Contig ID
5'-most EST
                   seb70\overline{0}653537.h1
                   BLASTX
Method
NCBI GI
                   q4376203
BLAST score
                   210
                   9.0e-17
E value
                   77
Match length
% identity
                   47
                   (U35226) putative cytochrome P-450 [Nicotiana
NCBI Description
                   plumbaginifolia]
                   9507
Seq. No.
Contig ID
                   16204 1.R1040
                   ncj700981150.hl
5'-most EST
                   BLASTX
Method
                   q3687235
NCBI GI
BLAST score
                   560
                   3.0e-57
E value
Match length
                   149
% identity
                   (AC005169) putative copia-like transposable element
NCBI Description
                   [Arabidopsis thaliana]
                   9508
Seq. No.
                   16204 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy206f05b1
Method
                   BLASTX
                   g3687235
NCBI GI
BLAST score
                   382
E value
                   1.0e-36
                   116
Match length
% identity
                   (AC005169) putative copia-like transposable element
NCBI Description
                   [Arabidopsis thaliana]
                   9509
Seq. No.
                   16204 3.R1040
Contig ID
                   crh700854648.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3687235
                   145
BLAST score
E value
                   3.0e-09
Match length
                   44
% identity
                   (AC005169) putative copia-like transposable element
NCBI Description
                   [Arabidopsis thaliana]
                   9510
Seq. No.
                   16208 1.R1040
Contig ID
5'-most EST
                   LIB3170-078-Q1-K1-D8
Method
                   BLASTX
                   q1483150
NCBI GI
BLAST score
                   450
E value
                   1.0e-44
Match length
                   109
% identity
                   (D84417) monodehydroascorbate reductase [Arabidopsis
NCBI Description
```

% identity NCBI Description

thaliana] Seq. No. 9511 16208 2.R1040 Contig ID LIB3109-046-Q1-K1-A11 5'-most EST BLASTX Method q1483150 NCBI GI 263 BLAST score 7.0e-23 E value 54 Match length 93 % identity NCBI Description (D84417) monodehydroascorbate reductase [Arabidopsis thaliana] Seq. No. 9512 Contig ID 16209 1.R1040 5'-most EST kl1701214815.hl Method BLASTX NCBI GI q4335734 BLAST score 386 E value 7.0e-37 Match length 182 45 % identity NCBI Description (AC006248) putative calmodulin [Arabidopsis thaliana] 9513 Seq. No. Contig ID 16213 1.R1040 5'-most EST zhf700959796.h1 Method BLASTX NCBI GI q4262240 BLAST score 535 E value 2.0e-54 Match length 139 % identity NCBI Description (AC006200) putative stress protein [Arabidopsis thaliana] Seq. No. 9514 Contig ID 16213 2.R1040 5'-most EST $k1170\overline{1}214913.h1$ Method BLASTX NCBI GI q4262240 BLAST score 487 E value 4.0e-49 Match length 161 30 % identity NCBI Description (AC006200) putative stress protein [Arabidopsis thaliana] 9515 Seq. No. Contig ID 16228 1.R1040 5'-most EST sat701012934.h1 Method BLASTX NCBI GI g2190550 BLAST score 1063 E value 1.0e-116 Match length 274

(AC001229) ESTs gb T45673, gb N37512 come from this gene.

[Arabidopsis thaliana]

9516 Seq. No. Contig ID 16230 1.R1040 5'-most EST rry700808402.hl BLASTX Method q4115934 NCBI GI BLAST score 614 1.0e-63 E value Match length 137 77 % identity (AF118223) contains similarity to Methanobacterium NCBI Description thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana] 9517 Seq. No. Contig ID 16247 1.R1040 5'-most EST trc700561396.hl Method BLASTX q3075402 NCBI GI BLAST score 304 4.0e-27 E value 104 Match length % identity (AC004484) unknown protein [Arabidopsis thaliana] NCBI Description 9518 Seq. No. 16247 2.R1040 Contig ID 5'-most EST $smc70\overline{0}747392.h1$ Method BLASTX q3075402 NCBI GI BLAST score 207 4.0e-16 E value 79 Match length % identity 53 (AC004484) unknown protein [Arabidopsis thaliana] NCBI Description 9519 Seq. No. 16248 1.R1040 Contig ID 5'-most EST $LIB30\overline{5}0-010-Q1-E1-F2$ Method BLASTX NCBI GI g1364059 307 BLAST score 6.0e-28 E value 129 Match length % identity 46 dioscorin class A precursor - Dioscorea cayenensis NCBI Description >gi 433463 emb CAA53781 (X76187) storage protein [Dioscorea cayenensis] Seq. No. 9520 16252 1.R1040 Contig ID 5'-most EST uC-gmropic045h07b1

Seq. No. 9521

Contig ID 16253_1.R1040

5'-most EST LIB3049-004-Q1-E1-H3

```
9522
Seq. No.
                  16264 1.R1040
Contig ID
                  LIB3106-093-Q1-K1-G8
5'-most EST
                  BLASTX
Method
                  g2880049
NCBI GI
                  235
BLAST score
                  1.0e-19
E value
                  91
Match length
                  55
% identity
                  (AC002340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  9523
Seq. No.
                  16268 1.R1040
Contig ID
                  LIB3170-067-Q1-K1-G10
5'-most EST
Method
                  BLASTX
                  g1174867
NCBI GI
                  334
BLAST score
                  5.0e-31
E value
                  72
Match length
                  85
% identity
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING
NCBI Description
                  PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2
                  KD PROTEIN) >gi_633687_emb_CAA55862 (X79275)
                  ubiquinol--cytochrome c reductase [Solanum tuberosum]
                  >gi 1094912 prf 2107179A cytochrome c
                  oxidase:SUBUNIT=8.2kD [Solanum tuberosum]
                  9524
Seq. No.
                  16268 2.R1040
Contig ID
                  hrw701060207.h1
5'-most EST
Method
                  BLASTX
                  g1174867
NCBI GI
BLAST score
                  267
                  2.0e-23
E value
                  67
Match length
                  78
% identity
NCBI Description
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING
                  PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2
                  KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275)
                  ubiquinol--cytochrome c reductase [Solanum tuberosum]
                  >gi_1094912_prf__2107179A cytochrome c
                  oxidase:SUBUNIT=8.2kD [Solanum tuberosum]
                  9525
Seq. No.
                  16270 1.R1040
Contig ID
                  LIB3106-069-P1-K1-G3
5'-most EST
                  BLASTX
Method
                  g2104536
NCBI GI
BLAST score
                  318
                  3.0e-29
E value
Match length
                  120
% identity
                  53
NCBI Description
                   (AF001308) predicted glycosyl transferase [Arabidopsis
                  thaliana]
```

Seq. No.

```
Contig ID
                   16272 1.R1040
                   LIB3170-028-Q1-K1-E3
5'-most EST
Method
                   BLASTX
                   q1684851
NCBI GI
BLAST score
                   265
                   5.0e-24
E value
Match length
                   91
% identity
                   (U77935) DnaJ-like protein [Phaseolus vulgaris]
NCBI Description
                   9527
Seq. No.
Contig ID
                   16288 1.R1040
5'-most EST
                   LIB3170-030-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g3123349
BLAST score
                   295
E value
                   1.0e-26
Match length
                   74
% identity
                   77
NCBI Description
                   (AJ005788) hypothetical protein [Cicer arietinum]
Seq. No.
                   9528
Contig ID
                   16293 1.R1040
5'-most EST
                   LIB3170-029-Q1-K1-B2
Method
                   BLASTN
NCBI GI
                   q4220468
BLAST score
                   45
E value
                   5.0e-16
Match length
                   113
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T8011 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   9529
Contig ID
                   16301 1.R1040
5'-most EST
                   LIB3049-035-Q1-E1-H6
Method
                   BLASTX
NCBI GI
                   g4335745
BLAST score
                   200
E value
                   2.0e-15
Match length
                   86
% identity
NCBI Description
                   (AC006284) putative hydrolase (contains an
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
                   9530
Seq. No.
                   16304 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy071d08b1
                   9531
Seq. No.
                   16304 2.R1040
Contig ID
5'-most EST
                   jC-gmf102220057a02a1
                   9532
Seq. No.
                   16312 1.R1040
Contig ID
                   leu701157523.h1
5'-most EST
```

```
. BLASTX
Method
NCBI GI
                  g170131
BLAST score
                  352
                  3.0e-33
E value
Match length
                  88
                  76
% identity
                  (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
NCBI Description
                   9533
Seq. No.
                   16317_1.R1040 ·
Contig ID
                  LIB3170-029-Q1-K1-C1
5'-most EST
                   9534
Seq. No.
                   16321 1.R1040
Contig ID
                   LIB3049-035-01-E1-F9
5'-most EST
                   9535
Seq. No.
Contig ID
                   16324 1.R1040
                   LIB3073-021-Q1-K1-F12
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2190548
BLAST score
                   244
                   2.0e-20
E value
Match length
                   68
                   66
% identity
                   (AC001229) EST gb ATTS1121 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   9536
                   16324 2.R1040
Contig ID
                   LIB3073-021-Q1-K1-F11
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2190548
BLAST score
                   359
E value
                   5.0e-34
Match length
                   106
                   62
% identity
                   (AC001229) EST gb_ATTS1121 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   9537
                   16328 1.R1040
Contig ID
                   jC-gmst02400007d01a1
5'-most EST
Seq. No.
                   9538
                   16335 2.R1040
Contig ID
                   awf700841716.h1
5'-most EST
                   9539
Seq. No.
Contig ID
                   16337 1.R1040
                   LIB3170-031-Q1-K1-A5
5'-most EST
Method
                   BLASTX
                   g1588365
NCBI GI
                   185
BLAST score
                   1.0e-13
E value
                   74
Match length
```

% identity

NCBI Description

```
NCBI Description signal peptidase:SUBUNIT=12kD [Homo sapiens]
                   9540
Seq. No.
                   16345 1.R1040
Contig ID
5'-most EST
                   crh70\overline{0}856185.h1
                   9541
Seq. No.
                   16346 1.R1040
Contig ID
                   LIB3049-035-Q1-E1-E12
5'-most EST
                   9542
Seq. No.
                   16355 1.R1040
Contig ID
5'-most EST
                   leu701148285.h1
Method
                   BLASTX
NCBI GI
                   g4510363
BLAST score
                   623
E value
                   1.0e-64
Match length
                   134
% identity
                   84
                   (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   9543
Seq. No.
                   16355_2.R1040
Contig ID
5'-most EST
                   uC-gmropic022c11b1
Method
                   BLASTX
NCBI GI
                   g4510363
BLAST score
                   503
E value
                   8.0e-51
Match length
                   106
                   89
% identity
                   (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   9544
Seq. No.
                   16355 3.R1040
Contig ID
                   trc700565054.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4510363
BLAST score
                   700
E value
                   9.0e-74
Match length
                   146
                   88
% identity
NCBI Description
                   (AC007017) putative DNA-binding protein [Arabidopsis
                   thaliana]
                   9545
Seq. No.
                   16355 4.R1040
Contig ID
5'-most EST
                   trc700565456.h1
                   BLASTN
Method
NCBI GI
                   g4510360
BLAST score
                   49
E value
                   2.0e-18
                   105
Match length
                   87
% identity
```

sequence, complete sequence

Arabidopsis thaliana chromosome II BAC F11F19 genomic

```
Seq. No.
                  9546
Contig ID
                  16355 5.R1040
5'-most EST
                  LIB3074-030-Q1-K2-B8
Method
                  BLASTX
NCBI GI
                  q4510363
BLAST score
                  427
                  4.0e-42
E value
                  93
Match length
                  80
% identity
NCBI Description
                   (AC007017) putative DNA-binding protein [Arabidopsis
                  thaliana]
                  9547
Seq. No.
Contig ID
                  16355 6.R1040
5'-most EST
                  epx701110325.hl
Method
                  BLASTN
NCBI GI
                  q4510360
BLAST score
                  65
                  3.0e-28
E value
Match length
                  109
                  90
% identity
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
NCBI Description
                  sequence, complete sequence
                  9548
Seq. No.
                  16359 1.R1040
Contig ID
5'-most EST
                  LIB3170-029-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3386596
BLAST score
                  163
                  1.0e-11
E value
Match length
                  47
% identity
NCBI Description
                  (AC004665) unknown protein [Arabidopsis thaliana]
                  >gi 3702346 (AC005397) unknown protein [Arabidopsis
                  thaliana]
                  9549
Seq. No.
Contig ID
                  16370 1.R1040
5'-most EST
                  LIB3170-030-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2244818
BLAST score
                  356
E value
                  6.0e-34
Match length
                  106
                  73
% identity
NCBI Description
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
                  9550
Seq. No.
Contiq ID
                  16374 1.R1040
5'-most EST
                  LIB3170-030-Q1-K1-E4
Seq. No.
                  9551
                  16379 1.R1040
Contig ID
```

vzy700753123.hl

```
9552
Seq. No.
                  16379 2.R1040
Contig ID
                  LIB3107-055-Q1-K1-F8
5'-most EST
                  9553
Seq. No.
                  16387 1.R1040
Contig ID
                  pxt700944294.hl
5'-most EST
                  BLASTX
Method
                  g629670
NCBI GI
                   223
BLAST score
                   3.0e-18
E value
                   84
Match length
                   58
% identity
NCBI Description
                  hypothetical protein - tomato
Seq. No.
                   9554
                   16391 1.R1040
Contig ID
                   uC-gmrominsoy060b04b1
5'-most EST
Method
                   BLASTX
                   q1935019
NCBI GI
                   526
BLAST score
                   2.0e-53
E value
                   190
Match length
                   59
% identity
                  (Z93774) sucrose transport protein [Vicia faba]
NCBI Description
                   9555
Seq. No.
Contig ID
                   16393 1.R1040
5'-most EST
                   crh700854076.hl
Method
                   BLASTX
                   g2673917
NCBI GI
BLAST score
                   609
                   2.0e-79
E value
Match length
                   206
% identity
                   35
                   (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   9556
                   16397 1.R1040
Contig ID
                   LIB3050-008-Q1-E1-C1
5'-most EST
Method
                   BLASTX
                   g2765240
NCBI GI
                   193
BLAST score
E value
                   9.0e-15
                   80
Match length
                   50
% identity
                   (Y12805) invertase inhibitor [Nicotiana tabacum]
NCBI Description
Seq. No.
                   9557
                   16398 1.R1040
Contig ID
5'-most EST
                   uC-gmropic055e11b1
Method
                   BLASTX
                   q4335750
NCBI GI
BLAST score
                   256
                   2.0e-21
E value
```

Match length

```
% identity
                   50 `
                   (AC006284) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                   thaliana]
                   9558
Seq. No.
                   16398 2.R1040
Contig ID
                   LIB3050-008-Q1-E1-B3
5'-most EST
                   BLASTX
Method
                   g4335750
NCBI GI
                   219
BLAST score
                   1.0e-17
E value
Match length
                   64
                   56
% identity
                   (AC006284) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                   thaliana]
                   9559
Seq. No.
                   16403 1.R1040
Contig ID
                   LIB3072-049-Q1-K1-E7
5'-most EST
                   9560
Seq. No.
                   16406 1.R1040
Contig ID
5'-most EST
                   uC-gmropic106g10b1
                   9561
Seq. No.
                   16407 1.R1040
Contig ID
5'-most EST
                   LIB3109-007-Q1-K1-D8
Method
                   BLASTX
NCBI GI
                   g1170089
BLAST score
                   637
E value
                   3.0e-66
Match length
                   212
% identity
                   57
NCBI Description
                   GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
                   >gi 481822 pir S39542 probable glutathione transferase (EC
                   2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase
                   [Arabidopsis thaliana] >gi 3201614 (AC004669) glutathione
                   S-transferase [Arabidopsis thaliana]
Seq. No.
                   9562
                   16407 2.R1040
Contig ID
5'-most EST
                   g4302960
Method
                   BLASTX
NCBI GI
                   g3201613
BLAST score
                   361
E value
                   5.0e-34
Match length
                   130
                   55
% identity
NCBI Description
                   (AC004669) glutathione S-transferase [Arabidopsis thaliana]
Seq. No.
                   9563
                   16410 1.R1040
Contig ID
                   seb700650214.hl
5'-most EST
Seq. No.
                   9564
```

16410 2.R1040

Contig ID

```
5'-most EST
                   LIB3170-029-Q1-K1-G6
                   9565
Seq. No.
                   16414 1.R1040
Contig ID
                   jex70\overline{0}908176.h1
5'-most EST
                   BLASTX
Method
                   g3738297
NCBI GI
                   201
BLAST score
                   1.0e-15
E value
                   67
Match length
                   24
% identity
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   9566
Seq. No.
                   16415 1.R1040
Contig ID
5'-most EST
                   LIB3049-034-Q1-E1-E5
Seq. No.
                   9567
                   16422 1.R1040
Contig ID
                   sat701007849.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3955021
BLAST score
                   304
                   1.0e-27
E value
Match length
                   72
% identity
                   (AJ010811) HB2 homeodomain protein [Populus tremula x
NCBI Description
                   Populus tremuloides]
Seq. No.
                   9568
Contig ID
                   16425 1.R1040
                   LIB3049-034-Q1-E1-C10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3080398
BLAST score
                   246
E value
                   6.0e-21
Match length
                   112
% identity
NCBI Description
                   (AL022603) putative protein [Arabidopsis thaliana]
Seq. No.
                   9569
                   16426 1.R1040
Contig ID
                   uC-gmronoir007b08b1
5'-most EST
Seq. No.
                   9570
                   16426 2.R1040
Contig ID
                   asn701138153.h1
5'-most EST
                   9571
Seq. No.
Contig ID
                   16428 1.R1040
                   awf700836372.hl
5'-most EST
Method
                   BLASTX
                   g2959370
NCBI GI
                   318
BLAST score
                   8.0e-29
E value
Match length
                   139
```

% identity

```
(AL022117) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  9572
Seq. No.
                  16428 2.R1040
Contig ID
                  dpv701101125.hl
5'-most EST
                  BLASTN
Method
                  q3510343
NCBI GI
BLAST score
                  49
                  2.0e-18
E value
                  89
Match length
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
                  9573
Seq. No.
                  16435 1.R1040
Contig ID
5'-most EST
                  LIB3092-043-Q1-K1-C12
                  BLASTX
Method
NCBI GI
                  q2673920
                  193
BLAST score
                  2.0e-14
E value
                  87
Match length
                  48
% identity
                   (ACO02561) similar to Drosophila couch potato protein
NCBI Description
                   [Arabidopsis thaliana]
                   9574
Seq. No.
                   16440 1.R1040
Contig ID
5'-most EST
                   zzp700832734.h1
                   9575
Seq. No.
                   16445 1.R1040
Contig ID
                   sat701011620.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                   q132944
                   469
BLAST score
                   4.0e-47
E value
                   92
Match length
                   92
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
                   9576
Seq. No.
                   16447 1.R1040
Contig ID
5'-most EST
                   zhf700952425.h1
                   BLASTX
Method
                   g2104691
NCBI GI
                   291
BLAST score
                   1.0e-25
E value
Match length
                   139
% identity
                   (U92794) alpha glucosidase II, beta subunit [Mus musculus]
NCBI Description
Seq. No.
                   9577
                   16453 1.R1040
Contig ID
```

fC-qmse7000757563f1

Seq. No. 9578 Contig ID 16453 2.R1040 zhf700963836.h1 5'-most EST 9579 Seq. No. Contig ID 16453 3.R1040 zsq701127106.hl 5'-most EST 9580 Seq. No. 16453 4.R1040 Contig ID 5'-most EST jC-gmro02910064h10d1 Seq. No. 9581 Contig ID 16453 5.R1040 5'-most EST fC-gmro700848077d4 Seq. No. 9582 Contig ID 16453 7.R1040 5'-most EST leu701144767.h1 9583 Seq. No. Contig ID 16466 1.R1040 5'-most EST sat701006587.h1 BLASTX Method NCBI GI q729704 BLAST score 250 4.0e-21 E value Match length 135 % identity DNA-BINDING PROTEIN HEXBP (HEXAMER-BINDING PROTEIN) NCBI Description >gi 1078700 pir A47156 hexamer-binding protein HEXBP -Leishmania major >gi 159342 (M94390) HEXBP DNA binding protein [Leishmania major] 9584 Seq. No. Contig ID 16469 1.R1040 5'-most EST kl1701206014.hl BLASTX Method NCBI GI g3292827 BLAST score 746 E value 4.0e-79 Match length 158 % identity NCBI Description (AL031018) putative protein [Arabidopsis thaliana] Seq. No. 9585 Contig ID 16473 1.R1040 5'-most EST LIB3170-030-Q1-K1-H3

Seq. No. 9586

Contig ID 16486 1.R1040 5'-most EST gsv701049029.h1

Method BLASTX
NCBI GI g2911081
BLAST score 149
E value 5.0e-09

```
Match length
                   257
% identity
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9587
                   16487 1.R1040
Contig ID
5'-most EST
                   LIB3170-029-Q1-K1-A6
                   9588
Seq. No.
                   16492 1.R1040
Contig ID
5'-most EST
                   LIB3049-033-Q1-E1-D6
Method
                   BLASTX
NCBI GI
                   q2621299
BLAST score
                   191
                   3.0e-14
E value
                   140
Match length
% identity
                   34
NCBI Description
                   (AE000812) conserved protein [Methanobacterium
                   thermoautotrophicum]
                   9589
Seq. No.
                   16499 1.R1040
Contig ID
                   k1170\overline{1}209813.h1
5'-most EST
                   9590
Seq. No.
                   16500 1.R1040
Contig ID
                  LIB3049-033-Q1-E1-E3
5'-most EST
Seq. No.
                   9591
Contig ID
                   16505 1.R1040
5'-most EST
                   jC-gmro02910037f04d1
Method
                   BLASTX
NCBI GI
                   q1706318
BLAST score
                   2055
                   0.0e+00
E value
                   501
Match length
% identity
                   77
NCBI Description
                  GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)
                  >gi_1362098_pir__S56177 probable glutamate decarboxylase -
                   tomato >gi_995555_emb_CAA56812_ (X80840) homology to
                  pyroxidal-5'-phosphate-dependant glutamate decarboxylases;
                  putative start codon [Lycopersicon esculentum]
                   9592
Seq. No.
Contig ID
                   16506 1.R1040
5'-most EST
                  LIB3049-033-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                  q4432846
BLAST score
                   171
                   4.0e-12
E value
Match length
                  105
% identity
NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   9593
Contig ID
                   16508 1.R1040
```

leu701146421.hl

Contig ID

```
9594
Seq. No.
                   16509 2.R1040
Contig ID
5'-most EST
                   LIB3049-028-Q1-E1-C8
                   BLASTX
Method
                   q3080439
NCBI GI
                   356
BLAST score
E value
                   7.0e-34
                   96
Match length
% identity
                   (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9595
                   16513 1.R1040
Contig ID
5'-most EST
                   gsv701056187.h1
Seq. No.
                   9596
                   16519 1.R1040
Contig ID
5'-most EST
                   LIB3049-033-Q1-E1-C7
                   9597
Seq. No.
                   16525 1.R1040
Contig ID
                  LIB3170-029-Q1-K1-F5
5'-most EST
                   9598
Seq. No.
                   16527 1.R1040
Contig ID
5'-most EST
                  pxt700941561.hl
Seq. No.
                   9599
                   16531 2.R1040
Contig ID
5'-most EST
                   jsh701064262.h1
                   9600
Seq. No.
                   16531 3.R1040
Contig ID
5'-most EST
                   LIB3065-014-Q1-N1-A7
                   9601
Seq. No.
                   16531 4.R1040
Contig ID
5'-most EST
                  LIB3049-003-Q1-E1-A10
                  BLASTN
Method
                  g498704
NCBI GI
BLAST score
                   33
E value
                   7.0e-09
                   53
Match length
% identity
                   91
NCBI Description S.oleracea slfa mRNA
                   9602
Seq. No.
                   16532 1.R1040
Contig ID
5'-most EST
                   k1170\overline{1}206566.h1
                  9603
Seq. No.
                   16533 1.R1040
Contig ID
5'-most EST
                  LIB3049-033-Q1-E1-A6
                   9604
Seq. No.
```

16547 1.R1040

```
asn701140281.hl
5'-most EST
                  9605
Seq. No.
                  16548 1.R1040
Contig ID
5'-most EST
                  LIB3109-055-Q1-K1-C8
                  BLASTX
Method
                  q2160182
NCBI GI
BLAST score
                   166
                   4.0e-11
E value
                  81
Match length
                   43
% identity
                  (AC000132) ESTs gb ATTS1236, gb T43334, gb N97019, gb AA395203
NCBI Description
                  come from this gene. [Arabidopsis thaliana]
                   9606
Seq. No.
                   16549 1.R1040
Contig ID
                   q5175367
5'-most EST
                   BLASTX
Method
NCBI GI
                   g124429
                   1339
BLAST score
                   1.0e-148
E value
                   342
Match length
                   75
% identity
                  37 KD CHLOROPLAST INNER ENVELOPE MEMBRANE PROTEIN PRECURSOR.
NCBI Description
                   (E37) >gi_99543_pir__S14409 membrane protein, 37K,
                   precursor, chloroplast inner envelope - spinach
                   >gi 21228 emb CAA40283 (X56963) 37 kD inner envelope
                   membrane polypeptide [Spinacia oleracea]
                   9607
Seq. No.
                   16549 3.R1040
Contig ID
                   kmv700740656.h1
5'-most EST
                   9608
Seq. No.
                   16559 1.R1040
Contig ID
                   zhf700954620.h1
5'-most EST
                   9609
Seq. No.
                   16563 1.R1040
Contig ID
5'-most EST
                   LIB3109-033-Q1-K1-A1
                   BLASTN
Method
                   g3819163
NCBI GI
                   551
BLAST score
                   0.0e + 00
E value
                   591
Match length
% identity
NCBI Description
                  Glycine max cctd gene
                   9610
Seq. No.
Contig ID
                   16571 1.R1040
5'-most EST
                   LIB3049-002-Q1-E1-G9
Method
                   BLASTX
                   q3599491
NCBI GI
BLAST score
                   1465
                   1.0e-163
E value
                   338
Match length
% identity
                   80
```

BLAST score

Method

NCBI GI

```
NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]
Seq. No.
                   9611
                   16573 1.R1040
Contig ID
                  LIB3049-032-Q1-E1-G10
5'-most EST
                  BLASTX
Method
                   q4538981
NCBI GI
                   162
BLAST score
                   6.0e-11
E value
                   59
Match length
                   56
% identity
                   (AL049487) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9612
Contig ID
                   16574 1.R1040
5'-most EST
                   leu701149875.hl
Seq. No.
                   9613
                   16574 2.R1040
Contig ID
                   LIB3107-077-Q1-K1-E3
5'-most EST
Seq. No.
                   9614
Contig ID
                   16576 1.R1040
5'-most EST
                   LIB3049-032-Q1-E1-G12
Seq. No.
                   9615
                   16576 2.R1040
Contig ID
5'-most EST
                   xpa700795012.hl
Seq. No.
                   9616
Contig ID
                   16581 1.R1040
5'-most EST
                   LIB3074-040-Q1-K1-C2
Method
                   BLASTN
NCBI GI
                   g1666172
BLAST score
                   101
                   2.0e-49
E value
                                                     ٠:٠
                   289
Match length
% identity
NCBI Description
                  N.plumbaginifolia mRNA for BTF3-like transcription factor
Seq. No.
                   9617
                   16582 1.R1040
Contig ID
                   rlr700897329.h1
5'-most EST
Method
                   BLASTX
                   g3094014
NCBI GI
BLAST score
                   160
                   4.0e-17
E value
                   91
Match length
                   51
% identity
NCBI Description
                   (AF060862) unknown [Homo sapiens]
                   9618
Seq. No.
                   16582_3.R1040
Contig ID
```

LIB3049-032-Q1-E1-D11

BLASTX

206

q3094014



```
3.0e-16
                                                                              E value
Match length
                   71
                   54
% identity
                   (AF060862) unknown [Homo sapiens]
NCBI Description
                   9619
Seq. No.
                   16593 1.R1040
Contig ID
5'-most EST
                   LIB3170-029-Q1-K1-B5
                   9620
Seq. No.
                   16610 1.R1040
Contig ID
                   LIB3051-058-Q1-K2-G8
5'-most EST
                   BLASTX
Method
                   g2833469
NCBI GI
                   143
BLAST score
                   1.0e-08
E value
                   119
Match length
                   32
% identity
                   HYPOTHETICAL 22.2 KD PROTEIN SLR0305
NCBI Description
                   >gi_1001792_dbj_BAA10672_ (D64005) hypothetical protein
                   [Synechocystis sp.]
                   9621
Seq. No.
                   16631 1.R1040
Contig ID
                   LIB3139-094-P1-N1-E8
5'-most EST
                   BLASTX
Method
                   g4559384
NCBI GI
                   924
BLAST score
                   1.0e-100
E value
Match length
                   244
% identity
                   73
                   (AC006526) unknown protein [Arabidopsis thaliana]
NCBI Description
                   9622
Seq. No.
                   16631 2.R1040
Contig ID
                   g5509744
5'-most EST
                   9623
Seq. No.
                   16631 3.R1040
Contig ID
5'-most EST
                   wrg700787781.h2
                   9624
Seq. No.
                   16637 1.R1040
Contig ID
                   asn70\overline{1}133352.h1
5'-most EST
Seq. No.
                   16640 1.R1040
Contig ID
                   LIB3049-031-Q1-E1-G3
5'-most EST
                   9626
Seq. No.
Contig ID
                   16644 1.R1040
                   wvk700681309.h2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3510261
BLAST score
                   397
```

2.0e-38

127

E value Match length

```
58
% identity
                   (AC005310) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9627
Seq. No.
                   16644 2.R1040
Contig ID
                   jC-gm\overline{r}o02910016f10a1
5'-most EST
Method
                   BLASTX
                   g3522950
NCBI GI
                   292
BLAST score
                   2.0e-26
E value
                   99
Match length
% identity
                   62
                   (AC004411) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9628
Contig ID
                   16648 1.R1040
                   LIB3049-031-Q1-E1-D8
5'-most EST
                   9629
Seq. No.
                   16649.1.R1040
Contig ID
                   k1170\overline{1}213122.h1
5'-most EST
Seq. No.
                   9630
                   16655 1.R1040
Contig ID
                   bth700847436.h1
5'-most EST
Seq. No.
                   9631
Contig ID
                   16656 1.R1040
5'-most EST
                   LIB3049-031-Q1-E1-E6
Method
                   BLASTX
NCBI GI
                   q4558564
BLAST score
                   284
E value
                   2.0e-25
Match length
                   129
% identity
                   48
                   (AC007138) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   9632
Contig ID
                   16657 1.R1040
5'-most EST
                   LIB3093-001-Q1-K1-F1
Seq. No.
                   9633
                   16660 1.R1040
Contig ID
5'-most EST
                   LIB3107-030-Q1-K1-H10
Method
                   BLASTX
                   g3193296
NCBI GI
BLAST score
                   163
E value
                   5.0e-11
Match length
                   119
% identity
                   34
                  (AF069298) similar to pectinesterase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9634
```

16664 1.R1040

LIB3049-031-Q1-E1-F12

Contig ID 5'-most EST

NCBI GI

```
9635
Seq. No.
Contig ID
                   16678 1.R1040
                   fC-gmse700667261f4
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3297819
                   787
BLAST score
                   7.0e-84
E value
Match length
                   169
% identity
                   (AL031032) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   9636
Contig ID
                   16678 2.R1040
5'-most EST
                   LIB3049-031-Q1-E1-D4
                   BLASTX
Method
                   g3297819
NCBI GI
BLAST score
                   462
E value
                   4.0e-46
Match length
                   105
% identity
                   (AL031032) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   9637
Seq. No.
                   16682 1.R1040
Contig ID
5'-most EST
                   LIB3049-031-Q1-E1-A5
Seq. No.
                   9638
                   16684 1.R1040
Contig ID
5'-most EST
                   LIB3106-105-Q1-K1-A9
Seq. No.
                   9639
Contig ID
                   16684 2.R1040
5'-most EST
                   LIB3107-008-Q1-K1-C12
                   9640
Seq. No.
                   16688 _1.R1040
Contig ID
5'-most EST
                   ary700764359.hl
                   BLASTX
Method
NCBI GI
                   g3420052
BLAST score
                   615
E value
                   4.0e-64
Match length
                   150
% identity
                   77
NCBI Description
                   (AC004680) putative ubiqinone reductase [Arabidopsis
                   thaliana]
                   9641
Seq. No.
                   16690 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{4}9-031-Q1-E1-B2
                   9642
Seq. No.
Contig ID
                   16691 1.R1040
                   LIB30\overline{4}9-031-Q1-E1-B3
5'-most EST
                   BLASTX
Method
```

q1723832

NCBI GI

```
181
BLAST score
                  2.0e-13
E value
                  93
Match length
% identity
                  HYPOTHETICAL 15.9 KD PROTEIN IN OLE1-DUP1 INTERGENIC REGION
NCBI Description
                  >gi 2132531 pir S64058 probable membrane protein YGL054c -
                  yeast (Saccharomyces cerevisiae) >gi 1322550 emb CAA96756
                   (Z72576) ORF YGL054c [Saccharomyces cerevisiae]
                  9643
Seq. No.
                  16698 1.R1040
Contig ID
5'-most EST
                  LIB3049-030-Q1-E1-G6
Seq. No.
                  16703 1.R1040
Contig ID
5'-most EST
                  LIB3049-030-Q1-E1-H1
Seq. No.
                  9645
Contig ID
                  16703 2.R1040
                  2DC-01-Q1-E1-G3
5'-most EST
                  9646
Seq. No.
                  16709 1.R1040
Contig ID
5'-most EST
                  LIB3107-041-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q4206197
                   926
BLAST score
                  1.0e-100
E value
Match length
                  217
% identity
                   (AF071527) putative pre-mRNA splicing factor [Arabidopsis
NCBI Description
                  thaliana]
                   9647
Seq. No.
Contig ID
                   16710 1.R1040
                  LIB3170-031-Q1-K1-G1
5'-most EST
Seq. No.
                   9648
                   16719 1.R1040
Contig ID
5'-most EST
                  LIB3049-030-Q1-E1-E5
                   9649
Seq. No.
                   16721 1.R1040
Contig ID
5'-most EST
                   jC-qmro02910040d06a1
                   BLASTX
Method
NCBI GI
                   q4468993
BLAST score
                   1496
                   1.0e-167
E value
Match length
                   347
% identity
NCBI Description
                   (AL035605) putative protein [Arabidopsis thaliana]
Seq. No.
                   9650
Contig ID
                   16721 2.R1040
5'-most EST
                   jC-qmle01810024h06a1
Method
                   BLASTX
```

q4468993

```
BLAST score
                   954
                   1.0e-103
E value
                   229
Match length
                   77
% identity
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
                   9651
Seq. No.
                   16727 1.R1040
Contig ID
                   LIB3109-043-Q1-K1-F12
5'-most EST
                   BLASTX
Method
                   g4455287
NCBI GI
                   380
BLAST score
                   2.0e-36
E value
                   140
Match length
                   54
% identity
                   (AL035527) putative protein [Arabidopsis thaliana]
NCBI Description
                   9652
Seq. No.
                   16727 3.R1040
Contig ID
                   hrw701058080.h1
5'-most EST
                   9653
Seq. No.
                   16732 1.R1040
Contig ID
                   LIB3170-030-Q1-K1-E1
5'-most EST
                   BLASTX
Method
                   g2618689
NCBI GI
BLAST score
                   545
                   4.0e-56
E value
Match length
                   108
% identity
                   (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                   9654
Seq. No.
                   16746 1.R1040
Contig ID
                   uC-gmropic023f01b1
5'-most EST
                   BLASTX
Method
                   g3046695
NCBI GI
BLAST score
                   284
                   1.0e-24
E value
Match length
                   136
                   49
% identity
                   (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9655
                   16746 2.R1040
Contig ID
                   LIB3056-001-Q1-B1-H4
5'-most EST
                    9656
Seq. No.
                   16746_3.R1040
Contig ID
                   LIB30\overline{9}4-038-Q1-K1-F3
5'-most EST
                   BLASTX
Method
                    g3046695
NCBI GI
BLAST score
                    223
                    7.0e-18
E value
                    135
Match length
                    33
 % identity
                    (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
```

9657 Seq. No. 16753 1.R1040 Contig ID LIB3170-031-Q1-K1-B1 5'-most EST 9658 Seq. No. 16754 1.R1040 Contig ID LIB3170-030-Q1-K1-B1 5'-most EST 9659 Seq. No. 16759 1.R1040 Contig ID gsv701051528.hl 5'-most EST BLASTX Method g2827544 NCBI GI 661 BLAST score 4.0e-69 E value Match length 153 82 % identity (AL021635) HSP associated protein like [Arabidopsis NCBI Description thaliana] 9660 Seq. No. 16764 1.R1040 Contig ID $LIB30\overline{4}9-030-Q1-E1-A5$ 5'-most EST BLASTX Method g4454026 NCBI GI 283 BLAST score 5.0e-25 E value Match length 76 72 % identity (AL035394) phosphatase like protein [Arabidopsis thaliana] NCBI Description 9661 Seq. No. 16764 2.R1040 Contig ID $jC-gm\overline{l}e01810007h11d1$ 5'-most EST BLASTX Method g4454026 NCBI GI BLAST score 268 E value 2.0e-23 Match length 60 83 % identity (AL035394) phosphatase like protein [Arabidopsis thaliana] NCBI Description 9662 Seq. No. 16765 1.R1040 Contig ID LIB3049-030-Q1-E1-A6 5'-most EST BLASTX Method NCBI GI g2194123 502 BLAST score 2.0e-50 E value 201 Match length % identity 54 (AC002062) Similar to Secale chloroplast ribosomal protein NCBI Description L12 (gb_SCL121A). EST gb_H36579 comes from this gene.

[Arabidopsis thaliana]

9663

Seq. No.

```
16772 1.R1040
Contig ID
5'-most EST
                  ary700764475.hl
                  BLASTX
Method
NCBI GI
                  g4262226
BLAST score
                  249
                  4.0e-21
E value
                  86
Match length
% identity
                   (AC006200) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  9664
Contig ID
                  16772 2.R1040
5'-most EST
                   jC-gmro02910007b02a1
Method
                  BLASTX
NCBI GI
                  g4262226
BLAST score
                  244
                  1.0e-20
E value
Match length
                  83
                  58
% identity
NCBI Description
                   (AC006200) putative protein kinase [Arabidopsis thaliana]
                  9665
Seq. No.
Contig ID
                  16779 1.R1040
5'-most EST
                  dpv701100971.hl
                  BLASTX
Method
NCBI GI
                  g2160180
BLAST score
                  567
                  2.0e-58
E value
Match length
                  158
                  66
% identity
NCBI Description
                   (ACO00132) No definition line found [Arabidopsis thaliana]
                  9666
Seq. No.
Contig ID
                  16783 2.R1040
5'-most EST
                  LIB3139-117-P1-N1-G6
Method
                  BLASTX
NCBI GI
                  q3367576
BLAST score
                  515
E value
                  1.0e-51
Match length
                  145
% identity
                  67
                   (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  9667
                  16783 5.R1040
Contig ID
5'-most EST
                  fC-gmle700557414r2
                  9668
Seq. No.
                  16783 6.R1040
Contig ID
5'-most EST
                  hyd700727566.h1
Method
                  BLASTX
NCBI GI
                  g3367576
BLAST score
                  781
E value
                  9.0e-83
Match length
                  475
% identity
NCBI Description
                   (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]
```

```
9669
Seq. No.
                   16783 9.R1040
Contig ID
                   ssr700554109.hl
5'-most EST
                   9670
Seq. No.
                   16783 10.R1040
Contig ID
                   uC-gmropic054g12b1
5'-most EST
                   9671
Seq. No.
                   16787 1.R1040
Contig ID
                   LIB3049-029-Q1-E1-H5
5'-most EST
                   9672
Seq. No.
                   16789 1.R1040
Contig ID
                   LIB3049-029-Q1-E1-H8
5'-most EST
Seq. No.
                   9673
                   16792 1.R1040
Contig ID
                   LIB3049-008-Q1-E1-E6
5'-most EST
                   9674
Seq. No.
Contig ID
                   16795 1.R1040
                   uC-gmrominsoy098a04b1
5'-most EST
Method
                   BLASTX
                   g2252634
NCBI GI
                   447
BLAST score
E value
                   3.0e-44
Match length
                   174
% identity
                   (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9675
Seq. No.
                   16797 1.R1040
Contig ID
                   pmv70\overline{0}890089.h1
5'-most EST
                   9676
Seq. No.
                   16798 1.R1040
Contig ID
5'-most EST
                   crh70\overline{0}851588.h1
                   9677
Seq. No.
                   16803 1.R1040
Contig ID
                   jsh701063770.h1
5'-most EST
                   9678
Seq. No.
                   16815 1.R1040
Contig ID
                   pcp700993566.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1168750
                   170
BLAST score
E value
                   7.0e-12
                   97
Match length
                   40
% identity
                   CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY
NCBI Description
                   SUBUNIT) >gi 458230 (U04380) calcineurin B [Naegleria
```

gruberi]

```
Seq. No.
                   9679
                   16815 2.R1040
Contig ID
5'-most EST
                  hyd700726431.h1
                   BLASTX
Method
                   q1168750
NCBI GI
                   206
BLAST score
                   5.0e-16
E value
                   121
Match length
                   40
% identity
                  CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY
NCBI Description
                   SUBUNIT) >gi_458230 (U04380) calcineurin B [Naegleria
                   gruberi]
                   9680
Seq. No.
Contig ID
                   16816 1.R1040
5'-most EST
                   zzp700835437.hl
                   BLASTX
Method
NCBI GI
                   g2673920
BLAST score
                   287
                   1.0e-25
E value
                   70
Match length
% identity
                   80
                   (AC002561) similar to Drosophila couch potato protein
NCBI Description
                   [Arabidopsis thaliana]
                   9681
Seq. No.
                   16817 1.R1040
Contig ID
5'-most EST
                   LIB3170-020-Q1-K1-A7
                   9682
Seq. No.
                   16820 1.R1040
Contig ID
                   LIB3049-029-Q1-E1-E3
5'-most EST
Seq. No.
                   9683
                   16822 1.R1040
Contig ID
                   jC-gmle01810009h10a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4454020
BLAST score
                   448
E value
                   3.0e-44
Match length
                   154
% identity
                   (AL035396) putative protein [Arabidopsis thaliana]
NCBI Description
                   9684
Seq. No.
                   16826 1.R1040
Contig ID
                   LIB3049-029-Q1-E1-F1
5'-most EST
                   9685
Seq. No.
                   16828_1.R1040
Contig ID
5'-most EST
                   LIB3170-026-Q1-K1-B12
                   BLASTX
Method
NCBI GI
                   q4335764
BLAST score
                   443
                   1.0e-43
E value
                   207
Match length
```

% identity

```
(AC006284) putative WRKY DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  9686
Seq. No.
                  16830 1.R1040
Contig ID
                  leu701152566.hl
5'-most EST
                  BLASTX
Method
                  q3482967
NCBI GI
                  659
BLAST score
                  4.0e-69
E value
                  154
Match length
                  77
% identity
                   (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
                  protein phosphatase 2C [Arabidopsis thaliana]
                  9687
Seq. No.
                  16830 2.R1040
Contig ID
                  LIB3049-029-Q1-E1-C12
5'-most EST
                  BLASTX
Method
                  g3482967
NCBI GI
BLAST score
                  456
E value
                  2.0e-45
                  114
Match length
                  75
% identity
                   (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
                  protein phosphatase 2C [Arabidopsis thaliana]
                   9688
Seq. No.
                  16830 4.R1040
Contig ID
                  kl1701213354.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3482967
                   276
BLAST score
                   2.0e-24
E value
Match length
                  67
% identity
NCBI Description
                   (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
                   thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
                  protein phosphatase 2C [Arabidopsis thaliana]
                   9689
Seq. No.
                   16836 1.R1040
Contig ID
                   leu70\overline{1}153534.h1
5'-most EST
                  BLASTX
Method
                   g4508078
NCBI GI
                   470
BLAST score
                   5.0e-47
E value
                  96
Match length
                   89
% identity
NCBI Description
                   (AC005882) 64134 [Arabidopsis thaliana]
                   9690
Seq. No.
                   16836 2.R1040
Contig ID
                   LIB3107-013-Q1-K1-D12
5'-most EST
```

BLASTX

Method

```
NCBI GI
                   g4508078
BLAST score
                   210
                   1.0e-16
E value
Match length
                   45
                   89
% identity
                   (AC005882) 64134 [Arabidopsis thaliana]
NCBI Description
                   9691
Seq. No.
                   16843 1.R1040
Contig ID
5'-most EST
                   LIB3049-029-Q1-E1-A4
                   9692
Seq. No.
                   16844 1.R1040
Contig ID
                   gsv701055528.h1
5'-most EST
                   9693
Seq. No.
Contig ID
                   16845 1.R1040
                   LIB3049-029-Q1-E1-A6
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4539324
                   298
BLAST score
                   2.0e-37
E value
                   131
Match length
                   68
% identity
                   (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
                   9694
Seq. No.
Contig ID
                   16846 1.R1040
                   fua701040502.hl
5'-most EST
                   9695
Seq. No.
                   16847 1.R1040
Contig ID
                   LIB3049-029-Q1-E1-A8
5'-most EST
Method
                   BLASTX
                   g3953463
NCBI GI
                   810
BLAST score
                   2.0e-86
E value
Match length
                   319
% identity
                   50
                   (AC002328) F20N2.8 [Arabidopsis thaliana]
NCBI Description
                   9696
Seq. No.
                   16847 2.R1040
Contig ID
5'-most EST
                   pmv700891029.h1
                   BLASTX
Method
                   g3953463
NCBI GI
BLAST score
                   138
                   1.0e-08
E value
Match length
                   34
% identity
                   62
                   (AC002328) F20N2.8 [Arabidopsis thaliana]
NCBI Description
                   9697 '
Seq. No.
                   16848 1.R1040
Contig ID
                   LIB3109-033-Q1-K1-G4
5'-most EST
```

9698

Seq. No.

```
Contig ID
                  16849 1.R1040
5'-most EST
                  LIB3170-025-Q1-J1-G12
Seq. No.
                  9699
                  16850 1.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy117q02b1
                  BLASTX
Method
NCBI GI
                  q2832357
                  203
BLAST score
                   2.0e-15
E value
Match length
                  96
% identity
                   (Y14071) HMG protein [Arabidopsis thaliana] >gi 3068715
NCBI Description
                   (AF049236) unknown [Arabidopsis thaliana]
                  9700
Seq. No.
Contig ID
                   16850 3.R1040
5'-most EST
                  LIB3093-038-Q1-K1-H12
                  9701
Seq. No.
Contig ID
                  16850 5.R1040
5'-most EST
                  awf700837862.h1
Seq. No.
                  9702
Contig ID
                  16850 6.R1040
                                                        167
5'-most EST
                  wrg700791125.hl
                   9703
Seq. No.
Contig ID
                   16851 1.R1040
5'-most EST
                  LIB3049-029-Q1-E1-B12
                  BLASTX
Method
NCBI GI
                  q3033375
BLAST score
                   255
E value
                   7.0e-29
Match length
                   129
% identity
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   9704
Contig ID
                   16852 1.R1040
5'-most EST
                  LIB3049-029-Q1-E1-B2
Method
                  BLASTX
NCBI GI
                  q4185143
BLAST score
                  244
                   1.0e-20
E value
Match length
                  93
% identity
```

(ACO05724) putative signal recognition particle receptor NCBI Description

beta subunit [Arabidopsis thaliana]

9705 Seq. No.

Contig ID 16854 1.R1040

LIB3049-029-Q1-E1-B5 5'-most EST

Seq. No. 9706

Contig ID 16855 1.R1040

```
5'-most EST
                   zsg701118742.hl
Method
                   BLASTX
                   q710626
NCBI GI
BLAST score
                   225
                   6.0e-19
E value
                   86
Match length
                   58
 % identity
                   (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
NCBI Description
                    (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                   thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis
                   thaliana]
 Seq. No.
                   9707
                   16857 1.R1040
Contig ID
                   taw700660090.hl
 5'-most EST
 Seq. No.
                   9708
                   16868 1.R1040
 Contig ID
 5'-most EST
                   rlr700898001.hl
                   9709
 Seq. No.
                   16868 2.R1040
 Contig ID
                   LIB3050-010-Q1-E1-B12
 5'-most EST
                   9710
Seq. No.
                   16886 1.R1040
 Contig ID
                   LIB3049-028-Q1-E1-G10
 5'-most EST
Method
                   BLASTX
NCBI GI
                   q3269297
 BLAST score
                   235
                   9.0e-20
 E value
                   82
Match length
                   52
 % identity
                   (AL030978) putative protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   16887 1.R1040
 Contig ID
 5'-most EST
                   LIB3109-052-Q1-K1-E11
 Seq. No.
                   16887 2.R1040
 Contig ID
 5'-most EST
                   gsv701045817.hl
                    9713
 Seq. No.
                    16894 1.R1040
 Contig ID
 5'-most EST
                   LIB3170-028-Q1-K1-G10
                   BLASTX
 Method
 NCBI GI
                   g1888357
 BLAST score
                    186
                    5.0e-14
 E value
 Match length
                    41
 % identity
 NCBI Description
                    (X98130) alpha-mannosidase [Arabidopsis thaliana]
                    >qi 1890154 emb CAA72432 (Y11767) alpha-mannosidase
                   precursor [Arabidopsis thaliana]
```

9714

Seq. No.

```
Contig ID
                   16897 1.R1040
                   sat701009333.hl
5'-most EST
Method
                   BLASTX
                   q629623
NCBI GI
                   155
BLAST score
                   3.0e-10
E value
                   70
Match length
                   50
% identity
                   chalcone reductase - alfalfa >gi_563538 emb CAA57784
NCBI Description
                   (X82368) chalcone reductase [Medicago sativa]
                   9715
Seq. No.
                   16898 1.R1040
Contig ID
                   ncj70\overline{0}983652.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4151319
BLAST score
                   892
E value
                   2.0e-96
Match length
                   250
                   73
% identity
                   (AF089084) putative auxin efflux carrier protein; AtPIN1
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
Contig ID
                   16900 1.R1040
5'-most EST
                   zzp700834260.h1
                   BLASTX
Method
NCBI GI
                   q927428
BLAST score
                   515
E value
                   3.0e-52
Match length
                   148
% identity
NCBI Description
                   (X86733) fis1 [Linum usitatissimum]
Seq. No.
                   9717
                   16902 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-074-Q1-K1-H2
                   BLASTX
Method
NCBI GI
                   q2853097
BLAST score
                   212
                   6.0e-17
E value
Match length
                   86
% identity
                   (AL021767) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                   9718
                   16902 2.R1040
Contig ID
                   LIB3139-049-P1-N1-B7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2853097
BLAST score
                   236
                   2.0e-19
E value
Match length
                   142
% identity
                    (AL021767) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
```

9719

Seq. No.

```
Contig ID
                  16902 3.R1040
5'-most EST
                  uC-qmflminsoy028c01b1
                  BLASTX
Method
                  g1353053
NCBI GI
BLAST score
                  157
                  1.0e-10
E value
Match length
                  62
                  47
% identity
                  HYPOTHETICAL 22.5 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION
NCBI Description
                  >gi 1077868 pir S55203 hypothetical protein YJR014w -
                  yeast (Saccharomyces cerevisiae) >gi 854588 emb_CAA60937
                  (X87611) ORF YJR83.12 [Saccharomyces cerevisiae]
                  >gi 1015646 emb CAA89538 (Z49514) ORF YJR014w
                  [Saccharomyces cerevisiae]
                  9720
Seq. No.
Contig ID
                  16909 1.R1040
5'-most EST
                  LIB3170-026-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  q2632019
BLAST score
                  335
                  7.0e-31
E value
Match length
                  228
% identity
                  (AJ002571) YkfB [Bacillus subtilis]
NCBI Description
                  >qi 2633652 emb CAB13155 (Z99110) similar to
                  chloromuconate cycloisomerase [Bacillus subtilis]
Seq. No.
                  9721
Contig ID
                  16914 1.R1040
5'-most EST
                  crh700853264.h1
                  BLASTN
Method
NCBI GI
                  q2687435
BLAST score
                  766
E value
                  0.0e + 00
Match length
                  874
                  97
% identity
                  Hamamelis virginiana large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
Seq. No.
                  9722
Contig ID
                  16916 1.R1040
5'-most EST
                  LIB3170-028-Q1-K1-A12
                  BLASTX
Method
NCBI GI
                  q4337206
BLAST score
                  162
E value
                  4.0e-11
Match length
                  63
                  54
% identity
NCBI Description
                   (AC006403) putative replication factor-A protein
                   [Arabidopsis thaliana]
Seq. No.
                  9723
                  16918 1.R1040
Contig ID
                  LIB3049-028-Q1-E1-C12
5'-most EST
Method
                  BLASTX
```

q2196466

NCBI GI

```
582
BLAST score
E value
                   5.0e-60
                   150
Match length
% identity
                   74
NCBI Description
                   (Y13673) TATA binding protein-associated factor
                   [Arabidopsis thaliana]
Seq. No.
                   16919 1.R1040
Contig ID
5'-most EST
                   LIB3049-028-Q1-E1-C3
Method
                   BLASTX
                   q4115371
NCBI GI.
BLAST score
                   829
                   2.0e-88
E value
                   597
Match length
                   39
% identity
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9725
Contig ID
                   16921 1.R1040
                   ncj70\overline{0}986793.h1
5'-most EST
                   BLASTX
Method
                   q2191165
NCBI GI
BLAST score
                   347
                   5.0e-32
E value
                   125
Match length
                   55
% identity
                   (AF007270) A IG002P16.14 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   9726
Seq. No.
                   16921 2.R1040
Contig ID
                   pmv700893202.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2191165
BLAST score
                   329
                   3.0e-30
E value
                   126
Match length
                   52
% identity
NCBI Description
                   (AF007270) A IG002P16.14 gene product [Arabidopsis
                   thaliana]
                   9727
Seq. No.
                   16921 4.R1040
Contig ID
5'-most EST
                   jC-qmst02400050c02d1
Seq. No.
                   9728
Contig ID
                   16930 1.R1040
5'-most EST
                   LIB3049-013-Q1-E1-F4
Method
                   BLASTN
NCBI GI
                   g1747309
BLAST score
                   53
E value
                   6.0e-21
Match length
                   113
% identity
                   87
NCBI Description
                   Arabidopsis thaliana mRNA for Myb-like DNA binding protein,
```

complete cds

Method

BLASTX

```
Seq. No.
                   9729
Contig ID
                   16930 2.R1040
5'-most EST
                   LIB3049-028-Q1-E1-B7
Method
                   BLASTN
NCBI GI
                   g2160155
BLAST score
                   71
E value
                   1.0e-31
Match length
                   171
                   85
% identity
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
Contig ID
                   16933 1.R1040
5'-most EST
                   LIB3049-028-Q1-E1-A11
Method
                   BLASTX
NCBI GI
                   q3021513
BLAST score
                   703
                   3.0e-74
E value
Match length
                   189
% identity
                   (X96728) isocitrate dehydrogenase (NADP+) [Nicotiana
NCBI Description
                   tabacum]
                                               1.5
                   9731
Seq. No.
Contig ID
                   16937 1.R1040
5'-most EST
                   gsv701055145.hl
Seq. No.
                   9732
Contig ID
                   16939 1.R1040
5'-most EST
                   seb70\overline{0}651907.h1
                   BLASTX
Method
NCBI GI
                   q1903021
BLAST score
                   510
E value
                   1.0e-51
Match length
                   125
% identity.
                   (Y10216) hypothetical 3-isopropylmalate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   9733
Contig ID
                   16939 2.R1040
5'-most EST
                   LIB3049-028-Q1-E1-A8
                   BLASTX
Method
NCBI GI
                   q1903021
BLAST score
                   545
                   8.0e-56
E value
Match length
                   178
% identity
NCBI Description
                   (Y10216) hypothetical 3-isopropylmalate dehydrogenase
                   [Arabidopsis thaliana]
Seq. No.
                   9734
Contig ID
                   16939 3.R1040
5'-most EST
                   LIB3049-015-Q1-E1-D6
```

Contig ID

```
NCBI GI
                   g126201
BLAST score
                   465
                   2.0e-46
E value
                   147
Match length
                   65
% identity
NCBI Description
                   3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM
                   DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi 81676 pir S20510
                   3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor -
                   rape >gi 17827 emb CAA42596 (X59970) 3-isopropylmalate
                   dehydrogenase [Brassica napus]
                   9735
Seq. No.
                   16942 1.R1040
Contig ID
5'-most EST
                   k1170\overline{1}203442.h1
                   9736
Seq. No.
                   16943 1.R1040
Contig ID
5'-most EST
                   LIB3170-057-Q1-K1-E7
Method
                   BLASTN
NCBI GI
                   g2924651<sup>-</sup>
                   39
BLAST score
E value
                   3.0e-12
                   150
Match length
                   87
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K2A18, complete sequence [Arabidopsis thaliana]
                   9737
Seq. No.
                   16943 2.R1040
Contig ID
5'-most EST
                   txt700731937.h1
Method
                   BLASTN
                   g2924651
NCBI GI
BLAST score
                   35
                   4.0e-10
E value
Match length
                   59
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K2A18, complete sequence [Arabidopsis thaliana]
                   9738
Seq. No.
                   16943 3.R1040
Contig ID
5'-most EST
                   epx70\overline{1}108086.h1
Method
                   BLASTN
NCBI GI
                   g2924651
                   35
BLAST score
E value
                   4.0e-10
Match length
                   109
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K2A18, complete sequence [Arabidopsis thaliana]
                   9739
Seq. No.
Contig ID
                   16943 4.R1040
5'-most EST
                   uC-gmropic063e11b1
                   9740
Seq. No.
```

16947 1.R1040

E value

Match length

2.0e-17

151

```
5'-most EST
                   jex700904806.hl
                   9741
Seq. No.
                   16947 2.R1040
Contig ID
5'-most EST
                   sat701008764.hl
                   9742
Seq. No.
Contig ID
                   16950 1.R1040
5'-most EST
                   LIB3106-026-Q1-K1-G8
                   9743
Seq. No.
                   16950 2.R1040
Contig ID
5'-most EST
                   LIB3138-012-Q1-N1-D9
                   9744
Seq. No.
                   16952 1.R1040
Contig ID
5'-most EST
                   LIB3087-004-Q1-K1-C7
Seq. No.
                   9745
                   16955 1.R1040
Contig ID
                   LIB3049-027-Q1-E1-H1
5'-most EST
                   9746
Seq. No.
Contig ID
                   16967 1.R1040
                   sat701002995.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4049344
BLAST score
                   184
E value
                   4.0e-13
Match length
                   120
% identity
                   13
                   (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                   9747
Seq. No.
Contig ID
                   16967 2.R1040
5'-most EST
                   LIB3049-027-Q1-E1-E7
                   9748
Seq. No.
Contig ID
                   16970 1.R1040
5'-most EST
                   LIB3049-027-Q1-E1-F1
                   BLASTN
Method
                   g2656031
NCBI GI
BLAST score
                   34
                   2.0e-09
E value
Match length
                   83
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MXC20
Seq. No.
                   9749
Contig ID
                   16976 1.R1040
5'-most EST
                   eep70\overline{0868308.h1}
Method
                   BLASTX
NCBI GI
                   g4262233
BLAST score
                   218
```

BLAST score

173

```
% identity
                   40
                  (AC006200) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  9750
                  16984 1.R1040
Contig ID
                  LIB3049-048-Q1-E1-A3
5'-most EST
Seq. No.
                  9751
                  16987 1.R1040
Contig ID
                  LIB3049-027-Q1-E1-D4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4539306
BLAST score
                   406
E value
                   3.0e-39
Match length
                  128
% identity
                  (AL049480) pumilio-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9752
Contig ID
                   16987 2.R1040
                   sat701007693.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4539306
BLAST score
                   161
                   3.0e-11
E value
Match length
                   48
                   62
% identity
                  (AL049480) pumilio-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9753
Contig ID
                   16989 1.R1040
5'-most EST
                  LIB3167-023-P4-K4-D6
                  BLASTX
Method
NCBI GI
                  q2924772
BLAST score
                   686
E value
                   3.0e-72
Match length
                   143
% identity
NCBI Description
                  (AC002334) unknown protein [Arabidopsis thaliana]
Seq. No.
                   9754
Contig ID
                   16993 1.R1040
5'-most EST
                   leu701156949.hl
Method
                  BLASTN
NCBI GI
                  g20755
BLAST score
                   475
                   0.0e+00
E value
Match length
                   691
                  93
% identity
NCBI Description P.sativum mRNA rab for ras-related GTP-binding protein
                   9755
Seq. No.
Contig ID
                   16993 2.R1040
                  LIB3049-027-Q1-E1-E1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g20755
```

```
E value
                  2.0e-92
Match length
                  289
% identity
                  95
                  P.sativum mRNA rab for ras-related GTP-binding protein
NCBI Description
                  9756
Seq. No.
                  16993 3.R1040
Contig ID
                  zhf700964965.h1
5'-most EST
                  BLASTN
Method
                  g1370185
NCBI GI
BLAST score
                  55
                  3.0e-22
E value
                  107
Match length
                  89
% identity
NCBI Description
                  L.japonicus mRNA for small GTP-binding protein, RAB7C
                  9757
Seq. No.
                  16993 4.R1040
Contig ID
                  rca700999277.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g20755
BLAST score
                  245
E value
                  1.0e-135
Match length
                  366
                  94
% identity
                  P.sativum mRNA rab for ras-related GTP-binding protein
NCBI Description
Seq. No.
                  9758
Contig ID
                  16993 8.R1040
5'-most EST
                  cf1700863676.h1
Method
                  BLASTN
NCBI GI
                  g1370185
BLAST score
                  118
E value
                  9.0e-60
Match length
                  224
% identity
                  92
                  L.japonicus mRNA for small GTP-binding protein, RAB7C
NCBI Description
Seq. No.
                  9759
Contig ID
                  16997 1.R1040
5'-most EST
                  LIB3049-027-Q1-E1-E2
                  9760
Seq. No.
Contig ID
                  17003 1.R1040
5'-most EST
                  vwf700674904.h1
Method
                  BLASTX
NCBI GI
                  g2160166
BLAST score
                  806
E value
                  5.0e-86
Match length
                  258
% identity
                  60
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  9761
```

17007 1.R1040

BLASTX

uC-gmropic033f02b1

Contig ID 5'-most EST

Method

5'-most EST

```
NCBI GI
                   q4415912
BLAST score
                   312
E value
                   3.0e-29
                   189
Match length
                   38
% identity
                   (AC006282) putative protease [Arabidopsis thaliana]
NCBI Description
                   9762
Seq. No.
                   17010 1.R1040
Contig ID
                   LIB3049-002-Q1-E1-E1
5'-most EST
Seq. No.
                   9763
                   17014 1.R1040
Contig ID
                   LIB3170-040-Q1-K1-E5
5'-most EST
                   BLASTX
Method
                   g2245018
NCBI GI
                   166
BLAST score
E value
                   2.0e-11
                   89
Match length
                   43
% identity
NCBI Description (Z97341) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                   9764
                   17014 2.R1040
Contig ID
                   LIB3109-015-Q1-K1-A3
5'-most EST
                   BLASTX
Method
                   q3776027
NCBI GI
BLAST score
                   165
E value
                   1.0e-18
Match length
                   81
                   60
% identity
                   (AJ010475) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   9765
Seq. No.
                   17015 1.R1040
Contig ID
                   LIB30\overline{4}9-027-Q1-E1-C3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2583134
BLAST score
                   142
                   7.0e-09
E value
Match length
                   85
% identity
                   (AC002387) putative proline-rich protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   9766 ·
                   17017 1.R1040
Contig ID
                   k1170\overline{1}211990.h1
5'-most EST
Seq. No.
                   9767
                   17019 1.R1040
Contig ID
                   LIB3049-026-Q1-E1-G9
5'-most EST
                   9768
Seq. No.
                   17027 1.R1040
Contig ID
```

LIB3049-026-Q1-E1-H9

```
9769
Seq. No.
                   17027 2.R1040
Contig ID
                   g4292567
5'-most EST
                   9770
Seq. No.
                   17030 1.R1040
Contig ID
                   LIB3049-026-Q1-E1-G8
5'-most EST
                   BLASTX
Method
                   g2832682
NCBI GI
BLAST score
                   275
                   3.0e-24
E value
                   111
Match length
                   53
% identity
                   (AL021712) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9771
                   17039 1.R1040
Contig ID
                   LIB3049-002-Q1-E1-A12
5'-most EST
                   9772
Seq. No.
                   17041 1.R1040
Contig ID
                   LIB3170-027-Q2-K1-C9
5'-most EST
Method
                   BLASTX
                   q4454465
NCBI GI
BLAST score
                   161
                   8.0e-11
E value
                   95
Match length
% identity
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   9773
Seq. No.
                   17041 2.R1040
Contig ID
                   epx701106554.hl
5'-most EST
Method
                   BLASTX
                   g4454465
NCBI GI
                   193
BLAST score
                   1.0e-14
E value
Match length
                   104
% identity
                   40
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   9774
Seq. No.
                   17047 1.R1040
Contig ID
                   LIB3092-012-Q1-K1-C6
5'-most EST
Method
                   BLASTX
                   g2529683
NCBI GI
                   769
BLAST score
                   1.0e-81
E value
                   280
Match length
% identity
                   (AC002535) unknown protein [Arabidopsis thaliana]
NCBI Description
                   9775
Seq. No.
                   17056 1.R1040
Contig ID
5'-most EST
                   vzy700755484.hl
```

9776

Seq. No.

```
17056 2.R1040
Contig ID
5'-most EST
                  xpa700796954.hl
                  9777
Seq. No.
                  17058 1.R1040
Contig ID
5'-most EST
                  LIB3170-057-Q1-J1-C8
Seq. No.
                  9778
                  17059 1.R1040
Contig ID
                  leu701152740.h1
5'-most EST
Seq. No.
                  9779
                  17062 1.R1040
Contig ID
5'-most EST
                  LIB3049-026-Q1-E1-E1
                  9780
Seq. No.
Contig ID
                  17064 1.R1040
5'-most EST
                  jC-qmle01810037d04a2
Method
                  BLASTX
                  g1345970
NCBI GI
                  231
BLAST score
                   4.0e-19
E value
                  117
Match length
                   48
% identity
                  OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 870784 (U25817) omega-3 fatty acid desaturase [Sesamum
                   indicum]
                   9781
Seq. No.
Contig ID
                   17070 1.R1040
                   uC-gmrominsoy187a07b1
5'-most EST
                   BLASTX
Method
                   q4378166
NCBI GI
                   178
BLAST score
                   5.0e-13
E value
                   78
Match length
                   47
% identity
                   (AF102543) unknown [Zymomonas mobilis]
NCBI Description
                   9782
Seq. No.
                   17071 1.R1040
Contig ID
5'-most EST
                   leu701157142.hl
                   BLASTX
Method
                   q2651313
NCBI GI
BLAST score
                   546
E value
                   1.0e-55
                   268
Match length
% identity
                   (AC002336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9783
Seq. No.
                   17072 1.R1040
Contig ID
5'-most EST
                   LIB3170-027-Q2-K1-D9
                   9784
Seq. No.
                   17074 1.R1040
Contig ID
```

leu701157294.hl

5'-most EST

```
Method
                  BLASTX
                  g3132476
NCBI GI
BLAST score
                  711
                  4.0e-75
E value
                  208
Match length
                   68
% identity
                   (AC003096) unknown protein [Arabidopsis thaliana]
NCBI Description
                  9785
Seq. No.
                  17081 1.R1040
Contig ID
                  LIB3170-013-Q1-K1-G11
5'-most EST
                  BLASTX
Method
                   q629561
NCBI GI
                   481
BLAST score
                   3.0e-48
E value
Match length
                   168
                   54
% identity
                   SRG1 protein - Arabidopsis thaliana
NCBI Description
                   >gi 479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
                   thaliana]
                   9786
Seq. No.
                   17085 1.R1040
Contig ID
                   epx701105472.h1
5'-most EST
                   BLASTX
Method
                   g3834303
NCBI GI
                   135
BLAST score
                   5.0e-10
E value
Match length
                   96
% identity
                   (AC005679) F9K20.3 [Arabidopsis thaliana]
NCBI Description
                   9787
Seq. No.
                   17086 1.R1040
Contig ID
                   LIB3049-026-Q1-E1-C5
5'-most EST
                   BLASTX
Method
NCBI GI
                   g549638
BLAST score
                   205
                   5.0e-16
E value
Match length
                   130
                   38
% identity
                   HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC
NCBI Description
                   REGION >gi_539279_pir__S38159 hypothetical protein YKR081c
                   - yeast (Saccharomyces cerevisiae) >gi_415901_emb_CAA81632_
                   (Z27116) ORF YKR401 [Saccharomyces cerevisiae]
                   >gi 486561_emb_CAA82160 (Z28306) ORF YKR081c
                   [Saccharomyces cerevisiae]
                   9788
Seq. No.
Contig ID
                   17087 1.R1040
                   uC-gmflminsoy012h05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4220541
                   494
BLAST score
                   6.0e-50
E value
Match length
                   142
```

44

% identity

BLAST score

386

```
NCBI Description
                   (AL035356) Rab geranylgeranyl transferase like protein
                   [Arabidopsis thaliana]
                   9789
Seq. No.
                  17092 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy276d01b1
Method
                  BLASTX
                  g3297816
NCBI GI
                   1323
BLAST score
                  1.0e-146
E value
                  359
Match length
% identity
                  73
                  (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9790
                   17092 2.R1040
Contig ID
                  LIB3107-048-Q1-K1-A11
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3297816
BLAST score
                   379
                   2.0e-36
E value
Match length
                  103
                  73
% identity
NCBI Description
                  (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   17092 3.R1040
5'-most EST
                  uC-gmrominsoy233a03b1
Method
                   BLASTX
NCBI GI
                   q3297816
BLAST score
                   236
E value
                   1.0e-19
Match length
                   89
% identity
NCBI Description
                  (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                   9792
                   17094 1.R1040
Contig ID
5'-most EST
                   epx70\overline{1}105082.h1
Method
                   BLASTX
NCBI GI
                   q927575
BLAST score
                   323
E value
                   5.0e-30
Match length
                   100
                   63
% identity
                   (U12926) alpha galactosidase [Glycine max]
NCBI Description
Seq. No.
                   9793
                   17097 1.R1040
Contig ID
5'-most EST
                  LIB3093-013-Q1-K1-E9
Seq. No.
                   9794
Contig ID
                   17098 1.R1040
5'-most EST
                   LIB3049-026-Q1-E1-A10
Method
                  BLASTX
NCBI GI
                   q3702343
```

. ...

Method

NCBI GI

BLASTX

q3080439

```
E value
                   3.0e-37
Match length
                   157
% identity
                   52
                  (AC005397) putative homeotic gene regulator [Arabidopsis
NCBI Description
                   thaliana]
                   9795
Seq. No.
                   17106 1.R1040
Contig ID
                   LIB3139-109-P1-N1-F5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3212877
BLAST score
                   1136
E value
                   1.0e-124
Match length
                   304
% identity
                   71
NCBI Description
                   (AC004005) Lea-like protein [Arabidopsis thaliana]
Seq. No.
                   9796
Contig ID
                   17106 2.R1040
5'-most EST
                   kl1701207511.hl
Method
                   BLASTX
                   q3212877
NCBI GI
BLAST score
                   604
E value
                   9.0e-63
Match length
                   160
% identity
                   (AC004005) Lea-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9797
Contig ID
                   17106 5.R1040
                   uC-gmropic067h01b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3264769
BLAST score
                   194
E value
                   1.0e-14
Match length
                   49
                   78
% identity
                   (AF071894) late embryogenesis-like protein [Prunus
NCBI Description
                   armeniaca]
Seq. No.
                   9798
Contig ID
                   17111 1.R1040
5'-most EST
                   LIB3049-025-Q1-E1-F8
                   BLASTX
Method
NCBI GI
                   q4558591
BLAST score
                   164
E value
                   2.0e-11
Match length
                   61
% identity
NCBI Description
                   (AC006555) putative beta-1,3-glucanase [Arabidopsis
                   thaliana]
Seq. No.
                   9799
Contig ID
                   17114 1.R1040
5'-most EST
                   LIB3049-001-Q1-E1-C3
```

NCBI Description

```
154
BLAST score
E value
                   5.0e-10
                   68
Match length
% identity
                   (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                   9800
Seq. No.
                   17120 1.R1040
Contig ID
5'-most EST
                   LIB3049-025-Q1-E1-G7
                   BLASTX
Method.
NCBI GI
                   g3252868
BLAST score
                   284
E value
                   2.0e-25
                   78
Match length
                   60
% identity
                   (AF033536) putative zinc transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   17138 1.R1040
5'-most EST
                   LIB3109-019-Q1-K1-F12
Seq. No.
                   17140 1.R1040
Contig ID
5'-most EST
                   LIB3049-025-Q1-E1-E8
Method
                   BLASTX
                   g4204283
NCBI GI
                   217
BLAST score
                   4.0e-17
E value
Match length
                   75
% identity
                   (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9803
Seq. No.
                   17141 1.R1040
Contig ID
5'-most EST
                   LIB3049-025-Q1-E1-F10
                   9804
Seq. No.
                   17143 1.R1040
Contig ID
                   LIB3049-025-Q1-E1-F12
5'-most EST
                   BLASTX
Method
                   q2661840
NCBI GI
BLAST score
                   240
                   4.0e-20
E value
                   104
Match length
                   63
% identity
                   (Y15430) adenosine kinase [Physcomitrella patens]
NCBI Description
                   9805
Seq. No.
                   17143 2.R1040
Contig ID
5'-most EST
                   qsv70\overline{1}050303.h1
Method
                   BLASTX
NCBI GI
                   q2661840
BLAST score
                   335
E value
                   1.0e-31
Match length
                   91
% identity
```

(Y15430) adenosine kinase [Physcomitrella patens]

BLAST score

283

```
Seq. No.
                   9806
                   17156 1.R1040
Contig ID
5'-most EST
                   LIB3049-025-Q1-E1-C11
                   9807
Seq. No.
Contig ID
                   17158 1.R1040
5'-most EST
                   jC-qmf102220148h08a1
Seq. No.
                   9808
Contig ID
                   17158 3.R1040
5'-most EST
                   jC-gmf102220114b06a1
Seq. No.
Contig ID
                   17164 1.R1040
5'-most EST
                   LIB3049-025-Q1-E1-D11
Method
                   BLASTX
NCBI GI
                   q3769330
BLAST score
                   1936
                   0.0e + 00
E value
Match length
                   387
% identity
NCBI Description
                   (AB015131) alpha-amylase [Phaseolus vulgaris]
                   9810
Seq. No.
                   17168 1.R1040
Contig ID
                   LIB3170-025-Q1-K1-E9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2281103
BLAST score
                   239
                   8.0e-20
E value
Match length
                   115
% identity
                   42
                   (AC002333) Glucan endo-1,3-beta glucosidase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   9811
Seq. No.
                   17170 1.R1040
Contig ID
5'-most EST
                   LIB3049-013-Q1-E1-D5
                   9812
Seq. No.
Contig ID
                   17173 1.R1040
5'-most EST
                   LIB3106-026-Q1-K1-E3
                   BLASTX
Method
NCBI GI
                   q2649239
BLAST score
                   168
                   1.0e-11
E value
Match length
                   47
% identity
NCBI Description
                  (AE001011) rubredoxin (rd-2) [Archaeoglobus fulgidus]
Seq. No.
Contig ID
                   17175 1.R1040
5'-most EST
                   LIB3170-028-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   q3687237
```

5'-most EST

ande.

```
E value
                   8.0e-25
Match length
                   120
% identity
                   58
                   (AC005169) putative Cys3His zinc-finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   9814
Seq. No.
Contig ID
                   17175 2.R1040
                   crh700849930.hl
5'-most EST
                   BLASTX
Method
                   g3687237
NCBI GI
                   352
BLAST score
                   2.0e-33
E value
                   136
Match length
                   59
% identity
                   (AC005169) putative Cys3His zinc-finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   9815
Seq. No.
                   17177 1.R1040
Contig ID
5'-most EST
                   LIB3049-025-Q1-E1-A8
                   BLASTX
Method
NCBI GI
                   q1396054
BLAST score
                   218
E value
                   1.0e-17
Match length
                   50
                   76
% identity
                   (D86180) phosphoribosylanthranilate transferase [Pisum
NCBI Description
                   sativum]
Seq. No.
                   9816
Contig ID
                   17180_1.R1040
5'-most EST
                   jex70\overline{0}909029.h1
Seq. No.
                   9817
                   17180 2.R1040
Contig ID
5'-most EST
                  LIB3049-024-Q1-E1-H6
Seq. No.
                   9818
                   17185 1.R1040
Contig ID
5'-most EST
                  pcp700993957.hl
Seq. No.
                   9819
                   17186 1.R1040
Contig ID
5'-most EST
                  LIB3051-096-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                   g1362162
BLAST score
                   1869
E value
                   0.0e + 00
                   501
Match length
% identity
                   68
NCBI Description
                  beta-glucosidase BGQ60 precursor - barley >gi_804656
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                   9820
Contig ID
                  17186 2.R1040
```

LIB3051-111-Q1-K1-B10

E value

```
Method
                   BLASTX
NCBI GI
                   g1362162
                   382
BLAST score
                   6.0e-37
E value
Match length
                   103
% identity
                   beta-glucosidase BGQ60 precursor - barley >gi 804656
NCBI Description
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                   17187 1.R1040
Contig ID
                   gsv701055639.h1
5'-most EST
Method
                   BLASTX
                   g3776559
NCBI GI
                   692
BLAST score
                   5.0e-73
E value
                   157
Match length
% identity
NCBI Description
                   (ACO05388) Strong similarity to gene F14J9.26 gi_3482933
                   cdc2 protein kinase homolog from A. thaliana BAC
                   gb AC003970. ESTs gb Z35332 and gb F19907 come from this
                   gene. [Arabidopsis thaliana]
                   9822
Seq. No.
                   17192 1.R1040
Contig ID
                   LIB3138-079-P1-N1-H12
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2191187
BLAST score
                   175
E value
                   1.0e-12
Match length
                   95
                   43
 % identity
                   (AF007271) contains similarity to a DNAJ-like domain
NCBI Description
                   [Arabidopsis thaliana]
                   9823
Seq. No.
Contig ID
                   17194 1.R1040
                   LIB3170-026-Q1-J1-A8
 5'-most EST
                   9824
Seq. No.
                   17199 1.R1040
Contig ID
                   jC-gmst02400031h09d1
 5'-most EST
Method
                   BLASTX
                   g2760844
NCBI GI
                   247
BLAST score
E value
                   6.0e-21
                   68
Match length
 % identity
                   (AC003105) hypothetical protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   9825
                   17210 1.R1040
 Contig ID
                   LIB3109-053-Q1-K1-H10
 5'-most EST
Method
                   BLASTX
NCBI GI
                   q4406764
 BLAST score
                   494
```

6.0e-51

Seq. No.

Contig ID

9831

17231 1.R1040

```
Match length
                   157
% identity
                   36
NCBI Description
                   (AC006836) putative uridylyl transferase [Arabidopsis
                   thaliana]
                   9826
Seq. No.
                   17210 2.R1040
Contig ID
                   LIB3049-024-Q1-E1-F5
5'-most EST
Method
                   BLASTX
                   g4406764
NCBI GI
                   210
BLAST score
E value
                   9.0e-17
                   55
Match length
% identity
                   71
                   (AC006836) putative uridylyl transferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   9827
                   17212 1.R1040
Contig ID
5'-most EST
                   LIB3049-024-Q1-E1-E10
Method
                   BLASTX
NCBI GI
                   g2995953
BLAST score
                   294
E value
                   2.0e-26
Match length
                   92
% identity
NCBI Description
                   (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]
Seq. No.
                   9828
Contig ID
                   17224 1.R1040
5'-most EST
                   jC-qmst02400057e05a1
Method
                   BLASTX
NCBI GI
                   q4101564
BLAST score
                   287
E value
                   2.0e-25
Match length
                   112
                   56
% identity
NCBI Description
                   (AF004556) IFA-binding protein [Arabidopsis thaliana]
Seq. No.
Contig ID
                   17227 1.R1040
5'-most EST
                   LIB3049-024-Q1-E1-D8
Method
                   BLASTX
NCBI GI
                   q2465925
BLAST score
                   163
E value
                   2.0e-11
Match length
                   91
% identity
NCBI Description
                   (AF024649) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                   9830
Contig ID
                   17230 1.R1040
                   LIB3049-024-Q1-E1-C11
5'-most EST
```

BLAST score

358

```
5'-most EST
                  epx701108947.h1
                  9832
Seq. No.
                  17233 1.R1040
Contig ID
5'-most EST
                  uxk700669925.h1
                  BLASTX
Method
NCBI GI
                  q1175102
BLAST score
                  217
                   3.0e-17
E value
Match length .
                  187
                  37
% identity
                  HYPOTHETICAL PROTEIN HI0077 >gi 1074247 pir__G64000
NCBI Description
                  hypothetical protein HI0077 - Haemophilus influenzae
                   (strain Rd KW20) >gi 1573032 (U32693) H. influenzae
                  predicted coding region HI0077 [Haemophilus influenzae Rd]
Seq. No.
                  9833
                   17243 1.R1040
Contig ID
5'-most EST
                  LIB3170-026-Q1-K1-F7
                  9834
Seq. No.
                  17244 1.R1040
Contig ID
                  LIB3049-024-Q1-E1-B6
5'-most EST
                   9835
Seq. No.
                  17248 1.R1040
Contig ID
                  LIB3170-026-Q1-K1-G7
5'-most EST
Seq. No.
                   9836
Contig ID
                   17259 1.R1040
                  LIB3051-107-Q1-K1-D3
5'-most EST
                  BLASTX
Method
                  a1899188
NCBI GI
                   301
BLAST score
E value
                   2.0e-27
                   127
Match length
% identity
                  (U90212) DNA binding protein ACBF [Nicotiana tabacum]
NCBI Description
                   9837
Seq. No.
                   17259 2.R1040
Contig ID
5'-most EST
                   LIB3087-009-Q1-K1-E2
Method
                   BLASTX
                   q4455223
NCBI GI
BLAST score
                   396
E value
                   2.0e-38
                   116
Match length
% identity
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   9838
Seq. No.
                   17259 3.R1040
Contig ID
5'-most EST
                   jC-gmro02910003f05a1
Method
                   BLASTX
                   q2708532
NCBI GI
```

Method

BLASTX

```
7.0e-51
E value
Match length
                  159
                  33
% identity
                  (AF029351) putative RNA binding protein [Nicotiana tabacum]
NCBI Description
                  9839
Seq. No.
                  17259 4.R1040
Contig ID
                  zhf700963840.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1899188
BLAST score
                  539
                  4.0e-55
E value
Match length
                  157
% identity
                  (U90212) DNA binding protein ACBF [Nicotiana tabacum]
NCBI Description
Seq. No.
                  9840
                  17265 1.R1040
Contig ID
5'-most EST
                  uC-gmropic103d05b1
                  BLASTX
Method
                  a3023946
NCBI GI
                  195
BLAST score
                  6.0e-15
E value
Match length
                  100
% identity
                  46
                  HIRA PROTEIN (TUP1 LIKE ENHANCER OF SPLIT PROTEIN 1)
NCBI Description
                  >gi 2352031 (U94324) Tuple1/HirA [Fugu rubripes]
                  >gi 2352036 (U94325) Tuple1/HirA [Fugu rubripes]
Seq. No.
                  17266 1.R1040
Contig ID
                  hrw701058819.h1
5'-most EST
Seq. No.
                  9842
Contig ID
                  17268 1.R1040
5'-most EST
                  bth700849208.h1
                  BLASTX
Method
                  g2462762
NCBI GI
BLAST score
                  293
E value
                  2.0e-26
                  113
Match length
% identity
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  9843
Contig ID
                  17271 1.R1040
5'-most EST
                  bth700848656.h1
                  9844
Seq. No.
Contig ID
                  17271 2.R1040
5'-most EST
                  gsv701046787.hl
Seq. No.
                  9845
Contig ID
                  17274 1.R1040
5'-most EST
                  uC-qmropic024b07b1
```

5'-most EST

```
NCBI GI
                  g1632831
BLAST score
                  627
                  3.0e-65
E value
Match length
                  142
% identity
                  85
                  (Z49698) orf [Ricinus communis]
NCBI Description
                  9846
Seq. No.
                  17274 2.R1040
Contig ID
5'-most EST
                  LIB3049-012-Q1-E1-H6
Method
                  BLASTX
                  q4512684
NCBI GI
BLAST score
                  422
                  2.0e-41
E value
Match length
                  94
                  89
% identity
                   (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4559324_gb_AAD22986.1_AC007087_5 (AC007087) unknown
                  protein [Arabidopsis thaliana]
                  9847
Seq. No.
                  17276 1.R1040
Contig ID
5'-most EST
                  leu701149782.h1
                  BLASTX
Method
                  g4097547
NCBI GI
                  277
BLAST score
                  2.0e-24
E value
                  68
Match length
                   43
% identity
                   (U64906) ATFP3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  9848
                  17276 2.R1040
Contig ID
5'-most EST
                  LIB3073-008-Q1-K1-G7
                  BLASTX
Method
NCBI GI
                  q4097547
                  296
BLAST score
                  1.0e-26
E value
                  69
Match length
                   40
% identity
NCBI Description
                   (U64906) ATFP3 [Arabidopsis thaliana]
Seq. No.
                  9849
Contig ID
                  17278 1.R1040
                  LIB3049-023-Q1-E1-E12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2737973
BLAST score
                  460
                  7.0e-46
E value
Match length
                  146
                  66
% identity
NCBI Description
                  (U83625) protein kinase ZmMEK1 [Zea mays]
                  9850
Seq. No.
Contig ID
                  17290 1.R1040
```

jC-gmle01810009d08a1

E value

2.0e-15

```
9851
Seq. No.
                   17290 2.R1040
Contig ID
                  LIB3049-023-Q1-E1-A10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1345666
BLAST score
                  216
                   4.0e-17
E value
Match length
                  86
                   48
% identity
                  F-ACTIN CAPPING PROTEIN BETA SUBUNIT >gi_1016279 (U35240)
NCBI Description
                   capping protein beta [Drosophila melanogaster]
Seq. No.
                   9852
                   17291 1.R1040
Contig ID
                   jC-gmst02400063b11a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3643611
BLAST score
                   1243
E value
                   1.0e-137
                   298
Match length
                   76
% identity
                   (AC005395) putative casein kinase [Arabidopsis thaliana]
NCBI Description
                   9853
Seq. No.
                   17291 2.R1040
Contig ID
5'-most EST
                   q5126\overline{4}68
                   BLASTN
Method
                   g4220640
NCBI GI
BLAST score
                   33
E value
                   8.0e-09
                   61
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MPE11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   17291 3.R1040
Contig ID
5'-most EST
                   uC-gmropic014g08b1
Seq. No.
                   9855
                   17291 7.R1040
Contig ID
5'-most EST
                   uxk700672101.h1
                   BLASTX
Method
NCBI GI
                   q3643607
BLAST score
                   347
E value
                   5.0e-33
Match length
                   99
% identity
                   (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9856
                   17291 8.R1040
Contig ID
5'-most EST
                   bth700844667.h1
Method
                   BLASTX
NCBI GI
                   q3643611
BLAST score
                   121
```

```
57
Match length
                  70
% identity
                   (AC005395) putative casein kinase [Arabidopsis thaliana]
NCBI Description
                  9857
Seq. No.
                  17294 1.R1040
Contig ID
                  LIB3093-006-Q1-K1-H1
5'-most EST
                  BLASTN
Method
                  q3821780
NCBI GI
                   36
BLAST score
                   2.0e-10
E value
                   36
Match length
                   100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   9858
Seq. No.
                   17294 2.R1040
Contig ID
                   uaw700662762.hl
5'-most EST
                   BLASTX
Method
                   g1651934
NCBI GI
                   242
BLAST score
                   4.0e-20
E value
                   183
Match length
                   35
% identity
                   (D90901) hypothetical protein [Synechocystis sp.]
NCBI Description
                   9859
Seq. No.
                   17296 1.R1040
Contig ID
                   zzp700833170.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2505940
BLAST score
                   1181
                   1.0e-130
E value
                   309
Match length
                   75
% identity
                   (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]
NCBI Description
                   9860
Seq. No.
                   17297 1.R1040
Contig ID
                   hyd700726184.h1
5'-most EST
                   BLASTN
Method
                   g3849811
NCBI GI
BLAST score
                   33
                   6.0e-09
E value
                   61
Match length
% identity
                   Arabidopsis thaliana chromosome I BAC T2P11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   9861
Seq. No.
                   17306 1.R1040
Contig ID
                   LIB3051-042-Q1-K1-A9
5'-most EST
                   BLASTX
Method
                   g2865175
NCBI GI
BLAST score
                   230
                   1.0e-18
E value
```

116

Match length

```
% identity
                  40
                 (AB010945) AtRer1A [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  9862
                  17306 4.R1040
Contiq ID
                  6HA - 0\overline{2} - Q1 - B1 - E11
5'-most EST
                  9863
Seq. No.
                  17307 1.R1040
Contig ID
                  LIB3170-025-Q1-J1-D7
5'-most EST
                  BLASTN
Method
                  g4097568
NCBI GI
                  84
BLAST score
                  2.0e-39
E value
Match length
                  132
                  91
% identity
NCBI Description Glycine max farnesylated protein GMFP4 mRNA, partial cds
                  9864
Seq. No.
                  17308 1.R1040
Contig ID
                  LIB3049-023-Q1-E1-C2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2494238
BLAST score
                  353
                  3.0e-33
E value
Match length
                  184
                  41
% identity
                  PROBABLE PEROXISOMAL ENOYL-COA HYDRATASE
NCBI Description
                  >qi 2135896 pir I38882 peroxisomal enoyl-CoA
                  hydratase-like protein - human >gi_564065 (U16660)
                  peroxisomal enoyl-CoA hydratase-like protein [Homo sapiens]
                  >gi 2623168 (AF030249) putative dienoyl-CoA isomerase [Homo
                  sapiens] >gi 4503447_ref NP_001389.1_pECH1_ enoyl Coenzyme
                  A hydratase 1, peroxisomal
                   9865
Seq. No.
                   17319 1.R1040
Contig ID
                  LIB3170-028-Q1-K1-H6
5'-most EST
                   BLASTX
Method
                   g2497542
NCBI GI
BLAST score
                   232
                   5.0e-19
E value
Match length
                   47
% identity
                   PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR
NCBI Description
                   >gi 629696_pir__S44287 pyruvate kinase, plastid - common
                   tobacco >gi 482938_emb_CAA82223_ (Z28374) Pyruvate kinase;
                   plastid isozyme [Nicotiana tabacum]
                   9866
Seq. No.
                   17327 1.R1040
Contig ID
                   LIB3170-026-Q1-K1-A6
5'-most EST
                   9867
Seq. No.
                   17341 1.R1040
Contig ID
                   LIB3049-022-Q1-E1-F7
5'-most EST
```

9868 Seq. No. 17343 1.R1040 Contig ID 5'-most EST jC-gmf102220065g12d1 9869 Seq. No. 17344 1.R1040 Contig ID 5'-most EST gsv701054265.hl 9870 Seq. No. 17344 3.R1040 Contig ID hyd700728428.hl 5'-most EST Seq. No. 9871 17346 1.R1040 Contig ID 5'-most EST uC-gmrominsoy107d06b1 BLASTX Method NCBI GI g120941 BLAST score 336 E value 3.0e - 31Match length 97 60 % identity GAR1 PROTEIN >gi 83030_pir__S19634 nucleolar protein GAR1 -NCBI Description yeast (Saccharomyces cerevisiae) >gi_3728 emb_CAA45162_ (X63617) GAR1 [Saccharomyces cerevisiae] >gi_487935 (U00060) Garlp: Small nucleolar RNA protein required for pre-rRNA splicing [Saccharomyces cerevisiae] Seq. No. Contig ID 17346 2.R1040 5'-most EST asn701133850.hl BLASTX Method q120941 NCBI GI BLAST score 160 7.0e-11 E value Match length 44 % identity GAR1 PROTEIN >gi_83030 pir__S19634 nucleolar protein GAR1 -NCBI Description yeast (Saccharomyces cerevisiae) >gi_3728 emb_CAA45162 (X63617) GAR1 [Saccharomyces cerevisiae] >gi_487935 (U00060) Gar1p: Small nucleolar RNA protein required for pre-rRNA splicing [Saccharomyces cerevisiae] Seq. No. 9873 Contia ID 17349 1.R1040 5'-most EST LIB3050-022-Q1-K1-B1 9874 Seq. No. 17349 2.R1040 Contig ID

 $uxk70\overline{0}667230.h1$ 5'-most EST

9875 Seq. No.

17349 3.R1040 Contig ID crh700853991.h1 5'-most EST

9876 Seq. No.

17349 4.R1040 Contig ID $uxk70\overline{0}668251.h1$ 5'-most EST

```
9877
Seq. No.
Contig ID
                   17353 1.R1040
                   hyd700729857.hl
5'-most EST
Method
                   BLASTX
                   q112785
NCBI GI
BLAST score
                   395
                   5.0e-38
E value
                   178
Match length
                   42
% identity
                   DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA
NCBI Description
                   GLYCOSYLASE I, CONSTITUTIVE) (TAG I) >gi_67508_pir__DGECM1
                   3-methyladenine DNA glycosylase (EC 3.2.\overline{2}.-) \overline{1}-
                   Escherichia coli >gi_43030_emb_CAA27472_ (X03845) TAGI (aa
                   1-187) [Escherichia coli] \overline{>}gi_147920 (\overline{J02606})
                   3-methyladenine-DNA glycosylase I (tag) [Escherichia coli]
                   >qi 466687 (U00039) 3-methyladenine-DNA glycosylase I,
                   constitutive [Escherichia coli] >gi_1789971 (AE000432)
                   3-methyl-adenine DNA glycosylase I, constitutive
                   [Escherichia coli]
                   9878
Seq. No.
Contig ID
                   17355 1.R1040
                   fua701040371.hl
5'-most EST
                   9879
Seq. No.
                   17355 2.R1040
Contig ID
5'-most EST
                   jsh701067431.hl
Seq. No.
                   9880
                   17356 1.R1040
Contig ID
                   LIB3065-019-Q1-N1-A5
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3901012
BLAST score
                   551
                   1.0e-113
E value
Match length
                   276
% identity
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                   sylvatica]
Seq. No.
                   9881
                   17359 1.R1040
Contig ID
                   LIB3049-022-Q1-E1-C8
5'-most EST
Seq. No.
                   9882
                   17364 1.R1040
Contig ID
                   LIB3049-022-Q1-E1-B12
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1703190
                   159
BLAST score
                   8.0e-11
E value
                   105
Match length
                   33
% identity
                   AF-10 PROTEIN >gi 538277 (U13948) zinc finger/leucine
NCBI Description
```

zipper protein [Homo sapiens]

Seq. No.

9889

```
9883
Seq. No.
                   17366 1.R1040
Contig ID
                   LIB3049-022-Q1-E1-B3
5'-most EST
Method
                   BLASTX
                   q2252631
NCBI GI
                   478
BLAST score
                   7.0e-48
E value
                   145
Match length
                   72
% identity
                   (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   9884
Seq. No.
                   17366 2.R1040
Contig ID
                   zhf700952405.hl
5'-most EST
                   9885
Seq. No.
Contig ID
                   17368 1.R1040
5'-most EST
                   ncj700977474.hl
                   9886
Seq. No.
                   17373 1.R1040
Contig ID
5'-most EST
                   asn701132787.hl
                   BLASTX
Method
NCBI GI
                   g2827139
BLAST score
                   3734
                   0.0e + 00
E value
                   779
Match length
% identity
                   (AF027172) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana] >gi_4049343 emb_CAA22568_ (AL034567)
                   cellulose synthase catalytic subunit (RSW1) [Arabidopsis
                   thaliana]
                   9887
Seq. No.
                   17373 2.R1040
Contig ID
                   jC-gmst02400003a09d1
5'-most EST
                   BLASTX
Method
                   g2827143
NCBI GI
BLAST score
                   157
E value
                   2.0e-10
                   42
Match length
% identity
                    (AF027174) cellulose synthase catalytic subunit
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   9888
Contig ID
                   17374 1.R1040
                   wvk70\overline{0}686102.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g791097
BLAST score
                   41
                   7.0e-14
E value
Match length
                   77
% identity
                   P.vulgaris plsB mRNA
NCBI Description
```

5'-most EST

```
17375 1.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy157h02b1
                   BLASTX
Method
NCBI GI
                   q481762
BLAST score
                   162
                   7.0e-11
E value
                   181
Match length
% identity
                   28
                  beta-adaptin 1 - fruit fly (Drosophila melanogaster)
NCBI Description
                   >gi 434902 emb CAA53509_ (X75910) beta-adaptin Drosophila 1
                   [Drosophila melanogaster]
                   9890
Seq. No.
                   17377 1.R1040
Contig ID
                   leu701144426.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3746059
BLAST score
                   556
E value
                   4.0e-57
                   151
Match length
                   65
% identity
                   (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana] >gi 4432812 gb AAD20662 (AC006593) putative
                   cysteinyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                   17377 2.R1040
Contig ID
                   leu70\overline{1}152494.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3746059
BLAST score
                   237
                   1.0e-19
E value
                   105
Match length
                   49
% identity
                   (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana] >gi 4432812 gb AAD20662_ (AC006593) putative
                   cysteinyl-tRNA synthetase [Arabidopsis thaliana]
                   9892
Seq. No.
Contig ID
                   17381 1.R1040
5'-most EST
                   LIB3049-021-Q1-E1-H5
                   9893
Seq. No.
                   17384 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{4}9-021-Q1-E1-H8
                   9894
Seq. No.
                   17385 1.R1040
Contig ID
5'-most EST
                   ncj700978967.h1
                   9895
Seq. No.
                   17390 1.R1040
Contig ID
5'-most EST
                   LIB3170-028-Q1-K1-C5
Seq. No.
                   9896
Contig ID
                   17391 1.R1040
```

LIB3049-022-01-E1-A3

```
9897
Seq. No.
                  17394 1.R1040
Contig ID
5'-most EST
                  zhf700953342.hl
                  9898
Seq. No.
                  17399 1.R1040
Contig ID
                  jC-qmle01810084a09a1
5'-most EST
                  BLASTX
Method
                  g121083
NCBI GI
                  3312
BLAST score
                  0.0e + 00
E value
                  693
Match length
% identity
                  GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE
NCBI Description
                  DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)
                  >gi 282926 pir A42109 glycine dehydrogenase
                  (decarboxylating) (EC 1.4.4.2) component P precursor -
                  garden pea >gi_20741_emb_CAA42443_ (X59773) component of
                  aminomethyltransferase [Pisum sativum]
                  9899
Seq. No.
                  17399 2.R1040
Contig ID
5'-most EST
                  LIB3138-016-Q1-N1-D8
                  BLASTN
Method
                  g20738
NCBI GI
                  69
BLAST score
                  3.0e-30
E value
                  97
Match length
% identity
                  P.sativum gdcP gene for P-protein of glycine decarboxylase
NCBI Description
                  enzyme complex
                   9900
Seq. No.
                  17399 3.R1040
Contig ID
                  wrg700788492.hl
5'-most EST
                  BLASTN
Method
                   g20738
NCBI GI
                   197
BLAST score
                   1.0e-106
E value
Match length
                   364
% identity
                   P.sativum gdcP gene for P-protein of glycine decarboxylase
NCBI Description
                   enzyme complex
                   9901
Seq. No.
                   17399 4.R1040
Contig ID
                   q5753163
5'-most EST
                   BLASTN
Method
NCBI GI
                   g20740
BLAST score
                   154
                   9.0e-81
E value
                   634
Match length
% identity
                   Pisum sativum mRNA for P protein, a part of glycine
NCBI Description
```

cleavage complex

Seq. No. 9902

17407 1.R1040 Contig ID 5'-most EST pcp700994349.hl

Method BLASTX g3880625 NCBI GI 346 BLAST score 4.0e-32 E value 146 Match length

% identity (Z93785) predicted using Genefinder; similar to RNA NCBI Description

recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this

49

9903 Seq. No.

17407 2.R1040 Contig ID

5'-most EST uC-qmflminsoy042h09b1

Method BLASTX NCBI GI q3880625 BLAST score 317 6.0e-29 E value Match length 105

% identity 57

(293785) predicted using Genefinder; similar to RNA NCBI Description

recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this

9904 Seq. No.

Contig ID 17407 3.R1040

5'-most EST jC-qmro02910047b12a1

Method BLASTX NCBI GI g3880625 BLAST score 262 E value 7.0e-23 Match length 85 58 % identity

(293785) predicted using Genefinder; similar to RNA NCBI Description

> recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this

ge

9905 Seq. No.

17407 4.R1040 Contig ID

LIB3049-021-Q1-E1-G5 5'-most EST

Seq. No. 9906

17407 5.R1040 Contig ID 5'-most EST zhf700961647.h1

Method BLASTX q3880625 NCBI GI 167 BLAST score E value 1.0e-11 54 Match length

Seq. No.

Contig ID

9912

17428 1.R1040

```
% identity
                  57
NCBI Description
                  (Z93785) predicted using Genefinder; similar to RNA
                  recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST
                  EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823
                  comes from this gene; cDNA EST EMBL: D27559 comes from this
                  qe
                  9907
Seq. No.
Contig ID
                  17411 1.R1040
5'-most EST
                  eep700868642.h1
                  BLASTX
Method
NCBI GI
                  q3250695
BLAST score
                  375
                  7.0e-36
E value
Match length
                  115
% identity
NCBI Description
                  (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
                  9908
                  17411 2.R1040
Contig ID
                  dpv701100557.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3250695
BLAST score
                  220
                  1.0e-17
E value
Match length
                  82
% identity
                  52
NCBI Description
                  (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
                  9909
                  17417 1.R1040
Contig ID
                  uC-gmropic110c07b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  a3953471
BLAST score
                  1156
                  1.0e-127
E value
                  423
Match length
% identity
NCBI Description
                  (AC002328) F2202.16 [Arabidopsis thaliana]
                  9910
Seq. No.
                  17418 1.R1040
Contig ID
                  LIB3051-008-Q1-E1-E8
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2961388
BLAST score
                  263
                  7.0e-23
E value
Match length
                  75
                  68
% identity
                  (AL022141) putative protein [Arabidopsis thaliana]
NCBI Description
                  9911
Seq. No.
Contig ID
                  17423 1.R1040
5'-most EST
                  LIB3170-028-Q1-K1-H4
```

```
5'-most EST
                  LIB3049-021-Q1-E1-E8
Method
                  BLASTX
NCBI GI
                  q2642450
BLAST score
                   452
                   7.0e-45
E value
Match length
                  121
% identity
                   74
                   (AC002391) putative metal ion transporter (Nramp)
NCBI Description
                   [Arabidopsis thaliana] >qi 3169188 (AC004401) putative
                  metal ion transporter (Nramp) [Arabidopsis thaliana]
                   9913
Seq. No.
                   17436 1.R1040
Contig ID
                  LIB3170-026-Q1-K1-H3
5'-most EST
Seq. No.
                   9914
Contig ID
                   17437 1.R1040
5'-most EST
                   awf700840951.h1
Method
                  BLASTX
NCBI GI
                  q2088647
BLAST score
                   655
E value
                   1.0e-68
Match length
                   171
% identity
NCBI Description
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
                   >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
Seq. No.
                   9915
Contig ID
                   17442 1.R1040
5'-most EST
                  pcp700991595.hl
Seq. No.
                   9916
Contig ID
                   17448 1.R1040
5'-most EST
                   LIB3049-008-Q1-E1-A11
Method
                   BLASTX
NCBI GI
                   g2500717
BLAST score
                   266
E value
                   3.0e-23
Match length
                   124
                   49
% identity
NCBI Description
                  STS14 PROTEIN PRECURSOR >qi 2129995 pir S65052
                  pistil-specific protein sts14 precursor - potato
                   >gi 1236785 emb CAA57976 (X82652) sts14 [Solanum
                   tuberosum] >gi 1589691 prf 2211417A sts14 gene [Solanum
                   tuberosum]
                   9917
Seq. No.
Contig ID
                   17453 1.R1040
5'-most EST
                  LIB3170-026-Q1-K1-F3
                   9918
Seq. No.
Contig ID
                   17456 1.R1040
                  LIB30\overline{4}9-021-Q1-E1-A4
5'-most EST
Seq. No.
                   9919
```

17457 1.R1040

Contig ID

% identity

NCBI Description

62

```
5'-most EST
                   bth700845843.h1
Method
                   BLASTX
NCBI GI .
                   q2995198
                   225
BLAST score
                   3.0e-18
E value
                   124
Match length
                   37
% identity
                   (Y11588) apoptosis specific protein [Homo sapiens]
NCBI Description
                   9920
Seq. No.
                   17459 1.R1040
Contig ID
                   LIB3106-074-Q1-K1-D5
5'-most EST
                   BLASTX
Method
                   g4098517
NCBI GI
BLAST score
                   771
E value
                   5.0e-82
                   180
Match length
% identity
                   (U79114) auxin-binding protein ABP19 [Prunus persica]
NCBI Description
                   9921
Seq. No.
                   17460 1.R1040
Contig ID
5'-most EST
                   smc70\overline{0}750129.h1
Method
                   BLASTX
                   g3170178
NCBI GI
BLAST score
                   175
                   2.0e-12
E value
Match length
                   95
% identity
                   40
                   (AF039689) antigen NY-CO-7 [Homo sapiens]
NCBI Description
                   9922
Seq. No.
Contig ID
                   17460 2.R1040
5'-most EST
                   LIB3049-021-Q1-E1-A9
                   9923
Seq. No.
                   17462 1.R1040
Contig ID
                   LIB3050-013-Q1-E1-A1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2288986
BLAST score
                   710
                   8.0e-75
E value
Match length
                   191
% identity
                   (AC002335) glyoxalase II isolog [Arabidopsis thaliana]
NCBI Description
                   9924
Seq. No.
                   17462 2.R1040
Contig ID
5'-most EST
                   g5677233
Method
                   BLASTX
                   g2570338
NCBI GI
BLAST score
                   325
E value
                   6.0e-30
                   101
Match length
```

(U90927) glyoxalase II isozyme [Arabidopsis thaliana]

NCBI GI

```
Seq. No.
                   9925
Contig ID
                   17462 3.R1040
5'-most EST
                   LIB3055-011-Q1-N1-F3
                   BLASTX
Method
                   g2570338
NCBI GI
BLAST score
                   767
E value
                   1.0e-81
Match length
                   221
% identity
                   65
                   (U90927) glyoxalase II isozyme [Arabidopsis thaliana]
NCBI Description
                   9926
Seq. No.
                   17462 4.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy170e07b1
Method
                   BLASTX
NCBI GI
                   q2288986
BLAST score
                   211
E value
                   1.0e-16
Match length
                   60
% identity
                   (AC002335) glyoxalase II isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   9927
                   17462 7.R1040
Contig ID
5'-most EST
                   LIB3049-021-Q1-E1-B10
                   BLASTX
Method
NCBI GI
                   q2570338
BLAST score
                   185
E value
                   5.0e-14
Match length
                   56
                   57
% identity
                   (U90927) glyoxalase II isozyme [Arabidopsis thaliana]
NCBI Description
                   9928
Seq. No.
Contig ID
                   17465 1.R1040
5'-most EST
                   gsv701047950.hl
                                           47.
Seq. No.
                   9929
                           .,,-
Contig ID
                   17472 1.R1040
5'-most EST
                   ssr70\overline{0}560174.h1
Seq. No.
                   9930
Contiq ID
                   17473 1.R1040
5'-most EST
                   LIB3049-020-Q1-E1-G8
Method
                   BLASTX
NCBI GI
                   q3643603
BLAST score
                   398
                   9.0e-39
E value
Match length
                   134
% identity
                   (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                   9931
Seq. No.
                   17476 1.R1040
Contig ID
                   LIB3051-061-Q1-K1-C10
5'-most EST
Method
                   BLASTX
                   g2952433
```

E value

2.0e-09

```
453
BLAST score
                   5.0e-45
E value
                  119
Match length
                  76
% identity
                   (AF051135) putative ubiquitin activating enzyme E1
NCBI Description
                   [Arabidopsis thaliana]
                   9932
Seq. No.
                   17476 2.R1040
Contig ID
                   LIB3109-005-Q1-K1-C9
5'-most EST
                   BLASTX
Method
                   q2952433
NCBI GI
BLAST score
                   306
                   6.0e-28
E value
                   87
Match length
% identity
                   (AF051135) putative ubiquitin activating enzyme E1
NCBI Description
                   [Arabidopsis thaliana]
                   9933
Seq. No.
                   17478 1.R1040
Contig ID
                   LIB3170-026-Q1-K1-C3
5'-most EST
                   9934
Seq. No.
                   17479 1.R1040
Contig ID
                   k11701207665.h1
5'-most EST
                   BLASTX
Method
                   q3695388
NCBI GI
BLAST score
                   250
E value
                   4.0e-21
                   58
Match length
% identity
                   (AF096371) No definition line found [Arabidopsis thaliana]
NCBI Description
                   9935
Seq. No.
                   17481 1.R1040
Contig ID
                   pcp700989792.hl
5'-most EST
                   BLASTX
Method
                   g4101626
NCBI GI
BLAST score
                   626
                   5.0e-65
E value
Match length
                   255
% identity
                   48
                   (AF005096) desaturase/cytochrome b5 protein [Ricinus
NCBI Description
                   communisl
                   9936
Seq. No.
                   17483 1.R1040
Contig ID
                   pmv700890620.hl
5'-most EST
Seq. No.
                   9937
                   17486 1.R1040
Contig ID
                   LIB3049-020-Q1-E1-H9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3184096
BLAST score
                   147
```

```
Match length
                  129
% identity
                  26
                  (AL023777) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  9938
Seq. No.
                  17488 1.R1040
Contig ID
                  LIB3170-027-Q2-K1-F3
5'-most EST
                  9939
Seq. No.
                  17492 1.R1040
Contig ID
                  LIB3049-020-Q1-E1-F7
5'-most EST
Method
                  BLASTX
                  q3420047
NCBI GI
                  244
BLAST score
E value
                   9.0e-21
Match length
                  106
                  56
% identity
                   (AC004680) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  9940
Seq. No.
                   17494 1.R1040
Contig ID
                  LIB3170-028-Q1-K1-F3
5'-most EST
                   9941
Seq. No.
                   17498 1.R1040
Contig ID
                   LIB3049-020-Q1-E1-F9
5'-most EST
Seq. No.
                   9942
Contig ID
                   17499 1.R1040
                   LIB3049-020-Q1-E1-G10
5'-most EST
                   9943
Seq. No.
                   17500 1.R1040
Contig ID
5'-most EST
                   LIB3049-020-Q1-E1-G11
Method
                   BLASTX
NCBI GI
                   g3269286
BLAST score
                   403
                   5.0e-39
E value
Match length
                  132
% identity
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   9944
Seq. No.
                   17503 1.R1040
Contiq ID
                   LIB3049-020-Q1-E1-G3
5'-most EST
                   9945
Seq. No.
                   17508 1.R1040
Contig ID
                   jex700906877.hl
5'-most EST
Method
                   BLASTN
                   g1370171
NCBI GI
BLAST score
                   317
E value
                   1.0e-178
                   694
Match length
                   88
% identity
```

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1X

BLAST score

242

```
9946
Seq. No.
Contig ID
                  17509 1.R1040
                  rlr700898646.h1
5'-most EST
Seq. No.
                  9947
                  17509 2.R1040
Contig ID
5'-most EST
                  LIB3049-009-Q1-E1-B8
                  9948
Seq. No.
                  17512 1.R1040
Contiq ID
5'-most EST
                  LIB3049-010-Q1-E1-B11
Seq. No.
                  9949
                  17512 2.R1040
Contig ID
                  LIB3049-033-Q1-E1-B6
5'-most EST
Method
                  BLASTN
NCBI GI
                  q3702736
BLAST score
                  37
E value
                  2.0e-11
                  77
Match length
                  87
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRI1, complete sequence [Arabidopsis thaliana]
                  9950
Seq. No.
Contig ID
                  17515 1.R1040
5'-most EST
                  LIB3049-020-Q1-E1-E7
                  BLASTX
Method
NCBI GI
                  g2914703
BLAST score
                  146
                  3.0e-09
E value
                  27
Match length
% identity
                  100
NCBI Description
                  (AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.
                  9951
                  17517 1.R1040
Contig ID
5'-most EST
                  LIB3170-025-Q1-J1-D3
                  9952
Seq. No.
                  17519 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220082f03d1
Method
                  BLASTX
                  g3915039
NCBI GI
BLAST score
                  371
E value
                  2.0e-35
                  124
Match length
% identity
                  SUGAR CARRIER PROTEIN C >gi 169718 (L08196) sugar carrier
NCBI Description
                  protein [Ricinus communis]
                  9953
Seq. No.
Contig ID
                  17530 1.R1040
5'-most EST
                  uC-gmrominsoy310d04b1
Method
                  BLASTX
NCBI GI
                  q4454464
```

```
2.0e-20 '
E value
Match length
                  123
% identity
                   46
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   17530 2.R1040
Contig ID
5'-most EST
                  LIB3049-020-Q1-E1-D2
Seq. No.
                  9955
                  17531 1.R1040
Contig ID
                  LIB3072-047-Q1-K1-B6
5'-most EST
                   9956
Seq. No.
                   17533 1.R1040
Contig ID
                   sat701008660.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2494304
BLAST score
                   439
E value
                   3.0e-43
                   178
Match length
                   52
% identity
                  TRANSLATION INITIATION FACTOR EIF-2B ALPHA SUBUNIT (EIF-2B
NCBI Description
                   GDP-GTP EXCHANGE FACTOR) >gi 2144003 pir I59376
                   translation initiation factor eIF-2B alpha-subunit - rat
                   >gi 623033 (U05821) translation initiation factor eIF-2B
                   alpha-subunit [Rattus norvegicus] >gi_1050328 (L41679)
                   GTP-exchange protein [Rattus norvegicus]
                   >gi_1096885_prf__2112359A initiation factor eIF-2B [Rattus
                   norvegicus]
                   9957
Seq. No.
                   17534 1.R1040
Contig ID
                   fC-gm\overline{f}1700906023a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4140326
BLAST score
                   641
                   2.0e-66
E value
Match length
                   314
% identity
                   (AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to
NCBI Description
                   many (archae) bacterial, worm and yeast hypothetical
                   proteins) [Homo sapiens]
                   9958
Seq. No.
Contig ID
                   17535 1.R1040
5'-most EST
                   uC-gmrominsoy133d06b1
Method
                   BLASTX
                   q462253
NCBI GI
BLAST score
                   165
E value
                   3.0e-11
                   151
Match length
                   27
% identity
NCBI Description
                  TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP
```

>gi 284975 pir S26660 HCNGP protein - mouse

>gi 57912 emb CAA48198 (X68061) HCNGP [Mus musculus]

```
9959
Seq. No.
Contig ID
                  17548 1.R1040
                  uaw700665763.hl
5'-most EST
Seq. No.
                  9960
                  17557 1.R1040
Contig ID
5'-most EST
                  LIB3109-014-Q1-K1-G8
                  9961
Seq. No.
                  17562 1.R1040
Contiq ID
5'-most EST
                  LIB3170-026-Q1-K1-F2
                  BLASTN
Method
NCBI GI
                  q3413472
BLAST score
                  142
                  5.0e-74
E value
                  308
Match length
                  87
% identity
NCBI Description Glycine max mRNA for tyrosine phosphatase
                  9962
Seq. No.
                  17563 1.R1040
Contig ID
                  LIB3049-020-Q1-E1-A1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3510253
BLAST score
                  373
                 . 1.0e-35
E value
Match length
                  114
% identity
                  67
NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]
                  9963
Seq. No.
                  17565 1.R1040
Contig ID
                  leu701146507.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q1370177
BLAST score
                   434
                  0.0e+00
E value
                  796
Match length
                  92
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB5A
                   9964
Seq. No.
                  17567 1.R1040
Contig ID
5'-most EST
                  LIB3170-027-Q2-K1-G2
Seq. No.
                   9965
                  17568 1.R1040
Contig ID
5'-most EST
                  LIB3049-020-Q1-E1-A3
                   9966
Seq. No.
Contig ID
                  17570 1.R1040
5'-most EST
                  LIB3107-029-Q1-K1-G9
Seq. No.
                   9967
Contig ID
                   17573 1.R1040
5'-most EST
                   LIB3170-027-Q2-K1-B2
Method
                   BLASTX
```

Seq. No.

Contig ID

9973

17580 2.R1040

```
NCBI GI
                  q731667
BLAST score
                  153
                  3.0e-10
E value
                  87
Match length
                  39
% identity
                  ATP-DEPENDENT RRNA HELICASE RRP3 >gi_626623 pir S46713
NCBI Description
                  hypothetical protein YHR065c - yeast (Saccharomyces
                  cerevisiae) >gi 487961 (U00061) Yhr065cp [Saccharomyces
                  cerevisiae]
                  9968
Seq. No.
                  17575 1.R1040
Contig ID
                  LIB3049-019-Q1-E1-G1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4580523
BLAST score
                  185
                   4.0e-28
E value
                  338
Match length
                   41
% identity
                   (AF036305) scarecrow-like 8 [Arabidopsis thaliana]
NCBI Description
                  9969
Seq. No.
                  17576 1.R1040
Contig ID
5'-most EST
                  LIB3170-026-Q1-K1-D2
                  9970
Seq. No.
                  17578 1.R1040
Contig ID
5'-most EST
                  LIB3049-019-Q1-E1-G12
                  9971
Seq. No.
Contig ID
                  17579 1.R1040
5'-most EST
                  k1170\overline{1}214122.h1
Method
                  BLASTX
                  q3876865
NCBI GI
BLAST score
                  255
                  2.0e-21
E value
Match length
                  187
% identity
                  36
                   (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177
NCBI Description
                  comes from this gene; cDNA EST EMBL: C09822 comes from this
                  gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST
                  yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co
                  9972
Seq. No.
                  17580 1.R1040
Contig ID
5'-most EST
                  LIB3109-055-Q1-K1-C11
                  BLASTX
Method
                  g2924363
NCBI GI
BLAST score
                  417
                  1.0e-40
E value
                  88
Match length
% identity
                   (AJ224683) zeta-carotene desaturase [Narcissus
NCBI Description
                  pseudonarcissus]
```

```
5'-most EST
                  ssr700560212.hl
Method
                  BLASTX
                  g1053093
NCBI GI
BLAST score
                  189
E value
                  4.0e-14
                  69
Match length
% identity
                  59
                  (U38550) zeta-carotene desaturase precursor [Arabidopsis
NCBI Description
                  9974
Seq. No.
                  17581 1.R1040
Contig ID
5'-most EST
                  LIB3049-019-Q1-E1-G5
                  9975
Seq. No.
                  17582 1.R1040
Contig ID
5'-most EST
                  bth700847081.h1
                  BLASTX
Method
NCBI GI
                  a2160150
                  346
BLAST score
                  2.0e-32
E value
                  163
Match length
                   48
% identity
                   (AC000375) EST gb T43829 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                   9976
Seq. No.
                  17582 2.R1040
Contig ID
5'-most EST
                  LIB3109-014-Q1-K1-A6
                   9977
Seq. No.
                  17583 1.R1040
Contig ID
                  LIB3049-019-01-E1-G7
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3075399
                   157
BLAST score
                   1.0e-10
E value
                   97
Match length
% identity
                   (AC004484) SF16-like protein [Arabidopsis thaliana]
NCBI Description
                   9978
Seq. No.
                   17584 1.R1040
Contig ID
                   LIB3049-019-Q1-E1-G8
5'-most EST
                   BLASTX
Method
NCBI GI
                   q192185
                   429
BLAST score
                   4.0e-42
E value
                   155
Match length
% identity
                   (M75122) acid beta-galactosidase [Mus musculus]
NCBI Description
                   9979
Seq. No.
Contig ID
                   17590 1.R1040
                   LIB3087-007-Q1-K1-C3
5'-most EST
```

BLASTX

q1711507

Method NCBI GI

BLAST score

55

```
338
BLAST score
E value
                  1.0e-31
Match length
                  106
% identity
                  62
                  SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19)
NCBI Description
                  >qi 624221 (U19030) signal recognition particle 19 kDa
                  protein subunit SRP19 [Oryza sativa]
                   9980
Seq. No.
Contig ID
                   17597 1.R1040
5'-most EST
                   sat701005120.hl
Seq. No.
                   9981
                   17603 1.R1040
Contig ID
                   k11701202580.hl
5'-most EST
Seq. No.
                   9982
Contig ID
                   17606 1.R1040
5'-most EST
                   jex70\overline{0}904276.h1
                   BLASTX
Method
                  q3355477
NCBI GI
                  357
BLAST score
                   2.0e-33
E value
Match length
                   96
% identity
                   45
                   (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   9983
Contig ID
                   17607 1.R1040
                   jsh701066283.h1
5'-most EST
                   BLASTN
Method
                   q2564049
NCBI GI
                   33
BLAST score
E value
                   5.0e-09
                   109
Match length
% identity
                   83
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLE2, complete sequence [Arabidopsis thaliana]
                   9984
Seq. No.
                   17609 1.R1040
Contig ID
                   LIB3049-019-Q1-E1-C8
5'-most EST
Method
                   BLASTX
                   a4539359
NCBI GI
BLAST score
                   239
                   4.0e-20
E value
                   81
Match length
% identity
                   (AL049525) putative protein [Arabidopsis thaliana]
NCBI Description
                   9985
Seq. No.
Contig ID
                   17610 1.R1040
5'-most EST
                   uC-gmropic088g05b1
Method
                   BLASTN
NCBI GI
                   q2924733
```

```
8.0e-22
E value
Match length
                  172
                  86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUF9, complete sequence [Arabidopsis thaliana]
                  9986
Seq. No.
                  17612 1.R1040
Contig ID
                  LIB3139-031-P1-N1-F7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3367522
BLAST score
                  1074
                   1.0e-117
E value
Match length
                   322
                   64
% identity
                   (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana)
                   9987
Seq. No.
                   17619 1.R1040
Contig ID
                   LIB3065-027-Q1-N1-B1
5'-most EST
                   BLASTX
Method
                   q1050918
NCBI GI
BLAST score
                   302
                   4.0e-27
E value
                   92
Match length
% identity
                   (X92648) lipid transfer protein [Helianthus annuus]
NCBI Description
Seq. No.
                   17619 2.R1040
Contig ID
5'-most EST
                   LIB3170-014-Q1-K1-G11
                   BLASTX
Method
                   q3914136
NCBI GI
BLAST score
                   284
                   5.0e-25
E value
                   100
Match length
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                   >qi 2632171 emb CAA05771 (AJ002958) lipid transfer protein
                   [Cicer arietinum]
                   9989
Seq. No.
                   17619 3.R1040
Contig ID
                   uaw700665883.hl
5'-most EST
Method
                   BLASTX
                   g2407271
NCBI GI
BLAST score
                   168
                   6.0e-12
E value
Match length
                   78
% identity
                   49
                   (AF017358) lipid transfer protein [Oryza sativa]
NCBI Description
                   9990
Seq. No.
```

17621 1.R1040

LIB3049-019-Q1-E1-C2

Contig ID

5'-most EST

```
9991
Seq. No.
                   17622 1.R1040
Contig ID
                   jC-gmle01810087g12a1
5'-most EST
                   BLASTX
Method
                   g3875304
NCBI GI
                   556
BLAST score
                   5.0e-57
E value
                   164
Match length
                   60
% identity
                   (274030) predicted using Genefinder; cDNA EST EMBL:C07609
NCBI Description
                   comes from this gene; cDNA EST EMBL:C09023 comes from this
                   gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST
                   yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com
                   9992
Seq. No.
                   17632 1.R1040
Contig ID
                   LIB3049-019-Q1-E1-B8
5'-most EST
                   9993
Seq. No.
                   17633 1.R1040
Contig ID
                   LIB3170-028-Q1-K1-D2
5'-most EST
                   9994
Seq. No.
                   17651 1.R1040
Contig ID
                   LIB3049-019-Q1-E1-A3
5'-most EST
                   9995
Seq. No.
                   17654 1.R1040
Contig ID
                   LIB3049-018-Q1-E1-F3
5'-most EST
                   9996
Seq. No.
                   17655 1.R1040
Contig ID
                   LIB3170-027-Q2-K1-E1
5'-most EST
                   9997
Seq. No.
                   17663 1.R1040
Contig ID
                   LIB3170-047-Q1-J1-C2
5'-most EST
                   9998
Seq. No.
                   17665 1.R1040
Contig ID
                   LIB3049-018-Q1-E1-G7
5'-most EST
                   9999
Seq. No.
                   17666 1.R1040
Contig ID
                   pcp70\overline{0}990149.h1
5'-most EST
                   10000
Seq. No.
                   17672 1.R1040
Contig ID
                   LIB3049-018-Q1-E1-E12
5'-most EST
                   10001
Seq. No.
                   17673 1.R1040
Contig ID
                   LIB30\overline{4}9-018-Q1-E1-E2
5'-most EST
                   10002
Seq. No.
                   17673 2.R1040
Contig ID
```

rca700998058.hl

5'-most EST

Contig ID

5'-most EST

```
Method
                  BLASTX
NCBI GI
                  g2623295
                  247
BLAST score
E value
                  3.0e-22
Match length
                  107
                  59
% identity
                  (AC002409) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  10003
                  17675 1.R1040
Contig ID
5'-most EST
                  leu701147592.h1
                  10004
Seq. No.
                  17675 2.R1040
Contig ID
5'-most EST
                  sat701007648.hl
                  10005
Seq. No.
                  17676 1.R1040
Contig ID
                  LIB3049-018-Q1-E1-E5
5'-most EST
Method
                  BLASTX
                  g2245086
NCBI GI
BLAST score
                  581
E value
                  8.0e-60
Match length
                  144
% identity
                  78
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  10006
Seq. No.
                  17688 1.R1040
Contig ID
5'-most EST
                  k11701203922.h2
                  10007
Seq. No.
Contig ID
                  17689 1.R1040
5'-most EST
                  LIB3170-025-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2104446
BLAST score
                  213
                  1.0e-16
E value
                  271
Match length
% identity
                  24
                  (Z95396) WD-repeat protein [Schizosaccharomyces pombe]
NCBI Description
                  10008
Seq. No.
                  17694 1.R1040
Contig ID
                   fua701042211.hl
5'-most EST
                  BLASTN
Method
NCBI GI
                  q4519187
BLAST score
                  37
E value
                   4.0e-11
Match length
                  106
                  89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K1G2, complete sequence
Seq. No.
                   10009
```

17704 1.R1040

LIB3049-018-Q1-E1-A12

Method

BLASTX

```
Method
                   BLASTX
NCBI GI
                   q2492511
BLAST score
                   580
E value
                   7.0e-60
Match length
                   182
                   63
% identity
NCBI Description
                   CELL DIVISION PROTEIN FTSH HOMOLOG 2
                   >gi_1652282_dbj_BAA17205_ (D90904) cell division protein
                   FtsH [Synechocystis sp.]
Seq. No.
                   10010
                   17719 1.R1040
Contig ID
5'-most EST
                   LIB3049-018-01-E1-A11
Seq. No.
                   10011
                   17720 1.R1040
Contig ID
5'-most EST
                   LIB3170-025-Q1-K1-E1
                   10012
Seq. No.
Contig ID
                   17721 1.R1040
5'-most EST
                   eep70\overline{0}864833.h1
Seq. No.
                   10013
Contig ID
                   17723 1.R1040
5'-most EST
                   LIB3170-021-Q1-K1-H11
Method
                   BLASTX
                   g4531442
NCBI GI
BLAST score
                   223
                   3.0e-18
E value
Match length
                   58
% identity
                   78
NCBI Description
                   (AC006224) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   10014
Contig ID
                   17725 1.R1040
5'-most EST
                   LIB3170-022-Q1-K1-H11
                   10015
Seq. No.
Contig ID
                   17736 1.R1040
5'-most EST
                   LIB3170-028-Q1-K1-B1
Seq. No.
                   10016
Contig ID
                   17738 1.R1040
5'-most EST
                   LIB3049-017-Q1-E1-G12
                   10017
Seq. No.
Contig ID
                   17740 1.R1040
5'-most EST
                   LIB3170-025-Q1-K1-D1
Seq. No.
                   10018
Contig ID
                   17744 1.R1040
5'-most EST
                   LIB3049-017-01-E1-F1
Seq. No.
                   10019
Contig ID
                   17755 1.R1040
                   seb700649613.h1
5'-most EST
```

Method

BLASTX

```
g4539306
NCBI GI
                   147
BLAST score
                   3.0e-09
E value
Match length
                   120
                   41
% identity
NCBI Description
                   (AL049480) pumilio-like protein [Arabidopsis thaliana]
                   10020
Seq. No.
Contig ID
                   17761 1.R1040
5'-most EST
                   q5510\overline{3}63
Method
                   BLASTX
NCBI GI
                   g1653142
BLAST score
                   213
E value
                   1.0e-16
Match length
                   135
% identity
                   (D90911) hypothetical protein [Synechocystis sp.]
NCBI Description
                   10021
Seq. No.
Contig ID
                   17762 1.R1040
5'-most EST
                   LIB3049-017-Q1-E1-D11
                   10022
Seq. No.
Contig ID
                   17765 1.R1040
                   jC-gmro02910020d12a1
5'-most EST
                   10023
Seq. No.
                   17765 2.R1040
Contig ID
                   uC-gmrominsoy025d02b1
5'-most EST
Seq. No.
                   10024
                   17770 1.R1040
Contig ID
                   xpa70\overline{0}793759.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2897875
BLAST score
                   228
E value
                   8.0e-19
Match length
                   79
                   52
% identity
NCBI Description
                   (U90274) histone acetyltransferase HAT B [Zea mays]
Seq. No.
                   10025
                   17771 1.R1040
Contig ID
5'-most EST
                   epx701110128.hl
                   10026
Seq. No.
Contig ID
                   17772 1.R1040
5'-most EST
                   LIB3170-022-Q1-K1-H3
                   10027
Seq. No.
                   17774 1.R1040
Contig ID
5'-most EST
                   LIB3170-021-Q1-J1-H9
Seq. No.
                   10028
                   17777 1.R1040
Contig ID
                   LIB3049-017-Q1-E1-A9
5'-most EST
```

```
g2252840
NCBI GI
BLAST score
                   248
E value
                   3.0e-21
Match length
                   105
% identity
                   45
NCBI Description
                   (AF013293) contains regions of similarity to Haemophilus
                   influenzae permease (SP:P38767) [Arabidopsis thaliana]
                   10029
Seq. No.
                   17781 1.R1040
Contig ID
5'-most EST
                   ncj700982438.hl
Seq. No.
                   10030
                   17783 1.R1040
Contig ID
5'-most EST
                   g5688018
Method
                   BLASTX
NCBI GI
                   q3549665
BLAST score
                   414
E value
                   4.0e-40
Match length
                   373
% identity
                   33
NCBI Description
                   (AL031394) hypothetical protein [Arabidopsis thaliana]
                   10031
Seq. No.
Contig ID
                   17785 1.R1040
5'-most EST
                   k1170\overline{1}203177.h1
Method
                   BLASTX
NCBI GI
                   q3928150
BLAST score
                   628
E value
                   1.0e-65
Match length
                   161
% identity
                   75
                   (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
                   10032
Seq. No.
                   17786_1.R1040
Contig ID
5'-most EST
                   uC-gmropic056f06b1
Method
                   BLASTX
NCBI GI
                   g2243118
BLAST score
                   1170
E value
                   1.0e-128
Match length
                   316
% identity
                   68
NCBI Description
                   (Y10984) glutathione synthetase [Brassica juncea]
                   10033
Seq. No.
Contig ID
                   17786_2.R1040
5'-most EST
                   LIB3093-018-Q1-K2-H4
                   BLASTX
Method
NCBI GI
                   g2243118
BLAST score
                   193
E value
                   1.0e-22
Match length
                   87
% identity
NCBI Description
                   (Y10984) glutathione synthetase [Brassica juncea]
```

10034

Seq. No.

```
Contig ID
                    17787 1.R1040
5'-most EST
                    LIB3049-017-Q1-E1-B9
Method
                    BLASTX
NCBI GI
                    q4432840
BLAST score
                    191
E value
                    2.0e-14
Match length
                    67
                    51
% identity
NCBI Description
                    (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                    10035
Contig ID
                    17789 1.R1040
5'-most EST
                    LIB3049-017-Q1-E1-C10
Seq. No.
                    10036
                    17796 1.R1040
Contig ID
5'-most EST
                    zhf700960425.hl
                    10037
Seq. No.
                    17796 2.R1040
Contig ID
                    leu701146313.h1
5'-most EST
                    10038
Seq. No.
                    17798 1.R1040
Contig ID
                    LIB3093-025-Q1-K1-H8
5'-most EST
                    10039
Seq. No.
                    17798 2.R1040
Contig ID
                    LIB3170-022-Q1-K1-H4
5'-most EST
                    10040
Seq. No.
                    17801 1.R1040
Contig ID
5'-most EST
                    ncj70\overline{0}983102.h1
                    10041
Seq. No.
                    17804 1.R1040
Contig ID
5'-most EST
                    LIB30\overline{4}9-017-Q1-E1-A12
Method
                    BLASTX
NCBI GI
                    g3242785
BLAST score
                    552
E value
                    2.0e-56
Match length
                    129
% identity
                    80
NCBI Description
                    (AF055355) respiratory burst oxidase protein C [Arabidopsis
                    thaliana]
Seq. No.
                    10042
Contig ID
                    17806_1.R1040
5'-most EST
                    jC-gmf102220072g04a1
                    10043
Seq. No.
                    17807_1.R1040
Contig ID
5'-most EST
                    LIB3049-017-Q1-E1-A4
Method
                    BLASTX
                    q2245141
NCBI GI
BLAST score
                    452
```

5.0e-45

E value

```
Match length
                    105
                    77
% identity
                   (297344) acetylornithine deacetylase [Arabidopsis thaliana]
NCBI Description
                    10044
Seq. No.
                    17815 1.R1040
Contig ID
                   pxt700944221.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2673920
BLAST score
                   232
E value
                    5.0e-19
Match length
                   97
                    49
% identity
                    (AC002561) similar to Drosophila couch potato protein
NCBI Description
                    [Arabidopsis thaliana]
                   10045
Seq. No.
                    17815 2.R1040
Contig ID
                   LIB30\overline{4}9-016-Q1-E1-F9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2673920
BLAST score
                   159
E value
                    1.0e-10
Match length
                   67
% identity
                   49
NCBI Description
                    (AC002561) similar to Drosophila couch potato protein
                    [Arabidopsis thaliana]
                   10046
Seq. No.
Contig ID
                   17818_1.R1040
5'-most EST
                   LIB3170-050-Q1-K1-A7
                   BLASTX
Method
NCBI GI
                   g3858937
BLAST score
                    649
E value
                    7.0e-68
Match length
                   216
% identity
                    62
NCBI Description
                   (AL021636) putative protein [Arabidopsis thaliana]
                   10047
Seq. No.
Contig ID
                   17819 1.R1040
5'-most EST
                   LIB30\overline{5}1-032-Q1-K1-E6
                   10048
Seq. No.
Contig ID
                   17825 1.R1040
5'-most EST
                   LIB3049-016-Q1-E1-G8
Seq. No.
                   10049
Contig ID
                   17827 1.R1040
5'-most EST
                   rca700999233.h1
Method
                   BLASTN
NCBI GI
                   a3176071
BLAST score
                   555
                   0.0e + 00
E value
Match length
                   1085
% identity
NCBI Description
                   Medicago sativa mRNA for protein phosphatase 1, beta
```

subunit Seq. No. 10050 Contig ID 17827_2.R1040 5'-most EST dpv701101871.h1

Method BLASTN
NCBI GI g3176071
BLAST score 114
E value 4.0e-57
Match length 242
% identity 87

NCBI Description Medicago sativa mRNA for protein phosphatase 1, beta

subunit

Seq. No. 10051

Contig ID 17827 3.R1040

5'-most EST LIB3106-074-Q1-K1-H3

Method BLASTN
NCBI GI g3176071
BLAST score 165
E value 1.0e-87
Match length 332
% identity 92

NCBI Description Medicago sativa mRNA for protein phosphatase 1, beta

subunit

Seq. No. 10052

Contig ID 17827_4.R1040 5'-most EST kl1701214536.h1

Method BLASTX
NCBI GI g3176074
BLAST score 480
E value 2.0e-48
Match length 138
% identity 70

NCBI Description (AJ002486) protein phosphatase 1, catalytic gsmms subunit

[Medicago sativa]

Seq. No. 10053

Contig ID 17829 1.R1040

5'-most EST LIB3138-034-Q1-N1-E3

Method BLASTX
NCBI GI g3860250
BLAST score 277
E value 2.0e-24
Match length 83
% identity 59

NCBI Description (AC005824) putative chloroplast prephenate dehydratase

[Arabidopsis thaliana]

Seq. No. 10054

Contig ID 17829 2.R1040

5'-most EST jC-gmle01810019d08a2

Method BLASTX
NCBI GI g3860250
BLAST score 271
E value 1.0e-23

```
Match length
                   90
                   53
% identity
                   (AC005824) putative chloroplast prephenate dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   10055
Seq. No.
                   17830 1.R1040
Contig ID
                  LIB3049-016-Q1-E1-E10
5'-most EST
Method
                  BLASTX
                   g1621438
NCBI GI
BLAST score
                   125
E value
                   3.0e-09
Match length
                  138
                   30
% identity
                   (U71603) mitochondrial transport protein amc-1 [Emericella
NCBI Description
                  nidulans]
                  10056
Seq. No.
                   17832 1.R1040
Contig ID
5'-most EST
                  LIB3049-016-Q1-E1-E12
Method
                  BLASTX
NCBI GI
                   g4454480
BLAST score
                   279
                   2.0e-24
E value
Match length
                   90
% identity
                   61
NCBI Description
                   (AC006234) putative (1-4)-beta-mannan endohydrolase
                   [Arabidopsis thaliana]
                   10057
Seq. No.
                   17839 1.R1040
Contig ID
5'-most EST
                   epx701105337.hl
                  10058
Seq. No.
                   17841 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810020a05d1
Seq. No.
                  10059
                  17841 3.R1040
Contig ID
5'-most EST
                  LIB3049-016-Q1-E1-F10
Method
                  BLASTX
                  g1174850
NCBI GI
BLAST score
                   743
E value
                   9.0e-79
Match length
                  149
                   92
% identity
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN
                  LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)
Seq. No.
                  10060
Contig ID
                   17841 4.R1040
5'-most EST
                  LIB3109-047-Q1-K1-D8
Method
                  BLASTX
                  q1174850
NCBI GI
                   753
BLAST score
                   7.0e-80
E value
```

149

Match length

5'-most EST

```
% identity
                  93
                  UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)
                  10061
Seq. No.
                  17841 5.R1040
Contig ID
                  sat701006343.hl
5'-most EST
                  BLASTX .
Method
NCBI GI
                  g431270
                  390
BLAST score
E value
                  1.0e-37
                  80
Match length
% identity
                  89
                  (L19356) ubiquitin conjugating enzyme [Arabidopsis
NCBI Description
                  thaliana]
                  10062
Seq. No.
                  17841 6.R1040
Contig ID
5'-most EST
                  zhf700954546.h1
                  BLASTX
Method
                  g136644
NCBI GI
BLAST score
                  202
                  5.0e-16
E value
                  42
Match length
% identity
                  88
                  UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_100765_pir__A34506
                  23K ubiquitin carrier protein E2 - wheat >gi 170782
                  (M28059) ubiquitin carrier protein [Triticum vulgare]
                  10063
Seq. No.
                  17841 7.R1040
Contig ID
                  uC-gmronoir023h05b1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g431269
BLAST score
                  46
E value
                  8.0e-17
Match length
                  105
                  92
% identity
                  Arabidopsis thaliana ubiquitin conjugating enzyme (UBC5)
NCBI Description
                  gene, complete cds
Seq. No.
                  10064
                  17843 1.R1040
Contig ID
5'-most EST
                  wrg700786292.h2
Method
                  BLASTX
NCBI GI
                  g4406815
BLAST score
                  731
E value
                  2.0e-77
Match length
                  209
                  67
% identity
                  (AC006201) putative peptide methionine sulfoxide reductase
NCBI Description
                  [Arabidopsis thaliana]
                  10065
Seq. No.
Contig ID
                  17843 2.R1040
```

LIB3170-021-Q1-K1-H2

5'-most EST

Method

```
Method
                   BLASTX
NCBI GI
                   q4406815
BLAST score
                   275
E value
                   3.0e-24
Match length
                   81
% identity
NCBI Description
                   (AC006201) putative peptide methionine sulfoxide reductase
                   [Arabidopsis thaliana]
Seq. No.
                   10066
                   17845 2.R1040
Contig ID
5'-most EST
                   pxt700946337.hl
Method
                   BLASTX
NCBI GI
                   q3288888
BLAST score
                   145
E value
                   4.0e-09
Match length
                   116
                   28
% identity
                   (AC005253) R26445_1 [Homo sapiens]
NCBI Description
                   10067
Seq. No.
                   17849 1.R1040
Contig ID
5'-most EST
                   trc700565235.h1
Method
                   BLASTX
NCBI GI
                   q4559356
BLAST score
                   163
E value
                   6.0e-11
Match length
                   146
                   10
% identity
                   (AC006585) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   10068
Seq. No.
                   17855 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400076f04a1
Method
                   BLASTX
NCBI GI
                   q4218121
BLAST score
                   148
E value
                   3.0e-09
Match length
                   43
% identity
                   56
                   (AL035353) putative protein [Arabidopsis thaliana]
NCBI Description
                   10069
Seq. No.
                   17855 2.R1040
Contig ID
5'-most EST
                   LIB3049-016-Q1-E1-D10
Method
                   BLASTX
NCBI GI
                   g4218121
BLAST score
                   413
                   3.0e-40
E value
Match length
                   152
% identity
                   55
NCBI Description
                   (AL035353) putative protein [Arabidopsis thaliana]
                   10070
Seq. No.
Contig ID
                   17856 1.R1040
```

LIB3107-035-Q1-K1-E9

BLASTX

% identity

77

```
NCBI GI
                   q4206210
BLAST score
                   336
E value
                   2.0e-31
Match length
                   128
% identity
                   54
                   (AF071527) putative calcium channel [Arabidopsis thaliana]
NCBI Description
                   >gi_4263043_gb_AAD15312_ (AC005142) putative calcium
                   channel [Arabidopsis thaliana]
Seq. No.
                   10071
                   17860 1.R1040
Contig ID
5'-most EST
                   LIB3049-016-Q1-E1-D5
Seq. No.
                   10072
                   17861 1.R1040
Contig ID
                   LIB3049-016-Q1-E1-D6
5'-most EST
Seq. No.
                   10073
Contig ID
                   17863 1.R1040
5'-most EST
                   vzy70\overline{0}755952.h1
Method
                   BLASTX
NCBI GI
                   q465820
BLAST score
                   587
E value
                   1.0e-60
Match length
                   161
% identity
                   63
NCBI Description
                   HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III
                   >gi_280536_pir__S28301 hypothetical protein C40H1.6 -
                   Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154)
                   C40H1.6 [Caenorhabditis elegans]
                   10074
Seq. No.
Contig ID
                   17868 1.R1040
5'-most EST
                   leu70\overline{1}156625.h1
Method
                   BLASTX
NCBI GI
                   q3860273
BLAST score
                   172
E value
                   2.0e-12
Match length
                   95
% identity
NCBI Description
                   (AC005824) hypothetical protein [Arabidopsis thaliana]
                   >gi_4314398_gb_AAD15608_ (AC006232) hypothetical protein
                   [Arabidopsis thaliana]
Seq. No.
                   10075
Contig ID
                   17869 1.R1040
5'-most EST
                   LIB3170-023-Q1-K1-H5
Seq. No.
                   10076
                   17881 1.R1040
Contig ID
5'-most EST
                   leu701144861.hl
Method
                   BLASTX
NCBI GI
                   q1255954
BLAST score
                   490
E value
                   3.0e-49
Match length
                   116
```

```
NCBI Description (Z70677) thioredoxin [Ricinus communis]
                  10077
Seq. No.
                  17881 2.R1040
Contig ID
5'-most EST
                  jC-gmst02400004a08d1
                  BLASTX
Method
                  g586099
NCBI GI
BLAST score
                  224
                  4.0e-18
E value
Match length
                  54
                  78
% identity
                  THIOREDOXIN H-TYPE 2 (TRX-H2) >gi_486690_pir__S34812
NCBI Description
                  thioredoxin h2 - common tobacco >gi 297519 emb_CAA77847_
                   (Z11803) THIOREDOXIN [Nicotiana tabacum]
                  >gi_447151_prf__1913431A thioredoxin [Nicotiana tabacum]
                  10078
Seq. No.
                  17882 1.R1040
Contig ID
                  hyd700727023.hl
5'-most EST
                  BLASTX
Method
                  g1200205
NCBI GI
BLAST score
                  347
                  3.0e-32
E value
                  124
Match length
                  55
% identity
                   (X95753) DAG [Antirrhinum majus]
NCBI Description
Seq. No.
                  10079
                  17886 1.R1040
Contig ID
                  LIB3049-015-Q1-E1-H6
5'-most EST
                  10080
Seq. No.
                  17888_1.R1040
Contig ID
5'-most EST
                  uC-gmropic022f04b1
Method
                  BLASTX
NCBI GI
                   g2632252
BLAST score
                   761
E value
                  7.0e-81
                   199
Match length
                   70
% identity
                   (Y12464) serine/threonine kinase [Sorghum bicolor]
NCBI Description
                   10081
Seq. No.
                   17888 2.R1040
Contig ID
                   kmv700740252.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3885328
BLAST score
                   1525
                   1.0e-170
E value
Match length
                   338
                   83
% identity
                   (AC005623) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   10082
Seq. No.
```

17888 3.R1040

LIB3138-127-Q1-N1-C4

Contig ID

5'-most EST

```
Seq. No.
                   10083
Contig ID
                   17888 4.R1040
5'-most EST
                   jC-gmle01810044e03a1
Seq. No.
                   17888 6.R1040
Contig ID
5'-most EST
                   jC-gmle01810075e03d1
Method
                   BLASTX
NCBI GI
                   q3885328
BLAST score
                   210
E value
                   1.0e-16
Match length
                   43
% identity
NCBI Description
                   (AC005623) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   10085
Contig ID
                   17888 8.R1040
5'-most EST
                   zzp70\overline{0}831282.h1
Method
                   BLASTX
NCBI GI
                   q3885328
BLAST score
                   207
E value
                   2.0e-16
Match length
                   43
% identity
NCBI Description
                   (AC005623) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
                   10086
Seq. No.
Contig ID
                   17889 1.R1040
                   jC-gmf102220138c12a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4220474
BLAST score
                   266
E value
                   5.0e-23
Match length
                   92
% identity
NCBI Description
                   (AC006069) putative myosin heavy chain [Arabidopsis
                   thalianal
Seq. No.
                   10087
                   17903 1.R1040
Contig ID
5'-most EST
                   fua701043040.h1
Seq. No.
                   10088
Contig ID
                   17903 2.R1040
5'-most EST
                   LIB3093-016-Q1-K1-H8
Seq. No.
                   10089
                   17907 1.R1040
Contig ID
5'-most EST
                   LIB3049-015-Q1-E1-G5
Method
                   BLASTX
                   g2148045
NCBI GI
BLAST score
                   165
                   2.0e-11
E value
Match length
                   120
```

% identity

53

```
% identity
                    30
                    self-incompatibility protein S3 precursor - Papaver rhoeas
NCBI Description
                   >gi_1107841_emb_CAA60578_ (X87100) S3 self-incompatibility
protein [Papaver rhoeas] >gi_1107843_emb_CAA60579_ (X87101)
                    S3 self-incompatibility protein [Papaver rhoeas]
                    10090
Seq. No.
                    17912 1.R1040
Contig ID
5'-most EST
                    jsh70\overline{1}069991.h2
Method
                    BLASTX
NCBI GI
                    q3858935
BLAST score
                    652
                    4.0e-68
E value
Match length
                    212
% identity
                    53
NCBI Description
                    (AL021636) synaptobrevin-like protein [Arabidopsis
                    thaliana] >gi_4103357 (AF025332) vesicle-associated
                    membrane protein 7C; synaptobrevin 7C [Arabidopsis
                    thaliana]
                    10091
Seq. No.
                    17912 2.R1040
Contig ID
5'-most EST
                    jsh70\overline{1}069609.h1
Method
                    BLASTX
NCBI GI
                    q3858935
BLAST score
                    182
E value
                    1.0e-13
Match length
                    55
                    58
% identity
NCBI Description
                    (AL021636) synaptobrevin-like protein [Arabidopsis
                    thaliana] >gi 4103357 (AF025332) vesicle-associated
                    membrane protein 7C; synaptobrevin 7C [Arabidopsis
                    thaliana]
                    10092
Seq. No.
Contig ID
                    17913 1.R1040
                    LIB31\overline{7}0-055-Q1-K1-F2
5'-most EST
Method
                    BLASTX
NCBI GI
                    q2315449
BLAST score
                    415
E value
                    3.0e-40
Match length
                    231
% identity
                    43
NCBI Description
                    (AF016448) similar to Saccharomyces cerevisiae nuclear
                    protein SNF7 (SP:P39929)in one region and the chromosome
                    segregation protein SMC2 (SP:P38989) in another
                    [Caenorhabditis elegans]
Seq. No.
                    10093
                    17913 2.R1040
Contig ID
5'-most EST
                    qsv701053216.h1
Method
                    BLASTX
NCBI GI
                    q3218396
BLAST score
                    191
E value
                    2.0e-14
Match length
                    74
```

NCBI Description

```
(AL023860) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   10094
Seq. No.
Contig ID
                   17921 1.R1040
                   jC-gmf102220092c07d1
5'-most EST
                   10095
Seq. No.
                   17923_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy186d03b1
Method
                   BLASTX
NCBI GI
                   g2129698
BLAST score
                   780
                   3.0e-83
E value
Match length
                   184
% identity
                   80
                   protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                   >gi_1054633_emb_CAA63387_ (X92728) protein kinase
                   [Arabidopsis thaliana]
                   10096
Seq. No.
Contig ID
                   17926_1.R1040
5'-most EST
                  LIB3049-015-Q1-E1-E8
                   10097
Seq. No.
Contig ID
                   17928_1.R1040
5'-most EST
                   pxt700941235.hl
Method
                   BLASTX
                   g3150410
NCBI GI
BLAST score
                   363
E value
                   5.0e - 34
Match length
                   236
% identity
                   33
NCBI Description
                   (AC004165) unknown protein [Arabidopsis thaliana]
                   10098
Seq. No.
                   17928 3.R1040
Contig ID
5'-most EST
                  LIB3049-015-Q1-E1-D4
                   10099
Seq. No.
Contig ID
                   17932 1.R1040
5'-most EST
                  LIB3170-022-Q1-K1-G4
                   10100
Seq. No.
Contig ID
                   17933 1.R1040
5'-most EST
                  LIB3049-015-Q1-E1-C12
Seq. No.
                   10101
Contig ID
                   17938_1.R1040
5'-most EST
                   jC-gmst02400050c04a1
                  BLASTX
Method
NCBI GI
                  g3643603
BLAST score
                  1113
E value
                   1.0e-122
Match length
                  295
% identity
                   74
```

(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.

10108

```
10102
Seq. No.
                  17941 1.R1040
Contig ID
                  LIB3049-015-Q1-E1-D1
5'-most EST
Method
                  BLASTX
                  q2213594
NCBI GI
BLAST score
                  307
                  5.0e-28
E value
Match length
                  64
% identity
                  81
NCBI Description
                  (AC000348) T7N9.14 [Arabidopsis thaliana]
                  10103
Seq. No.
                  17943 1.R1040
Contig ID
                  epx701107744.hl
5'-most EST
Method
                  BLASTX
                  q585973
NCBI GI
                  179
BLAST score
                  1.0e-12
E value
                  110
Match length
                  40
% identity
                  NCBI Description
                  fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A
                  fructokinase [Solanum tuberosum]
                  10104
Seq. No.
Contig ID
                  17945 1.R1040
5'-most EST
                  LIB3049-015-Q1-E1-D2
Method
                  BLASTX
NCBI GI
                  q4539351
BLAST score
                  369
E value
                  4.0e-35
Match length
                  154
                  50
% identity
NCBI Description
                  (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  10105
                  17946_1.R1040
Contig ID
                  uC-gmflminsoy022c08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4432863
BLAST score
                  179
                  5.0e-13
E value
Match length
                  60
% identity
                  53
                  (AC006300) putative phosphate/phosphoenolpyruvate
NCBI Description
                  translocator protein [Arabidopsis thaliana]
Seq. No.
                  10106
                  17955 1.R1040
Contig ID
5'-most EST
                  fde700874633.hl
Seq. No.
                  10107
                  17956 1.R1040
Contig ID
5'-most EST
                  gsv70\overline{1}053913.h1
```

Seq. No.

10117

```
17962 1.R1040
Contig ID
                   sat701011715.hl
5'-most EST
                   10109
Seq. No.
                   17962 2.R1040
Contig ID
                  LIB3049-015-Q1-E1-B2
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4210451
BLAST score
                   150
E value
                   2.0e-09
                   57
Match length
% identity
                   56
                   (AB016472) ARR2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10110
                   17966 1.R1040
Contig ID
5'-most EST
                   uC-gmropic112d10b1
Method
                   BLASTX
NCBI GI
                   g2245082
BLAST score
                   156
E value
                   7.0e-10
Match length
                  82
% identity
                   41
NCBI Description
                   (Z97343) SCARECROW homolog [Arabidopsis thaliana]
Seq. No.
                   10111
                   17966 2.R1040
Contig ID
5'-most EST
                  LIB3170-023-Q1-K1-G5
                   10112
Seq. No.
                   17966 3.R1040
Contig ID
5'-most EST
                   smc70\overline{0}747161.h1
                   10113
Seq. No.
                   17969 1.R1040
Contig ID
5'-most EST
                  LIB3049-013-Q1-E1-D7
Method
                  BLASTX
NCBI GI
                   g2252628
BLAST score
                   183
E value
                   1.0e-13
Match length
                   57
% identity
NCBI Description
                   (U95973) hypothetical protein [Arabidopsis thaliana]
                   10114
Seq. No.
                   17970 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy307f04b1
Seq. No.
                   10115
                   17971 1.R1040
Contig ID
5'-most EST
                   kl1701210033.h1
Seq. No.
                   10116
                   17971 2.R1040
Contig ID
5'-most EST
                  LIB3049-014-Q1-E1-G11
```

```
17976 1.R1040
Contig ID
                  leu701149308.hl
5'-most EST
Method
                  BLASTX
                  g2829924
NCBI GI
BLAST score
                  790
                  1.0e-111
E value
                  353
Match length
% identity
                  61
                  (AC002291) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  10118
Seq. No.
                  17980 1.R1040
Contig ID
5'-most EST
                  q5606496
Method
                  BLASTX
NCBI GI
                  q4176522
                  198
BLAST score
                   6.0e-15
E value
Match length
                  227
% identity
                  25
                   (AL035263) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                  17980 2.R1040
Contig ID
5'-most EST
                  trc700563873.hl
Seq. No.
                   17983 1.R1040
Contig ID
5'-most EST
                   iC-qmst02400043d01a1
                   10121
Seq. No.
Contig ID
                   17988 1.R1040
5'-most EST
                  LIB3170-023-Q1-K1-G7
                   10122
Seq. No.
                   17989 1.R1040
Contig ID
5'-most EST
                   LIB3093-016-Q1-K1-D4
Method
                   BLASTN
NCBI GI
                   q4263540
BLAST score
                   35
E value
                   5.0e-10
Match length
                   78
% identity
                   Arabidopsis thaliana chromosome II BAC T6A13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   10123
Seq. No.
Contig ID
                   17990 1.R1040
5'-most EST
                   uC-qmropic006b11b1
Method
                   BLASTX
NCBI GI
                   g2245032
BLAST score
                   286
E value
                   2.0e-25
Match length
                   116
% identity
                   51
                   (Z97342) gibberellin oxidase homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10124
```

Contig ID 17994_1.R1040 5'-most EST uC-gmropic070g10b1

Method BLASTX
NCBI GI g2435511
BLAST score 513
E value 1.0e-51
Match length 190
% identity 55

NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase

alpha subunit [Arabidopsis thaliana]

Seq. No. 10125

Contig ID 17994_2.R1040 5'-most EST leu701146423.h1

Method BLASTX
NCBI GI g2435511
BLAST score 452
E value 1.0e-46
Match length 192
% identity 54

NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase

alpha subunit [Arabidopsis thaliana]

Seq. No. 10126

Contig ID 17997_1.R1040 5'-most EST kl1701215377.h1

Method BLASTX
NCBI GI g1946355
BLAST score 487
E value 8.0e-49
Match length 220
% identity 41

NCBI Description (U93215) maize transposon MuDR mudrA protein isolog

[Arabidopsis thaliana] >gi_2880040 (AC002340) maize

transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 10127

Contig ID 17999 1.R1040

5'-most EST LIB3106-043-Q1-K1-H5

Seq. No. 10128

Contig ID 17999 2.R1040

5'-most EST LIB3049-014-Q1-E1-E8

Seq. No. 10129

Contig ID 18000_1.R1040 5'-most EST epx701107566.h1

Method BLASTX
NCBI GI g2494100
BLAST score 699
E value 1.0e-73
Match length 259
% identity 49

NCBI Description NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (NADP-GDH)

(NAD(P)H-DEPENDENT GLUTAMATE DEHYDROGENASE) >gi_1772845

(U82240) NAD(P)H-dependent glutamate dehydrogenase

[Prevotella ruminicola]

E value

```
Seq. No.
                   10130
Contig ID
                   18002 1.R1040
5'-most EST
                   LIB3049-002-Q1-E1-F4
                   10131
Seq. No.
                   18006 1.R1040
Contig ID
5'-most EST
                   uC-gmropic112c12b1
Method
                   BLASTX
                                 10
NCBI GI
                   g1246403
BLAST score
                   291
E value
                   8.0e-26
Match length
                   151
% identity
NCBI Description
                   (X94698) TINY [Arabidopsis thaliana] >qi 3406035 (AC005405)
                   TINY [Arabidopsis thaliana]
Seq. No.
                   10132
Contig ID
                   18012 1.R1040
5'-most EST
                   LIB3170-022-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   g2842490
BLAST score
                   406
E value
                   8.0e-40
Match length
                   83
% identity
                   88
                   (AL021749) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   10133
Seq. No.
                   18014 1.R1040
Contig ID
5'-most EST
                   kmv700737783.h1
                   BLASTX
Method
NCBI GI
                   q3176669
BLAST score
                   187
E value
                   6.0e-14
Match length
                   102
% identity
                   37
NCBI Description
                   (AC004393) End is cut off. [Arabidopsis thaliana]
Seq. No.
                   10134
Contig ID
                   18016 1.R1040
5'-most EST
                   LIB3107-013-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   q3461820
BLAST score
                   260
E value
                   2.0e-22
Match length
                   64
% identity
NCBI Description
                   (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   10135
Contig ID
                   18016 2.R1040
5'-most EST
                   LIB3109-020-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   g3461820
BLAST score
                   260
```

3.0e-22

```
64
Match length
                   69
% identity
                   (AC004138) unknown protein [Arabidopsis thaliana]
NCBI Description
                   10136
Seq. No.
                   18022 1.R1040
Contig ID
5'-most EST
                   LIB3106-049-Q1-K1-B11
Seq. No.
                   10137
                   18028 1.R1040
Contig ID
5'-most EST
                   LIB3049-013-Q1-E1-H3
                   10138
Seq. No.
                   18031 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy071b04b2
Method
                   BLASTX
                   g2916917
NCBI GI
                   633
BLAST score
E value
                   1.0e-80
Match length
                   373
% identity
                   44
NCBI Description
                   (AL022004) hypothetical protein Rv0858c [Mycobacterium
                   tuberculosis]
                   10139
Seq. No.
                   18036 1.R1040
Contig ID
5'-most EST
                   LIB3049-014-Q1-E1-A11
                   10140
Seq. No.
                   18040 1.R1040
Contig ID
5'-most EST
                   LIB3049-014-Q1-E1-A6
                   10141
Seq. No.
Contig ID
                   18041 1.R1040
5'-most EST
                   crh700854610.h1
Method
                   BLASTX
NCBI GI
                   g3482974
BLAST score
                   1155
E value
                   1.0e-127
Match length
                   323
                   70
% identity
NCBI Description
                   (AL031369) ATP-dependent Clp proteinase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   10142
Contig ID
                   18042_1.R1040
5'-most EST
                  LIB3049-014-Q1-E1-A8
                   BLASTX
Method
NCBI GI
                   g4558659
BLAST score
                   456
E value
                   2.0e-45
Match length
                   118
% identity
                   69
NCBI Description
                   (AC007063) unknown protein [Arabidopsis thaliana]
                   10143
Seq. No.
```

18047 1.R1040

Contig ID

Contig ID

```
5'-most EST
                    LIB3049-013-Q1-E1-F6
Seq. No.
                    10144
                    18050 1.R1040
Contig ID
                    LIB3049-013-Q1-E1-F9
5'-most EST
Method
                    BLASTX
                    g2492772
NCBI GI
BLAST score
                    527
E value
                    5.0e-54
Match length
                    104
                    93
% identity
                    GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
NCBI Description
                    (FALDH) (GSH-FDH) >gi_1498024 (U63931) glutathione-dependent formaldehyde dehydrogenase
                    [Arabidopsis thaliana]
Seq. No.
                    10145
                    18052 1.R1040
Contig ID
5'-most EST
                    LIB3049-013-Q1-E1-G9
Seq. No.
                    10146
Contig ID
                    18062 1.R1040
5'-most EST
                    LIB3106-039-Q1-K1-D3
Method
                    BLASTX
NCBI GI
                    q1001603
BLAST score
                    187
E value
                    6.0e-20
Match length
                    117
% identity
                    50
NCBI Description
                    (D64000) hypothetical protein [Synechocystis sp.]
                    10147
Seq. No.
Contig ID
                    18066 1.R1040
5'-most EST
                    leu70\overline{1}146028.h1
Method
                    BLASTN
NCBI GI
                    q3869069
BLAST score
                    34
E value
                    6.0e-09
Match length
                    167
% identity
NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                    MEB5, complete sequence [Arabidopsis thaliana]
                    10148
Seq. No.
                    18066 2.R1040
Contig ID
5'-most EST
                    jC-gmle01810024b06d1
Seq. No.
                    10149
                    18066 3.R1040
Contig ID
5'-most EST
                    LIB3170-065-01-K1-B5
Seq. No.
                    18066 4.R1040
Contia ID
                    kmv70\overline{0}742292.h1
5'-most EST
Seq. No.
```

18068 1.R1040

```
5'-most EST
                     uC-qmropic025h12b1
  Method
                     BLASTX
  NCBI GI
                     q984756
  BLAST score
                     761
  E value
                     1.0e-80
  Match length
                     396
  % identity
                     44
  NCBI Description
                     (Z54153) chilling-inducible protein [Oryza sativa]
  Seq. No.
                     18068 2.R1040

    Contig ID

                     gsv701054946.hl
  5'-most EST
  Method
                     BLASTX
  NCBI GI
                     q984756
  BLAST score
                     218
  E value
                     1.0e-17
  Match length
                     67
  % identity
  NCBI Description
                     (Z54153) chilling-inducible protein [Oryza sativa]
                     10153
  Seq. No.
                     18068 3.R1040
  Contig ID
  5'-most EST
                     zhf700964316.h1
  Method
                     BLASTX
  NCBI GI
                     q984756
  BLAST score
                     333
  E value
                     5.0e-31
  Match length
                     140
                     49
  % identity
  NCBI Description
                     (Z54153) chilling-inducible protein [Oryza sativa]
  Seq. No.
                     10154
                     18075 1.R1040
  Contig ID
  5'-most EST
                     jC-gmst02400025c10a1
  Method
                     BLASTX
  NCBI GI
                     g3420054
  BLAST score
                     219
  E value
                     1.0e-17
  Match length
                     125
  % identity
  NCBI Description
                     (AC004680) unknown protein [Arabidopsis thaliana]
                     10155
  Seq. No.
                     18076 1.R1040
  Contig ID
  5'-most EST
                     LIB3051-084-Q1-K1-E8
  Seq. No.
                     10156
                     18076 2.R1040
  Contig ID
  5'-most EST.
                     LIB3107-080-Q1-K1-D11
  Seq. No.
                     10157
                     18081 1.R1040
  Contig ID
  5'-most EST
                     LIB3049-013-Q1-E1-C2
  Seq. No.
                     10158
  Contig ID
                     18084 1.R1040
  5'-most EST
                     LIB3052-014-Q1-N1-G9
```

Method

BLASTX

```
BLASTX
Method
                  q3123908
NCBI GI
                   657
BLAST score
E value
                  1.0e-68
                  171
Match length
                   67
% identity
                   (AF038392) pre-mRNA splicing factor [Homo sapiens]
NCBI Description
                   10159
Seq. No.
Contig ID
                   18086 1.R1040
5'-most EST
                   gsv701044694.hl
                   10160
Seq. No.
                   18090 1.R1040
Contig ID
5'-most EST
                   LIB3106-026-Q1-K1-H5
                   BLASTX
Method
                   g2213594
NCBI GI
BLAST score
                   581
                   5.0e-60
E value
Match length
                   161
% identity
                   65
                   (AC000348) T7N9.14 [Arabidopsis thaliana]
NCBI Description
                   10161
Seq. No.
                   18092 1.R1040
Contig ID
5'-most EST
                   LIB3049-013-Q1-E1-D2
                   10162
Seq. No.
                   18098 1.R1040
Contig ID
                   LIB3049-013-Q1-E1-C12
5'-most EST
                   10163
Seq. No.
                   18100 1.R1040
Contig ID
                   sat701003273.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3785998
BLAST score
                   426
                   8.0e-42
E value
Match length
                   121
                   61
% identity
                   (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
                   10164
Seq. No.
                   18100 2.R1040
Contig ID
                   LIB3170-024-Q1-K1-F2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3785998
BLAST score
                   335
E value
                   3.0e-31
                   94
Match length
% identity
                   64
                   (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10165
                   18103 1.R1040
Contig ID
5'-most EST
                   trc700562330.h1
```

```
g3273202
NCBI GI
BLAST score
                   414
                   2.0e-40
E value
Match length
                   106
                   76
% identity
                   (AB010918) responce reactor4 [Arabidopsis thaliana]
NCBI Description
                   10166
Seq. No.
Contig ID
                   18103 2.R1040
5'-most EST
                   LIB30\overline{5}1-068-Q1-K1-E2
Method
                   BLASTX
NCBI GI
                   q3273202
BLAST score
                   179
                   1.0e-12
E value
Match length
                   162
% identity
                   31
NCBI Description
                   (AB010918) responce reactor4 [Arabidopsis thaliana]
                   10167
Seq. No.
                   18106_1.R1040
Contig ID
                   LIB3170-023-Q1-K1-F8
5'-most EST
                   BLASTN
Method
                   g3510347
NCBI GI
BLAST score
                   45
E value
                   4.0e-16
Match length
                   182
% identity
                   86
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MSJ11, complete sequence [Arabidopsis thaliana]
                   10168
Seq. No.
                   18109 1.R1040
Contig ID
                   uaw70\overline{0}663343.h1
5'-most EST
                   10169
Seq. No.
                   18112_1.R1040
Contig ID
5'-most EST
                   LIB3049-013-Q1-E1-C1
                   10170
Seq. No.
                   18114 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810005b01a1
Method
                   BLASTX
                   g4006826
NCBI GI
BLAST score
                   448
E value
                   2.0e-44
Match length
                   148
% identity
                   59
NCBI Description
                   (AC005970) unknown protein [Arabidopsis thaliana]
Seq. No.
                   10171
                   18116_1.R1040
Contig ID
                   leu70\overline{1}151307.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2645699
BLAST score
                   182
                   4.0e-13
E value
```

92.

Match length

NCBI GI

```
% identity
                   46
NCBI Description
                   (AF031933) glycine-rich RNA-binding protein [Euphorbia
                   esula]
                   10172
Seq. No.
                   18117 1.R1040
Contig ID
5'-most EST
                   leu70\overline{1}151765.h1
                   10173
Seq. No.
                   18122 1.R1040
Contig ID
                   epx70\overline{1}105809.h1
5'-most EST
Seq. No.
                   10174
                   18129 1.R1040
Contig ID
5'-most EST
                   LIB3049-013-Q1-E1-A12
                   10175
Seq. No.
                   18129 2.R1040
Contig ID
5'-most EST
                   pmv700891366.h1
Seq. No.
                   10176
                   18130_1.R1040
Contig ID
5'-most EST
                   k11701205527.h1
Seq. No.
                   10177
Contig ID
                   18136 1.R1040
5'-most EST
                   LIB3170-022-Q1-K1-E10
                   BLASTX
Method
NCBI GI
                   g4415912
BLAST score
                   169
E value
                   6.0e-12
Match length
                   65
                   62
% identity
NCBI Description
                   (AC006282) putative protease [Arabidopsis thaliana]
                   10178
Seq. No.
Contig ID
                   18138 1.R1040
5'-most EST
                   pxt700944466.hl
                   10179
Seq. No.
Contig ID
                   18139 1.R1040
5'-most EST
                   LIB3170-070-Q1-K2-B6
Method
                   BLASTX
NCBI GI
                   g3763916
BLAST score
                   293
E value
                   3.0e-26
Match length
                   103
% identity
                   51
NCBI Description
                   (AC004450) unknown protein [Arabidopsis thaliana]
                   >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   10180
                   18139 2.R1040
Contig ID
5'-most EST
                   hrw701061944.h1
Method
                   BLASTX
```

q3763916

```
BLAST score
                   158
                   1.0e-10
E value
Match length
                   79
% identity
                   39
                   (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   10181
                   18142 1.R1040
Contig ID
5'-most EST
                   pmv700890296.h1
                   10182
Seq. No.
                   18146 1.R1040
Contig ID
5'-most EST
                   LIB3049-012-Q1-E1-G7
                   10183
Seq. No.
                   18148 1.R1040
Contig ID
                   LIB3170-046-Q1-J1-D1
5'-most EST
Method
                   BLASTX
                   q3660469
NCBI GI
                   1827
BLAST score
E value
                   0.0e + 00
Match length
                   410
                   87
% identity
                   (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                   thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)
                   succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
                   10184
Seq. No.
                   18148 2.R1040
Contig ID
                   sat70\overline{1}012817.h1
5'-most EST
Method
                   BLASTX
                   q3660469
NCBI GI
BLAST score
                   423
E value
                   1.0e-41
Match length
                   97
% identity
                   82
                   (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                   thaliana] >gi 4512693 gb AAD21746.1_ (AC006569)
                   succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
                   10185
Seq. No.
Contig ID
                   18149 1.R1040
                   LIB3049-012-Q1-E1-D5
5'-most EST
                   10186
Seq. No.
Contig ID
                   18153 1.R1040
5'-most EST
                   gsv701046028.hl
                   10187
Seq. No.
                   18156 1.R1040
Contig ID
5'-most EST
                   ncj70\overline{0}975168.h1
                   BLASTX
Method
                   q3096931
NCBI GI
BLAST score
                   362
```

3.0e-34

E value

Method

BLASTX

```
Match length
                   111
% identity
                   59
NCBI Description
                   (AL023094) putative ribosomal protein S16 [Arabidopsis
                   thaliana]
                   10188
Seq. No.
                   18157 1.R1040
Contig ID
5'-most EST
                   jex70\overline{0}907657.h1
Method
                   BLASTX.
NCBI GI
                   g4455199
BLAST score
                   1108
E value
                   1.0e-121
Match length
                   283
% identity
                   78
NCBI Description
                   (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   10189
                   18157 2.R1040
Contig ID
5'-most EST
                   eep700868548.hl
Method
                   BLASTX
NCBI GI
                   q4522009
BLAST score
                   389
E value
                   9.0e-38
Match length
                   127
% identity
                   54
NCBI Description
                   (AC007069) unknown protein [Arabidopsis thaliana]
Seq. No.
                   10190
Contig ID
                   18158 1.R1040
5'-most EST
                   zzp700835245.h1
Method
                   BLASTX
NCBI GI
                   g3204101
BLAST score
                   251
E value
                   3.0e-21
Match length
                   102
% identity
                   58
NCBI Description
                   (AJ006760) hypothetical protein [Cicer arietinum]
Seq. No.
                   10191
                   18158 2.R1040
Contig ID
5'-most EST
                   gsv701045938.hl
Seq. No.
                   10192
Contig ID
                   18166 1.R1040
5'-most EST
                   LIB3109-016-Q1-K3-B5
Method
                   BLASTX
NCBI GI
                   g4567215
BLAST score
                   274
E value
                   3.0e-24
Match length
                   113
% identity
NCBI Description
                   (AC007113) putative presentlin [Arabidopsis thaliana]
                   10193
Seq. No.
                   18169 1.R1040
Contig ID
5'-most EST
                   g5753705
```

NCBI GI

g128405

```
NCBI GI
                   q2245101
BLAST score
                   517
E value
                   2.0e-52
Match length
                   144
                   71
% identity
NCBI Description
                   (Z97343) hypothetical protein [Arabidopsis thaliana]
                   10194
Seq. No.
Contig ID
                   18169 3.R1040
5'-most EST
                   LIB3170-022-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   q2245101
BLAST score
                   332
                   6.0e-31
E value
Match length
                   72
% identity
                   86
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                   10195
Seq. No.
                   18169 4.R1040
Contig ID
                   gsv701047470.hl
5'-most EST
                   10196
Seq. No.
                   18169_5.R1040
Contig ID
5'-most EST
                   eep700865796.h1
Method
                   BLASTX
                   g2245101
NCBI GI
                   231
BLAST score
                   3.0e-19
E value
                   49
Match length
% identity
                   90
NCBI Description
                   (Z97343) hypothetical protein [Arabidopsis thaliana]
                   10197
Seq. No.
                   18170_1.R1040
Contig ID
5'-most EST
                   jex70\overline{0}906004.h1
Method
                   BLASTX
                   g1808656 <sup>% }</sup>
NCBI GI
BLAST score
                   1381
                   1.0e-153
E value
                   311
Match length
% identity
                   83
                   (Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]
NCBI Description
                   10198
Seq. No.
                   18171 1.R1040
Contig ID
5'-most EST
                   LIB3049-012-Q1-E1-C10
Seq. No.
                   10199
                   18179 1.R1040
Contig ID
5'-most EST
                   LIB3049-012-Q1-E1-B5
Seq. No.
                   10200
                   18180 1.R1040
Contig ID
                   LIB3139-094-P1-N1-H7
5'-most EST
Method
                   BLASTX
```

```
457
BLAST score
                   3.0e-45
E value
Match length
                   166
% identity
                   57
                   NODULIN 21 (N-21) >gi_99942_pir__S08632 nodulin-21 -
NCBI Description
                   soybean >gi_18694_emb_CAA34506_ (X16488) nodulin-21 (AA
                   1-201) [Glycine max]
Seq. No.
                   10201
                   18183 1.R1040
Contig ID
5'-most EST
                   LIB3049-012-Q1-E1-A10
Method
                   BLASTX
                   q3096939
NCBI GI
BLAST score
                   333
E value
                   6.0e-31
                   87
Match length
                   72
% identity
                   (AL023094) putative protein [Arabidopsis thaliana]
NCBI Description
                   10202
Seq. No.
                   18183 2.R1040
Contig ID
5'-most EST
                   leu701150481.h1
Method
                   BLASTN
                   g3641835
NCBI GI
                   39
BLAST score
E value
                   2.0e-12
Match length
                   153
% identity
                   85
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20
                   (ESSAII project)
Seq. No.
                   10203
Contig ID
                   18188 1.R1040
                   LIB30\overline{4}9-012-Q1-E1-A5
5'-most EST
                   10204
Seq. No.
Contig ID
                   18188 2.R1040
                   hrw701060104.hl
5'-most EST
                   10205
Seq. No.
Contig ID
                   18192 1.R1040
                   LIB3109-038-Q1-K1-A12
5'-most EST
                   10206
Seq. No.
Contig ID
                   18194 1.R1040
                   LIB30\overline{5}6-002-Q1-B1-E5
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3327957
BLAST score
                   209
                   3.0e-16
E value
Match length
                   91
% identity
NCBI Description
                   (AF060490) TLS-associated protein TASR-2 [Mus musculus]
                   >gi 3327976 (AF067730) TLS-associated protein TASR-2 [Homo
                   sapiens]
```

10207

Seq. No.

Contig ID

```
Contig ID
                   18207 1.R1040
5'-most EST
                   uC-gmrominsoy090a03b1
Method
                   BLASTX
NCBI GI
                   g2281637
BLAST score
                   304
                   4.0e-27
E value
                   65
Match length
% identity
                   88
NCBI Description
                   (AF003099) AP2 domain containing protein RAP2.6
                   [Arabidopsis thaliana]
                   10208
Seq. No.
                   18207 2.R1040
Contig ID
5'-most EST
                   LIB3049-011-Q1-E1-H10
Seq. No.
                   18207 3.R1040
Contig ID
5'-most EST
                   uC-gmropic0001c10b1
Seq. No.
                   10210
                   18207 4.R1040
Contig ID
5'-most EST
                   jsh70\overline{1}067143.h1
Seq. No.
                   10211
Contig ID
                   18207 6.R1040
5'-most EST
                   LIB3051-050-01-K1-F3
Seq. No.
                   10212
                   18207 9.R1040
Contig ID
5'-most EST
                   LIB3139-101-P1-N1-G9
Seq. No.
                   10213
                   18216 1.R1040
Contig ID
                   hrw701062463.h1
5'-most EST
Seq. No.
                   10214
                   18216 2.R1040
Contig ID
5'-most EST
                   uaw700664293.h1
Seq. No.
                   10215
Contig ID
                   18217 1.R1040
5'-most EST
                   LIB3049-011-Q1-E1-E4
Method
                   BLASTX
NCBI GI
                   q2827715
BLAST score
                   539
E value
                   2.0e-55
Match length
                   128
% identity
NCBI Description
                   (AL021684) receptor protein kinase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   10216
                   18219 1.R1040
Contig ID
5'-most EST
                   LIB3170-023-Q1-K1-E4
                   10217
Seq. No.
```

18220 1.R1040

5'-most EST

```
5'-most EST
                   LIB3170-023-01-K1-E5
                   10218
Seq. No.
                   18221 1.R1040
Contig ID
5'-most EST
                   LIB3049-011-Q1-E1-F11
                   10219
Seq. No.
Contig ID
                   18223 1.R1040
5'-most EST
                   LIB3049-011-Q1-E1-F3
Seq. No.
                   10220
                   18231 1.R1040
Contig ID
                   jC-gmst02400060b11a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4510406
BLAST score
                   550
E value
                   3.0e-56
Match length
                   150
% identity
                   68
NCBI Description
                   (AC006587) putative protein kinase [Arabidopsis thaliana]
                   10221
Seq. No.
                   18231 2.R1040
Contig ID
5'-most EST
                   pmv700892967.hl
Method
                   BLASTX
NCBI GI
                   a3367520
BLAST score
                   440
E value
                   2.0e-47
Match length
                   174
                   60
% identity
NCBI Description
                   (AC004392) Similar to protein kinase APK1A,
                   tyrosine-serine-threonine kinase gb_D12522 from A.
                   thaliana. [Arabidopsis thaliana]
Seq. No.
                   10222
Contig ID
                   18231 3.R1040
5'-most EST
                   epx701104778.h1
Seq. No.
                   10223
Contig ID
                   18233 1.R1040
5'-most EST
                   LIB3049-011-01-E1-E3
Method
                   BLASTX
NCBI GI
                   q2462753
BLAST score
                   876
E value
                   1.0e-94
Match length
                   204
% identity
NCBI Description
                   (AC002292) putative polygalacturonase [Arabidopsis
                   thaliana]
                   10224
Seq. No.
Contig ID
                   18236 1.R1040
5'-most EST
                   LIB3049-011-Q1-E1-C6
                   10225
Seq. No.
                   18238 1.R1040
Contig ID
```

uC-gmflminsoy055f12b1

% identity

```
.Method
                    BLASTX
NCBI GI
                    q2288887
BLAST score
                    642
E value
                    5.0e-67
Match length
                    167
                    73
% identity
                    (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
NCBI Description
                    thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]
                    >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase
                    [Arabidopsis thaliana]
                    10226
Seq. No.
Contig ID
                    18241 1.R1040
5'-most EST
                    LIB3049-011-Q1-E1-D11
Method
                    BLASTX
NCBI GI
                    g1737492
BLAST score
                    1108
E value
                    1.0e-121
Match length
                    407
                    29
% identity
NCBI Description
                    (U81318) poly(A)-binding protein [Triticum aestivum]
                    10227
Seq. No.
                    18245 1.R1040
Contig ID
5'-most EST
                    LIB3049-011-Q1-E1-D6
                    BLASTX
Method
                    q3913732
NCBI GI
BLAST score
                    271
                    1.0e-23
E value
Match length
                    86
                    62
% identity
                    HYDROXYACYLGLUTATHIONE HYDROLASE MITOCHONDRIAL ISOZYME
NCBI Description
                    PRECURSOR (GLYOXALASE II) (GLX II) >gi_2570340 (U90928)
                    glyoxalase II mitochondrial isozyme [Arabidopsis thaliana]
Seq. No.
                    10228
                    18245 2.R1040
Contig ID
5'-most EST
                    k1170\overline{1}203505.h2
                    10229
Seq. No.
                    18246 1.R1040
Contig ID
5'-most EST
                    dpv70\overline{1}099471.h1
                    10230
Seq. No.
                    18246 3.R1040
Contig ID
5'-most EST
                    zhf70\overline{0}962535.h1
Seq. No.
                    10231
                    18254 1.R1040
Contig ID
5'-most EST
                    LIB3049-011-Q1-E1-A8
Method
                    BLASTX
NCBI GI
                    q3600039
BLAST score
                    232
E value
                    2.0e-19
Match length
                    54
```

BLAST score

```
NCBI Description (AF080119) similar to Schizosaccharomyces pombe isp4
                   protein (GB:D14061) [Arabidopsis thaliana]
Seq. No.
                   18256 1.R1040
Contig ID
                   xpa70\overline{0}792801.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2809233
BLAST score
                   239
E value
                   3.0e-20
                   75
Match length
% identity
NCBI Description
                   (AC002560) F21B7.2 [Arabidopsis thaliana]
Seq. No.
                   10233
Contig ID
                   18260 1.R1040
5'-most EST
                   LIB3170-081-Q1-K1-D3
Method
                   BLASTN
NCBI GI
                   q170007
BLAST score
                   112
E value
                   9.0e-56
Match length
                   196
% identity
                   90
NCBI Description
                   Soybean 18 kD late embryogenesis abundant (Lea) protein
                   mRNA, complete cds
                   10234
Seq. No.
                   18262 1.R1040
Contig ID
                   bth700845315.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4512685
BLAST score
                   279
                   1.0e-24
E value
Match length
                   150
% identity
                   42
NCBI Description
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
                   >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087)
                   hypothetical protein [Arabidopsis thaliana]
                   10235
Seq. No.
                   18264 1.R1040
Contig ID
5'-most EST
                   hrw701059985.h1
Method
                   BLASTX
NCBI GI
                   q3880215
BLAST score
                   156
E value
                   8.0e-10
Match length
                   142
% identity
NCBI Description
                   (Z82053) cDNA EST yk302b12.3 comes from this gene
                   [Caenorhabditis elegans]
                   10236
Seq. No.
Contig ID
                   18265 1.R1040
5'-most EST
                   uxk70\overline{0}673114.h1
Method
                   BLASTX
NCBI GI
                   g4510345
```

Match length

```
E value
                   6.0e-46
Match length
                   177
% identity
                   51
NCBI Description
                   (AC006921) unknown protein [Arabidopsis thaliana]
                   10237
Seq. No.
                   18265 2.R1040
Contig ID
5'-most EST
                   LIB3049-011-Q1-E1-C2
Method
                   BLASTX
NCBI GI
                   g4510345
BLAST score
                   465
E value
                   4.0e-46
Match length
                   176
% identity
                   51
NCBI Description
                   (AC006921) unknown protein [Arabidopsis thaliana]
                   10238
Seq. No.
                   18265 3.R1040
Contig ID
5'-most EST
                   rca70\overline{1}002474.h1
Method
                   BLASTX
NCBI GI
                   g4510345
                   456
BLAST score
E value
                   5.0e-45
Match length
                   172
                   52
% identity
NCBI Description
                   (AC006921) unknown protein [Arabidopsis thaliana]
                   10239
Seq. No.
                   18265 4.R1040
Contig ID
5'-most EST
                   epx701106091.h1
Method
                   BLASTX
NCBI GI
                   g4510345
BLAST score
                   189
E value
                   2.0e-15
Match length
                   55
% identity
                   72
NCBI Description
                   (AC006921) unknown protein [Arabidopsis thaliana]
                   10240
Seq. No.
                   18265 5.R1040
Contiq ID
5'-most EST
                   uC-gmropic099f11b1
Method
                   BLASTX
                   g4510345
NCBI GI
BLAST score
                   229
E value
                   5.0e-19
Match length
                   54
% identity
                   74
NCBI Description
                   (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                   10241
                   18266 1.R1040
Contig ID
5'-most EST
                   uC-qmropic018a05b1
Method
                   BLASTX
NCBI GI
                   g2642154
BLAST score
                   526
E value
                   4.0e-55
```

```
% identity
                   (AC003000) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3790595 (AF079186) RING-H2 finger protein RHC2a
                   [Arabidopsis thaliana]
                  10242
Seq. No.
                  18267 2.R1040
Contig ID
5'-most EST
                  zzp700832279.h1
Seq. No.
                  10243
                  18267 3.R1040
Contig ID
5'-most EST
                  zpv700757039.h1
Seq. No.
                  10244
Contig ID
                  18271 1.R1040
                  gsv701051833.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2952433
BLAST score
                  625
E value
                  2.0e-65
Match length
                  146
% identity
                  75
NCBI Description
                   (AF051135) putative ubiquitin activating enzyme E1
                   [Arabidopsis thaliana]
Seq. No.
                  10245
Contig ID
                  18272 1.R1040
5'-most EST
                  LIB3049-010-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                  q2980782
BLAST score
                  228
E value
                  1.0e-18
Match length
                  141
% identity
NCBI Description
                  (AL022198) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  10246
Contig ID
                  18290 1.R1040
5'-most EST
                  wvk700680196.h2
Method
                  BLASTX
NCBI GI
                  a3979937
BLAST score
                  154
E value
                  4.0e-10
Match length
                  67
% identity
                  43
NCBI Description
                   (AL034393) predicted using Genefinder; cDNA EST EMBL:D65716
                  comes from this gene; cDNA EST yk263b1.3 comes from this
                  gene; cDNA EST yk263b1.5 comes from this gene; cDNA EST
                  EMBL: D69251 comes from this gene [Caenorhabditis elegans]
                  10247
Seq. No.
Contig ID
                  18291 1.R1040
5'-most EST
                  LIB3170-021-01-K1-D12
                  10248
Seq. No.
```

18293 1.R1040

LIB3170-022-Q1-K1-D12

Contig ID 5'-most EST

Contig ID

```
10249
Seq. No.
Contig ID
                   18294 1.R1040
5'-most EST
                   g5342465
Method
                   BLASTX
                   g4416307
NCBI GI
BLAST score
                   193
E value
                   3.0e-14
Match length
                   203
% identity
                   27
NCBI Description
                   (AF105716) hypothetical protein [Zea mays]
                   10250
Seq. No.
Contig ID
                   18301 1.R1040
5'-most EST
                   LIB3049-010-Q1-E1-E1
Seq. No.
                   10251
                   18303 1.R1040
Contig ID
5'-most EST
                   LIB3139-040-P1-N1-F3
Seq. No.
                   10252
                   18306 1.R1040
Contig ID
5'-most EST
                   LIB3049-010-Q1-E1-E4
                   10253
Seq. No.
Contig ID
                   18311 1.R1040
5'-most EST
                   LIB3051-037-Q1-K1-B4
                   BLASTX
Method
NCBI GI
                   q3402711
BLAST score
                   165
E value
                   3.0e-11
Match length
                   46
                   76
% identity
NCBI Description
                   (AC004261) putative RNA-binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   10254
                   18312 1.R1040
Contig ID
5'-most EST
                  LIB3049-010-Q1-E1-D6
                   10255
Seq. No.
Contig ID
                   18314 1.R1040
5'-most EST
                  LIB3138-015-Q1-N2-H4
                  BLASTX
Method
NCBI GI
                   g2342724
BLAST score
                   1185
E value
                   1.0e-130
Match length
                   331
% identity
                   71
NCBI Description
                  (AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.
                   10256
                   18314 2.R1040
Contig ID
5'-most EST
                   jC-qmst02400069b04a1
Seq. No.
```

18319 1.R1040

Seq. No.

```
5'-most EST
                    uC-qmropic090e05b1
                    10258
Seq. No.
                    18319 2.R1040
Contig ID
 5'-most EST
                    LIB3049-010-Q1-E1-C7
                    10259
Seq. No.
                    18325 1.R1040
Contig ID
 5'-most EST
                    LIB3093-023-Q1-K1-D10
                    BLASTX
Method
NCBI GI
                    q3212866
BLAST score
                    430
E value
                    8.0e-42
Match length
                    267
 % identity
                    37
NCBI Description
                    (AC004005) unknown protein [Arabidopsis thaliana]
                    10260
Seq. No.
                    18325_2.R1040
Contig ID
 5'-most EST
                    k1170\overline{1}214357.h1
Method
                    BLASTX
                    g3212866
NCBI GI
BLAST score
                    231
E value
                    4.0e-28
                    205
Match length
'% identity
                    38
                    (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                    10261
Seq. No.
                    18333 1.R1040
Contig ID
 5'-most EST
                    leu70\overline{1}146986.h1
Method
                    BLASTX
                    g3738331
NCBI GI
BLAST score
                    322
                    9.0e-30
E value
Match length
                    72
 % identity
                    74
                    (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                    10262
Seq. No.
                    18340 1.R1040
Contig ID
 5'-most EST
                    kl1701208052.h1
Method
                    BLASTX
NCBI GI
                    q1176658
BLAST score
                    227
E value
                    3.0e-18
Match length
                    80
% identity
                    53
NCBI Description
                    HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
                    >gi 726363 (U23168) No definition line found
                    [Caenorhabditis elegans]
Seq. No.
                    10263
Contig ID
                    18340 2.R1040
5'-most EST
                    LIB3049-010-Q1-E1-B4
```

Match length

```
Contig ID
                   18340 3.R1040
5'-most EST
                   zsg701123960.hl
Seq. No.
                   10265
                   18346 1.R1040
Contig ID
                   pmv70\overline{0}890645.h1
5'-most EST
                   10266
Seq. No.
Contig ID
                   18349 1.R1040
5'-most EST
                   LIB3170-022-Q1-K1-D4
                   10267
Seq. No.
Contig ID
                   18350 1.R1040
5'-most EST
                   LIB3049-009-Q1-E1-G7
Method
                   BLASTX
NCBI GI
                   a1800223
BLAST score
                   310
E value
                   2.0e-28
Match length
                   126
% identity
                   55
                   (U65018) mannosyltransferase [Dictyostelium discoideum]
NCBI Description
Seq. No.
                   10268
Contig ID
                   18353 1.R1040
5'-most EST
                   LIB3049-009-Q1-E1-H11
                   10269
Seq. No.
                   18355 1.R1040
Contig ID
5'-most EST
                   uxk70\overline{0}668561.h1
Method
                   BLASTX
                   g1742187
NCBI GI
BLAST score
                   182
                   4.0e-13
E value
Match length
                   205
                   27
% identity
NCBI Description
                   (D90771) ORF_ID:o260#14; similar to [SwissProt Accession
                   Number P11666] [Escherichia coli] >gi_1742198_dbj_BAA14933_
                   (D90772) ORF ID:o260#14; similar to [SwissProt Accession
                   Number P1166\overline{6}] [Escherichia coli] >gi_1787591 (AE000231)
                   orf, hypothetical protein [Escherichia coli]
Seq. No.
                   10270
                   18356 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{4}9-009-Q1-E1-H3
Seq. No.
                   10271
Contig ID
                   18360 1.R1040
5'-most EST
                   fC-gmf1700898745a1
Seq. No.
                   10272
                   18363 1.R1040
Contig ID
5'-most EST
                   ssr70\overline{0}557079.h1
Method
                   BLASTX
NCBI GI
                   q4415912
BLAST score
                   180
E value
                   4.0e-13
```

% identity

```
% identity
                   50
                   (AC006282) putative protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10273
                   18364 1.R1040
Contig ID
                   LIB30\overline{9}2-002-Q1-K1-H9
5'-most EST
Method
                   BLASTX
                   q3201680
NCBI GI
BLAST score
                   640
                   6.0e-67
E value
Match length
                   163
% identity
                   72
NCBI Description
                   (AF060941) extra-large G-protein [Arabidopsis thaliana]
                   10274
Seq. No.
Contig ID
                   18364_2.R1040
5'-most EST
                   jC-gmro02910061g03a1
Method
                   BLASTX
NCBI GI
                   g3242709
BLAST score
                   602
E value
                   2.0e-62
Match length
                   197
                   63
% identity
NCBI Description
                   (AC003040) putative guanine nucleotide-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   10275
                   18369 1.R1040
Contig ID
                   awf70\overline{0}838918.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2244964
BLAST score
                   376
E value
                   6.0e-36
Match length
                   204
% identity
                   45
NCBI Description
                   (Z97340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   10276
Contig ID
                   18370 1.R1040
5'-most EST
                   gsv701046362.hl
Method
                   BLASTX
NCBI GI
                   g2982247
BLAST score
                   258
E value
                   7.0e-22
                   109
Match length
% identity
                   43
NCBI Description
                   (AF051206) probable thioredoxin H [Picea mariana]
Seq. No.
                   10277
                   18377 1.R1040
Contig ID
5'-most EST
                   LIB3049-009-Q1-E1-G1
Method
                   BLASTX
NCBI GI
                   q4115377
BLAST score
                   343
E value
                   6.0e-33
Match length
                   118
```

```
(AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   10278
Seq. No.
                   18378 1.R1040
Contig ID
5'-most EST
                   LIB3049-009-Q1-E1-G10
Seq. No.
                   10279
                   18380 1.R1040
Contig ID
                   LIB3049-009-Q1-E1-G12
5'-most EST
                   10280
Seq. No.
Contig ID
                   18387 1.R1040
5'-most EST
                   LIB3049-009-Q1-E1-D4
Seq. No.
                   10281
Contig ID
                   18389 1.R1040
5'-most EST
                   vzy700754587.hl
Method
                   BLASTX
NCBI GI
                   g3559811
BLAST score
                   1491
E value
                   1.0e-166
Match length
                   401
% identity
                   69
NCBI Description
                   (AJ010735) grl-protein [Arabidopsis thaliana]
Seq. No.
                   10282
                   18390 1.R1040
Contig ID
5'-most EST
                   LIB3065-006-Q1-N1-H12
Method
                   BLASTX
NCBI GI
                   q416922
BLAST score
                   348
                   7.0e-33
E value
Match length
                   96
% identity
NCBI Description
                   DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE)
                   (DUTP PYROPHOSPHATASE) (P18) >gi_282947_pir__JQ1599 dUTP
                   pyrophosphatase (EC 3.6.1.23) - tomato
                   >gi_251897_bbs 109276 (S40549) deoxyuridine triphosphatase,
                   dUTPase, P\overline{1}8 {\overline{E}C 3.6.1.23} [tomatoes, Tint Tim cultivar
                   LA154, Peptide, 169 aa] [Lycopersicon esculentum]
Seq. No.
                   10283
Contig ID
                   18391 1.R1040
5'-most EST
                   LIB3049-009-Q1-E1-D8
Method
                   BLASTX
NCBI GI
                   q3142297
BLAST score
                   363
E value
                   1.0e-34
Match length
                   96
% identity
NCBI Description
                   (AC002411) Contains similarity to serine/threonine protein
                   phosphatase gb X83099 from S. cerevisiae. [Arabidopsis
                   thaliana]
Seq. No.
                   10284
Contig ID
                   18395 1.R1040
5'-most EST
                   LIB3170-022-Q1-K1-D1
```

1801

Contig ID

```
Seq. No.
                   10285
                   18396 1.R1040
Contig ID
                   LIB3049-009-Q1-E1-E2
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1806143
BLAST score
                   142
E value
                   6.0e-74
Match length
                   274
                   88
% identity
NCBI Description M.sativa mRNA for cdc2 kinase homologue, cdc2MsE
                   10286
Seq. No.
                   18414 1.R1040
Contig ID
                   zhf700951883.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1944575
BLAST score
                   537
E value
                    4.0e-55
Match length
                   133
% identity
                   76
NCBI Description
                   (Z94058) pectinesterase [Lycopersicon esculentum]
Seq. No.
Contig ID
                   18415 1.R1040
5'-most EST
                   LIB3170-023-Q1-K1-D4
Seq. No.
                   10288
Contig ID
                   18420 1.R1040
5'-most EST
                   bth700845450.h1
Seq. No.
                   10289
                   18422 1.R1040
Contig ID
5'-most EST
                   LIB3170-023-Q1-K1-D10
Seq. No.
                   10290
Contig ID
                   18425 1.R1040
5'-most EST
                   pmv700889715.h1
Method
                   BLASTX
NCBI GI
                   q1352881
BLAST score
                   154
E value
                   5.0e-10
Match length
                   95
% identity
NCBI Description
                   HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC
                   REGION >gi_1078266_pir__S57063 probable membrane protein
                   YJR044c - yeast (Saccharomyces cerevisiae)
                   >gi_1015699_emb_CAA89572_ (Z49544) ORF YJR044c
[Saccharomyces cerevisiae] >gi_1197072 (L36344) ORF;
                   putative [Saccharomyces cerevisiae]
Seq. No.
                   10291
                   18425 2.R1040
Contig ID
5'-most EST
                   ncj70\overline{0}980410.h1
Seq. No.
                   10292
```

18426 1.R1040

NCBI GI

```
5'-most EST
                  uC-qmflminsoy005c06b1
Seq. No.
                  10293
                  18426 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy099e12b1
                  10294
Seq. No.
                  18427 1.R1040
Contig ID
                   fua701040106.hl
5'-most EST
Method
                  BLASTX
                  g3763940
NCBI GI
BLAST score
                  535
                   1.0e-54
E value
Match length
                  157
                   71
% identity
                   (AC004450) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Contig ID
                   18429 1.R1040
                  LIB3170-024-Q1-K1-D7
5'-most EST
                   10296
Seq. No.
                   18436 1.R1040
Contig ID
5'-most EST
                  LIB3109-006-Q1-K1-H9
Seq. No.
Contig ID
                   18438 1.R1040
5'-most EST
                   LIB3049-008-Q1-E1-G2
                   10298
Seq. No.
Contig ID
                   18439 1.R1040
5'-most EST
                   LIB3049-008-Q1-E1-G3
Method
                   BLASTX
NCBI GI
                   q2760835
BLAST score
                   298
E value
                   7.0e-27
                   134
Match length
% identity
                   46
                   (AC003105) unknown protein [Arabidopsis thaliana]
NCBI Description
                   10299
Seq. No.
Contig ID
                   18441 1.R1040
5'-most EST
                   wrg700790675.h2
Method
                   BLASTX
NCBI GI
                   q1764100
BLAST score
                   290
E value
                   1.0e-30
Match length
                   94
% identity
                   (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis
NCBI Description
                   thaliana]
                   10300
Seq. No.
                   18442 1.R1040
Contig ID
5'-most EST
                   LIB3049-008-Q1-E1-G6
Method
                   BLASTX
```

g3152605

```
BLAST score
                   295
E value
                   2.0e-26
Match length
                   154
% identity
                   47
                   (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   10301
Seq. No.
                   18444 1.R1040
Contig ID
5'-most EST
                   LIB3049-008-Q1-E1-G8
Method
                   BLASTX
                   g3355465
NCBI GI
BLAST score
                   305
E value
                   7.0e-28
Match length
                   125
% identity
NCBI Description
                   (AC004218) putative Ser/Thr protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   10302
Contig ID
                   18445 1.R1040
5'-most EST
                   asn70\overline{1}138856.h1
Method
                   BLASTX
NCBI GI
                   q1653775
BLAST score
                   220
                                  7.6
E value
                   1.0e-17
Match length
                   117
% identity
                   46
                   (D90916) thiol:disulfide interchange protein DsbD
NCBI Description
                   [Synechocystis sp.]
Seq. No.
                   10303
                   18446 1.R1040
Contig ID
                   LIB3138-080-P1-N1-C1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2245378
BLAST score
                   658
E value
                   1.0e-77
Match length
                   198
% identity
                   71
                   (U83245) auxin response factor 1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10304
                   18446 2.R1040
Contig.ID
5'-most EST
                   LIB3049-006-Q1-E1-B8
                   10305
Seq. No.
Contig ID
                   18447 1.R1040
5'-most EST
                   LIB3170-036-Q1-K2-B8
Method
                   BLASTX
NCBI GI
                   g3164222
BLAST score
                   252
E value
                   1.0e-21
Match length
                   64
% identity
NCBI Description
                   (AB008518) RMA1 [Arabidopsis thaliana] >gi 4206205
                   (AF071527) RMA1 RING zinc finger protein [Arabidopsis
```

thaliana]

```
Seq. No.
                   10306
                   18447 2.R1040
Contig ID
                   zhf70\overline{0}962429.h1
5'-most EST
                   10307
Seq. No.
                   18449_1.R1040
Contig ID
5'-most EST
                   LIB3170-024-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   g125606
BLAST score
                   197
E value
                   3.0e-15
Match length
                   63
                   63
% identity
NCBI Description
                   PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248
                   pyruvate kinase (EC 2.7.1.40) - potato
                   >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
                   tuberosum]
Seq. No.
                   10308
                   18450 1.R1040
Contig ID
5'-most EST
                   qsv70\overline{1}047939.h1
Method
                   BLASTX
                   g2760830
NCBI GI
BLAST score
                   1576
E value
                   1.0e-176
Match length
                   382
% identity
NCBI Description
                   (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
                   thaliana]
                   10309
Seq. No.
                   18460 1.R1040
Contig ID
                   LIB3170-023-Q1-K1-D8
5'-most EST
                   10310
Seq. No.
Contig ID
                   18461 1.R1040
                   smc70\overline{0}749767.h1
5'-most EST
                   10311
Seq. No.
Contig ID
                   18463 1.R1040
5'-most EST
                   LIB3109-022-Q1-K1-D8
Method .
                   BLASTX
NCBI GI
                   g3420054
BLAST score
                   269
                   2.0e-23
E value
Match length
                   183
% identity
NCBI Description
                   (AC004680) unknown protein [Arabidopsis thaliana]
                   10312
Seq. No.
Contig ID
                   18464 1.R1040
5'-most EST
                   LIB3049-008-Q1-E1-F3
                   10313
Seq. No.
                   18469 1.R1040
Contig ID
```

pmv700891633.hl

5'-most EST

```
BLASTX
Method
 NCBI GI
                    g3850063
 BLAST score
                    787
 E value
                    1.0e-83
 Match length
                    482
                    35
 % identity
 NCBI Description (AJ223830) ARE1 [Rattus norvegicus]
 Seq. No.
                    10314
                    18478 1.R1040
 Contig ID
                    LIB3170-024-Q1-J1-D1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g3834322
 BLAST score
                    180
                    4.0e-13
 E value
 Match length
                    46
 % identity
                    80
                    (AC005679) EST gb_R30300 comes from this gene. [Arabidopsis
 NCBI Description
                    thaliana]
                    10315
 Seq. No.
                    18481 1.R1040
 Contig ID
                    LIB3170-022-Q1-K1-C11
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q3080412
 BLAST score
                    209
 E value
                    3.0e-16
 Match length
                    129
 % identity
                    33
 NCBI Description
                    (AL022604) putative protein [Arabidopsis thaliana]
 Seq. No.
                    10316
                    18486 1.R1040
 Contig ID
 5'-most EST
                    jC-qmf102220148c03a1
 Method
                    BLASTX
 NCBI GI
                    q2289003
 BLAST score ·
                    414
 E value
                    2.0e-40
 Match length
                    129
 % identity
 NCBI Description
                    (AC002335) membrane transporter D1 isolog [Arabidopsis
                    thaliana]
                    10317
 Seq. No.
                    18488 1.R1040
 Contig ID
 5'-most EST
                    LIB3056-004-Q1-N1-B2
 Seq. No.
                    10318
                    18489 1.R1040
 Contig ID
                    LIB3092-043-Q1-K1-E6
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g4519673
 BLAST score
                    1106
 E value
                    1.0e-121
 Match length
                    280
 % identity
                    71
 NCBI Description
                    (AB017694) WREBP-2 [Nicotiana tabacum]
```

```
10319
Seq. No.
Contig ID
                   18497_1.R1040
5'-most EST
                   zzp700833272.h1
                   BLASTX
Method
                   g1914685
NCBI GI
                   763
BLAST score
                   2.0e-91
E value
Match length
                   242
% identity
                   77
NCBI Description
                   (Y12014) RAD23 protein, isoform II [Daucus carota]
                   10320
Seq. No.
                   18498 1.R1040
Contig ID
5'-most EST
                   jsh701064031.h1
                   BLASTX
Method
                   g3395441
NCBI GI
BLAST score
                   282
                   5.0e-25
E value
                   71
Match length
                   72
% identity
                   (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                   10321
Seq. No.
Contig ID
                   18499 1.R1040
5'-most EST
                   LIB3170-021-Q1-K1-C11
Method
                   BLASTN
NCBI GI
                   g2564045
                   47
BLAST score
E value
                   2.0e-17
                   184
Match length
                   85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K8K14, complete sequence [Arabidopsis thaliana]
                   10322
Seq. No.
Contig ID
                   18507 1.R1040
5'-most EST
                   LIB3170-023-Q1-K1-C5
Method
                  BLASTX
                   g3892045
NCBI GI
BLAST score
                   224
E value
                   2.0e-18
Match length
                   43
% identity
                   (AC002330) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   10323
Seq. No.
Contig ID
                   18509 1.R1040
5'-most EST
                   fua701038279.hl
Method
                   BLASTX
NCBI -GI
                   q416758
BLAST score
                   1808
E value
                   0.0e + 00
Match length
                   455
% identity
                   73
```

NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)

Contig ID 5'-most EST

```
thalianal
Seq. No.
                   10324
                   18510 1.R1040
Contig ID
                   LIB30\overline{4}9-007-Q1-E1-H6
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2760167
BLAST score
                   36
E value
                    6.0e-11
Match length
                   80
% identity
                   86
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCO15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   10325
                   18510 2.R1040
Contig ID
5'-most EST
                   hyd70\overline{0}730781.h1
Method
                   BLASTN
NCBI GI
                   q2760167
BLAST score
                   38
E value
                   5.0e-12
Match length
                   134
                   82
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCO15, complete sequence [Arabidopsis thaliana]
                   10326
Seq. No.
Contig ID
                   18511 1.R1040
5'-most EST
                   LIB3094-065-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   q3063701
BLAST score
                   544
E value
                   2.0e-55
Match length
                   144
% identity
                   73
NCBI Description
                   (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                   10327
                   18511 2.R1040
Contig ID
5'-most EST
                   LIB3170-020-Q1-J1-F4
Method
                   BLASTX
NCBI GI
                   q3063701
BLAST score
                   384
E value
                   5.0e-37
Match length
                   98
% identity
NCBI Description
                   (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                   10328
Contig ID
                   18518 1.R1040
5'-most EST
                   LIB3138-033-01-N1-C5
                   10329
Seq. No.
```

carboxypeptidase Y-like protein [Arabidopsis thaliana]
>gi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis

18519 1.R1040

LIB3049-007-Q1-E1-G9

```
10330
Seq. No.
                   18520 1.R1040
Contig ID
                   jex70\overline{0}910091.h1
5'-most EST
                   10331
Seq. No.
                   18529_1.R1040
Contig ID
                   uC-gmropic065c11b1
5'-most EST
Method
                   BLASTX
                   g1480670
NCBI GI
BLAST score
                   503
E value
                   1.0e-50
Match length
                   151
% identity
                   (U60267) delta 1-pyrroline-5-carboxylate synthetase
NCBI Description
                   [Lycopersicon esculentum]
                   10332
Seq. No.
                   18535 1.R1040
Contig ID
5'-most EST
                   bth700847296.h1
Method
                   BLASTX
NCBI GI
                   g3128209
BLAST score
                   324
                   8.0e-30
E value
Match length
                   81
% identity
                   74
                   (AC004077) unknown protein [Arabidopsis thaliana]
NCBI Description
                   10333
Seq. No.
                   18538 1.R1040
Contig ID
                   LIB3107-066-Q1-K1-F2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2494041
BLAST score
                   803
                   2.0e-85
E value
                   281
Match length
                   57
% identity
NCBI Description
                   DIAMINOPIMELATE EPIMERASE >gi_1653875_dbj_BAA18785_
                   (D90917) diaminopimelate epimerase [Synechocystis sp.]
                   10334
Seq. No.
                   18538 2.R1040
Contig ID
5'-most EST
                   tku700646390.h1
                   BLASTX
Method
                   g2494041
NCBI GI
BLAST score
                   361
E value
                   4.0e-34
Match length
                   88
                   72
% identity
                   DIAMINOPIMELATE EPIMERASE >gi_1653875_dbj_BAA18785_
NCBI Description
                   (D90917) diaminopimelate epimerase [Synechocystis sp.]
                   10335
Seq. No.
                   18538 3.R1040
Contig ID
5'-most EST
                   dpv701102513.h1
```

10336

Seq. No.

E value

3.0e-41

```
18540 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-079-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   g2464901
BLAST score
                   205
                   4.0e-16
E value
                   88
Match length
% identity
                   48
NCBI Description
                   (Z99708) putative protein [Arabidopsis thaliana]
                   10337
Seq. No.
                   18542 1.R1040
Contig ID
                   LIB3109-014-Q1-K1-E1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4191791
BLAST score
                   1202
E value
                   1.0e-132
Match length
                   324
% identity
                   69
NCBI Description
                   (AC005917) putative sf21 (Helianthus annuus) protein
                   [Arabidopsis thaliana]
Seq. No.
                   10338
                   18542 2.R1040
Contig ID
5'-most EST
                   uC-gmronoir040h10b1
Method
                   BLASTX
NCBI GI
                   q4191791
BLAST score
                   499
E value
                   1.0e-50
Match length
                   135
% identity
                   69
NCBI Description
                   (AC005917) putative sf21 {Helianthus annuus} protein
                   [Arabidopsis thaliana]
Seq. No.
                   10339
Contig ID
                   18542 4.R1040
5'-most EST
                   jC-gmst02400074g04d1
Seq. No.
                   10340
Contig ID
                   18542 5.R1040
5'-most EST
                   seb700651041.hl
Method
                   BLASTX
NCBI GI
                   q4191791
BLAST score
                   142
E value
                   7.0e-09
Match length
                   34
% identity
                   76
NCBI Description
                   (AC005917) putative sf21 {Helianthus annuus} protein
                   [Arabidopsis thaliana]
Seq. No.
                   10341
Contig ID
                   18542 6.R1040
5'-most EST
                   uC-gmrominsoy087f02b1
Method
                   BLASTX
NCBI GI
                   g4191791
BLAST score
                   304
```

BLAST score

```
120
Match length
                   71
% identity
                   (AC005917) putative sf21 {Helianthus annuus} protein
NCBI Description
                   [Arabidopsis thaliana]
                   10342
Seq. No.
                   18549 1.R1040
Contig ID
5'-most EST
                   g5058258
                   10343
Seq. No.
                   18549 2.R1040
Contig ID
5'-most EST
                   jC-qmst02400061a04a1
                   10344
Seq. No.
Contig ID
                   18549 3.R1040
5'-most EST
                   jC-gmro02910075f07a1
Seq. No.
                   10345
                   18549 4.R1040
Contig ID
5'-most EST
                   leu701149641.h1
Method
                   BLASTX
                   g3095111
NCBI GI
BLAST score
                   193
E value
                   2.0e-14
                   144
Match length
                   33
% identity
NCBI Description
                  (AF051894) 15 kDa selenoprotein [Homo sapiens]
                   10346
Seq. No.
Contig ID
                   18560 1.R1040
5'-most EST
                   uC-gmrominsoy112f04b1
Method
                   BLASTX
                   g3757515
NCBI GI
BLAST score
                   168
E value
                   2.0e-11
Match length
                   82
% identity
                   41
NCBI Description
                   (AC005167) hypothetical protein [Arabidopsis thaliana]
                   10347
Seq. No.
Contig ID
                   18566 1.R1040
5'-most EST
                   LIB3049-007-Q1-E1-A8
                   10348
Seq. No.
Contig ID
                   18567 1.R1040
5'-most EST
                   LIB3170-023-Q1-J1-C12
Seq. No.
                   10349
Contig ID
                   18569 1.R1040
                   LIB3093-013-Q1-K1-F1
5'-most EST
                  10350
Seq. No.
Contig ID
                   18572 1.R1040
                   LIB30\overline{5}0-023-Q1-K1-A8
5'-most EST
Method
                   BLASTX
                   g3237190
NCBI GI
```

```
E value
                   2.0e-19
Match length
                   92
                   51
% identity
NCBI Description
                   (AB014760) cystein proteinase inhibitor [Cucumis sativus]
                   10351
Seq. No.
                   18578 1.R1040
Contig ID
5'-most EST
                   LIB3109-006-Q1-K1-B8
Seq. No.
                   18583 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220068h02d1
                   10353
Seq. No.
Contig ID
                   18585 1.R1040
                   jC-gmf102220102f03a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g542020
BLAST score
                   493
E value
                   1.0e-49
Match length
                   155
% identity
                   62
NCBI Description
                   sucrose transport protein - castor bean
                   >gi_468562_emb_CAA83436_ (Z31561) sucrose carrier [Ricinus
                   communis]
Seq. No.
                   10354
                   18586 1.R1040
Contig ID
5'-most EST
                   q4314\overline{0}18
Method
                   BLASTX
NCBI GI
                   q3702343
BLAST score
                   1625
E value
                   0.0e + 00
Match length
                   468
% identity
                   76
NCBI Description
                   (AC005397) putative homeotic gene regulator [Arabidopsis
                   thaliana]
                   10355
Seq. No.
                   18590 1.R1040
Contig ID
5'-most EST
                   ncj700987760.hl
Seq. No.
                   10356
                   18590 2.R1040
Contig ID
5'-most EST
                   kl1701214752.h1
                   10357
Seq. No.
Contig ID
                   18593_1.R1040
5'-most EST
                   LIB3049-006-Q1-E1-H3
Method
                   BLASTX
                   g2244765
NCBI GI
BLAST score
                   285
E value
                   2.0e-25
Match length
                   94
% identity
                   54
```

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
                  10358
                  18595 1.R1040
Contig ID
                  kl1701213810.h1
5'-most EST
Method
                  BLASTX
                  g3582436
NCBI GI
BLAST score
                  1153
                   1.0e-148
E value
Match length
                   345
% identity
NCBI Description
                   (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
                   10359
Seq. No.
                  18598 1.R1040
Contig ID
5'-most EST
                  LIB3049-006-Q1-E1-G12
Seq. No.
                  10360
                  18610 1.R1040
Contig ID
5'-most EST
                  LIB3049-006-Q1-E1-F6
                  10361
Seq. No.
                  18611 1.R1040
Contig ID
5'-most EST
                  LIB3049-006-Q1-E1-F7
                  10362
Seq. No.
Contig ID
                  18613 1.R1040
5'-most EST
                  LIB3049-006-Q1-E1-G1
                  10363
Seq. No.
Contig ID
                  18615 1.R1040
5'-most EST
                   jC-qmro02800022f01a1
Method
                   BLASTX
                   g4415939
NCBI GI
                   533
BLAST score
E value
                   6.0e-54
Match length
                   250
                   55
% identity
NCBI Description
                   (AC006418) putative zinc finger protein [Arabidopsis
                   thaliana]
                   10364
Seq. No.
Contig ID
                   18615 3.R1040
5'-most EST
                   trc700565847.hl
Method
                   BLASTX
                   g4415939
NCBI GI
BLAST score
                   348
E value
                   8.0e-33
Match length
                   71
% identity
                   (AC006418) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   10365
Seq. No.
Contig ID
                   18615 4.R1040
5'-most EST
                   uC-gmropic068g10b1
Method
                  BLASTX
```

g4415939

380

NCBI GI BLAST score

```
E value
                   1.0e-36
Match length
                   118
                   67
% identity
                   (AC006418) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   10366
Seq. No.
                   18618_1.R1040
Contig ID
                   vzy700753764.hl
5'-most EST
                   BLASTX
Method
                   g3600052
NCBI GI
BLAST score
                   635
                   6.0e-66
E value
Match length
                   311
                   44
% identity
                   (AF080120) contains similarity to glycosyl hydrolases
NCBI Description
                   family 9 (Pfam: glycosyl_hydro5.hmm, score: 88.03)
                   [Arabidopsis thaliana]
                   10367
Seq. No.
                   18620 1.R1040
Contig ID
                   LIB3049-006-Q1-E1-D3
5'-most EST
                   10368
Seq. No.
                   18622 1.R1040.
Contig ID
                   leu701157390.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1708420
BLAST score
                   271
                   8.0e-24
E value
                   123
Match length
                   43
% identity
                   ISOFLAVONE REDUCTASE HOMOLOG P3 >gi 1361992 pir S57613
NCBI Description
                   isoflavonoid reductase homolog - Arabidopsis thaliana
                   >gi 886432 emb CAA89859 (Z49777) isoflavonoid reductase
                   homologue [Arabidopsis thaliana]
                   10369
Seq. No.
                   18623 1.R1040
Contig ID
                   LIB31\overline{3}9-117-P1-N1-G9
5'-most EST
Method
                   BLASTX
                   g2832623
NCBI GI
                   168
BLAST score
E value
                   1.0e-11
                   61
Match length
% identity
                   (AL021711) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   10370
Seq. No.
Contig ID
                   18624 1.R1040
5'-most EST
                   zhf700957067.h1
Method
                   BLASTN
NCBI GI
                   g2792154
BLAST score
                   593
                   0.0e + 00
E value
```

981

Match length

```
90
% identity
                  Sesbania rostrata mRNA for putative chalcone reductase
NCBI Description
Seq. No.
                  10371
                  18631 1.R1040
Contig ID
5'-most EST
                  LIB3049-006-Q1-E1-E3
                  BLASTN
Method
NCBI GI
                  q169157
BLAST score
                  136
                   2.0e-70
E value
Match length
                  376
% identity
                   87
                  Pisum sativum serine hydroxymethyltransferase mRNA,
NCBI Description
                   complete cds
                   10372
Seq. No.
                   18633 1.R1040
Contig ID
                  LIB3049-006-Q1-E1-D10
5'-most EST
                   10373
Seq. No.
Contig ID
                   18635 1.R1040
                   zzp700832155.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2213626
                   193
BLAST score
                   2.0e-14
E value
                   156
Match length
                   38
% identity
                   (AC000103) F21J9.18 [Arabidopsis thaliana]
NCBI Description
                   10374
Seq. No.
                   18635 2.R1040
Contig ID
                   uaw700660817.hl
5'-most EST
                   10375
Seq. No.
                   18645_1.R1040
Contig ID
                   LIB3049-006-Q1-E1-C5
5'-most EST
Method
                   BLASTX
                   g2880043
NCBI GI
BLAST score
                   734
                   1.0e-77
E value
Match length
                   300
% identity
                   46
                   (AC002340) putative 3-hydroxyisobutyryl-coenzyme A
NCBI Description
                   hydrolase [Arabidopsis thaliana]
                   10376
Seq. No.
Contig ID
                   18647 1.R1040
5'-most EST
                   LIB3049-006-Q1-E1-C7
                   10377
Seq. No.
                   18648 1.R1040
Contig ID
5'-most EST
                   LIB3092-061-Q1-K1-C1
                   10378
Seq. No.
                   18651 1.R1040
Contig ID
                   LIB3109-050-Q1-K1-G2
5'-most EST
```

```
10379
Seq. No.
Contig ID
                  18652 1.R1040
5'-most EST
                  LIB3170-023-Q1-K1-B9
                  10380
Seq. No.
                  18656_1.R1040
Contig ID
5'-most EST
                  LIB3049-006-Q1-E1-A3
Method
                  BLASTX
NCBI GI
                  q3548801
BLAST score
                  346
                   3.0e-32
E value
Match length
                  192
% identity
NCBI Description
                   (AC005313) putative transmembrane protein [Arabidopsis
                   thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative
                   integral membrane protein [Arabidopsis thaliana]
                   10381
Seq. No.
                   18656_2.R1040
Contig ID
                   leu701147073.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3461828
BLAST score
                   157
                   2.0e-10
E value
Match length
                  81
% identity
                   38
                   (AC004138) unknown protein [Arabidopsis thaliana]
NCBI Description
                   10382
Seq. No.
Contig ID
                   18657 1.R1040
                   uaw700665034.hl
5'-most EST
                   BLASTX
Method
                   q4468048
NCBI GI
BLAST score
                   336
E value
                   2.0e-31
Match length
                   152
% identity
                   (X78703) catechol O-methyltransferase [Vanilla planifolia]
NCBI Description
                   10383
Seq. No.
Contig ID
                   18659 1.R1040
5'-most EST
                   LIB3049-006-Q1-E1-A6
                   10384
Seq. No.
                   18663 1.R1040
Contig ID
5'-most EST
                   LIB3106-095-Q1-K1-F10
Seq. No.
                   10385
                   18669 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy031f01b1
Seq. No.
                   10386
                   18669 2.R1040
Contig ID
5'-most EST
                   LIB3106-013-Q1-K1-E6
```

10387

Seq. No.

```
Contig ID
                   18670 1.R1040
                   LIB3049-005-Q1-E1-G7
5'-most EST
Method
                   BLASTX
                   g1086147
NCBI GI
                   450
BLAST score
                   1.0e-44
E value
                   131
Match length
                   61
% identity
                   protein S2 - Phalaris coerulescens >gi 556833 emb_CAA57520
NCBI Description
                   (X81992) S2 [Phalaris coerulescens]
                   10388
Seq. No.
Contig ID
                   18670 2.R1040
                   LIB3107-015-Q1-K1-E10
5'-most EST
Seq. No.
                   10389
Contig ID
                   18670 3.R1040
                   vzy700751450.hl
5'-most EST
                   10390
Seq. No.
                   18678 1.R1040
Contig ID
5'-most EST
                   LIB3049-005-Q1-E1-H4
Method
                   BLASTX
                   g2498329
NCBI GI
BLAST score
                   593
                   1.0e-61
E value
Match length
                   127
% identity
                   91
                   PATTERN FORMATION PROTEIN EMB30 >gi 2129665 pir S65571
NCBI Description
                   pattern-formation protein GNOM - Arabidopsis thaliana
                   >gi 1209633 (U36433) GNOM gene product [Arabidopsis
                   thaliana] >gi 1335997 (U56140) similar to the Saccharomyces
                   cerevisiae Sec7 protein, GenBank Accession Number J03918
                   [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the
                   Saccharomyces cerevisiae \overline{\text{Sec}}7 protein, GenBank Accession
                   Number J03918 [Arabidopsis thaliana]
                   10391
Seq. No.
                   18680 1.R1040
Contig ID
                   LIB3094-043-Q1-K1-C9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4544399
BLAST score
                   745
E value
                   3.0e-79
                   177
Match length
% identity
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   10392
Seq. No.
Contig ID
                   18683 1.R1040
                   LIB30\overline{4}9-005-Q1-E1-H9
5'-most EST
                   10393
Seq. No.
                   18686 1.R1040
Contig ID
                   LIB3049-005-Q1-E1-F10
5'-most EST
```

BLASTX

Method

```
g629858
NCBI GI
BLAST score
                   533
E value
                   1.0e-54
Match length
                   127
                   80
% identity
                   protein kinase C inhibitor - maize
NCBI Description
                   10394
Seq. No.
Contig ID
                   18687 1.R1040
5'-most EST
                   LIB3049-005-Q1-E1-F11
Seq. No.
                   10395
                   18688 1.R1040
Contig ID
                   leu701151019.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2129675
                   638
BLAST score
                   1.0e-66
E value
Match length
                   192
                   69
% identity
NCBI Description
                   probable chlorophyll synthetase G4 - Arabidopsis thaliana
                   >gi_972938 (U19382) putative chlorophyll synthetase
                   [Arabidopsis thaliana] >gi_3068709 (AF049236) putative
                   chlorophyll synthetase [Arabidopsis thaliana]
                   10396
Seq. No.
Contig ID
                   18689 1.R1040
5'-most EST
                   LIB3049-005-Q1-E1-F2
                   10397
Seq. No.
                   18689 2.R1040
Contig ID
5'-most EST
                   asn70\overline{1}132169.h1
                   10398
Seq. No.
                   18691_1.R1040
Contig ID
5'-most EST
                   zsg70\overline{1}127305.h1
Method
                   BLASTX
                   g3927830
NCBI GI
BLAST score
                   506
E value
                   3.0e-57
Match length
                   200
% identity
NCBI Description
                   (AC005727) hypothetical protein [Arabidopsis thaliana]
                   10399
Seq. No.
                   18694 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy091e09b1
Method
                   BLASTN
                   g3941288
NCBI GI
BLAST score
                   376
E value
                   0.0e + 00
Match length
                   828
% identity
                   86
NCBI Description
                   Pisum sativum similarity to SCAMP37 (psam2) mRNA, complete
```

10400

Seq. No.

```
18694 2.R1040
Contig ID
5'-most EST
                   LIB3051-047-Q1-K1-H9
                   BLASTN
Method
NCBI GI
                   q3941288
BLAST score
                   92
                   5.0e-44
E value
Match length
                   249
                   87
% identity
NCBI Description
                   Pisum sativum similarity to SCAMP37 (psam2) mRNA, complete
                   10401
Seq. No.
                   18694 3.R1040
Contig ID
                   jC-qmro02910054h10a1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3941288
                   48
BLAST score
                   8.0e-18
E value
Match length
                   145
% identity
                   88
NCBI Description
                   Pisum sativum similarity to SCAMP37 (psam2) mRNA, complete
                   cds
                   10402
Seq. No.
Contig ID
                   18694_4.R1040
5'-most EST
                   jC-gmro02910054h10d1
                   BLASTN
Method
NCBI GI
                   q3941288
-BLAST score
                   215
E value
                   1.0e-117
Match length
                   379
% identity
                   89
                   Pisum sativum similarity to SCAMP37 (psam2) mRNA, complete
NCBI Description
                   cds
                   10403
Seq. No.
Contig ID
                   18702 1.R1040
5'-most EST
                   kl1701202317.hl
Method
                   BLASTX
                   g4490316
NCBI GI
BLAST score
                   554
E value
                   4.0e-57
Match length
                   229
% identity
                   53
                   (AL035678) nucellin-like protein [Arabidopsis thaliana]
NCBI Description
                   10404
Seq. No.
Contig ID
                   18702 2.R1040
                   LIB3170-047-Q1-J1-B3
5'-most EST
Method
                   BLASTX
                   g4490316
NCBI GI
BLAST score
                   247
E value
                   2.0e-33
                   131
Match length
                   53
% identity
```

NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]

NCBI GI

```
10405
Seq. No.
Contig ID
                   18704 1.R1040
5'-most EST
                  LIB3050-020-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                   g3860258
BLAST score
                   408
E value
                   9.0e-40
Match length
                  118
% identity
                   62
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
                   10406
Seq. No.
                   18704 2.R1040
Contig ID
5'-most EST
                   LIB3170-021-Q1-K1-B7
Method
                   BLASTX
                   q3860258
NCBI GI
BLAST score
                   162
                   3.0e-11
E value
                   52
Match length
% identity.
                   60
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   10407
Seq. No.
Contig ID
                   18705 1.R1040
                   uC-gmflminsoy080h11b1
5'-most EST
Method
                   BLASTX
                   q2827528
NCBI GI
BLAST score
                   436
                   9.0e-43
E value
Match length
                   216
% identity
                   44
                   (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                   10408
Seq. No.
                   18707 1.R1040
Contig ID
5'-most EST
                   kmv700741951.h1
                   10409
Seq. No.
                   18707 2.R1040
Contig ID
5'-most EST
                   zzp700836141.hl
                   10410
Seq. No.
                   18710_1.R1040
Contig ID
                   LIB3170-022-Q1-K1-B9
5'-most EST
Method
                   BLASTX
                   g3269284
NCBI GI
BLAST score
                   395
E value
                   2.0e-38
Match length
                   128
% identity
                   62
                   (AL030978) histone H2A- like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10411
                   18729 1.R1040
Contig ID
                   LIB3092-015-Q1-K1-G11
5'-most EST
                   BLASTX
Method
```

q4105798

```
931
BLAST score
                   1.0e-100
E value
                   249
Match length
% identity
                   57
                  (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                   10412
Seq. No.
                   18729 2.R1040
Contig ID
5'-most EST
                   LIB3109-007-Q1-K1-C1
Method
                   BLASTX
NCBI GI
                   q4105798
BLAST score
                   207
                   3.0e-16
E value
Match length
                   65
                   54
% identity
                   (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                   10413
Seq. No.
                   18732 1.R1040
Contig ID
5'-most EST
                   LIB3049-005-Q1-E1-C6
                   BLASTX
Method
NCBI GI
                   q1352881
BLAST score
                   146
                   7.0e-09
E value
Match length
                   110
                   28
% identity
NCBI Description
                   HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC
                   REGION >gi_1078266_pir__S57063 probable membrane protein ...
                   YJR044c - yeast (Saccharomyces cerevisiae)
                   >gi_1015699_emb_CAA89572_ (Z49544) ORF YJR044c
[Saccharomyces cerevisiae] >gi_1197072 (L36344) ORF;
                   putative [Saccharomyces cerevisiae]
                   10414
Seq. No.
                   18732 2.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}6-014-Q1-N1-D1
Seq. No.
                   10415
                   18738 1.R1040
Contig ID
5'-most EST
                   LIB3049-004-Q1-E1-H4
                   10416
Seq. No.
Contig ID
                   18741 1.R1040
5'-most EST
                   zpv700761129.h1
                   BLASTX
Method
NCBI GI
                   g3451411
BLAST score
                   530
E value
                   4.0e-54
Match length
                   145
% identity
NCBI Description
                   (Z98761) seryl-tRNA synthetase [Helianthus annuus]
                   10417
Seq. No.
                   18746 1.R1040
Contig ID
5'-most EST
                   LIB3049-005-Q1-E1-A5
Method
                   BLASTX
```

g1843628

NCBI GI

```
465
BLAST score
                   2.0e-46
E value
                   127
Match length
                   72
% identity
                   (U88061) SNF5 homolog BSH [Arabidopsis thaliana]
NCBI Description
                   10418
Seq. No.
                   18749 1.R1040
Contig ID
                   LIB3170-021-Q1-K1-B5
5'-most EST
                   10419
Seq. No.
                   18750 1.R1040
Contig ID
                   LIB3049-005-Q1-E1-B1
5'-most EST
Method
                   BLASTX
                   g3970680
NCBI GI
                   275
BLAST score
E value
                   3.0e-24
Match length
                   108
% identity
                   52
                   (AL034388) 67A9.b [Drosophila melanogaster]
NCBI Description
                   10420
Seq. No.
                   18750 2.R1040
Contig ID
                   pmv700889336.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3970680
BLAST score
                   105
E value
                   1.0e-11
Match length
                   99
% identity
                   (AL034388) 67A9.b [Drosophila melanogaster]
NCBI Description
                   10421
Seq. No.
                   18750 3.R1040
Contig ID
5'-most EST
                   uC-qmronoir064h03b1
Seq. No.
                   10422
                   18750 4.R1040
Contig ID `
5'-most EST
                   jex700906670.h1
                   10423
Seq. No.
Contig ID
                   18751 1.R1040
                   sat701011064.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3395938
BLAST score
                   781
E value
                   4.0e-83
Match length
                   251
% identity
                   50
                   (AF076924) polypyrimidine tract-binding protein homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   10424
                   18753 1.R1040
Contig ID
5'-most EST
                   LIB3170-022-Q1-K1-B2
```

BLASTX

q3269287

Method NCBI GI

BLAST score 174 E value 1.0e-12 58 Match length % identity 62 (AL030978) GH3 like protein [Arabidopsis thaliana] NCBI Description 10425 Seq. No. Contig ID 18754 1.R1040 5'-most EST uC-gmronoir063d11b1 10426 Seq. No. 18760 1.R1040 Contig ID trc700564090.hl 5'-most EST 10427 Seq. No. 18760 2.R1040 Contig ID 5'-most EST LIB3051-051-Q1-K1-H1 10428 Seq. No. 18768 1.R1040 Contig ID 5'-most EST LIB3049-004-Q1-E1-H2 Method BLASTX g3687240 NCBI GI BLAST score 227 E value 7.0e-19 100 Match length % identity 42 (AC005169) extensin-like protein [Arabidopsis thaliana] NCBI Description 10429 Seq. No. 18779 1.R1040 Contig ID 5'-most EST zzp700831511.hl Method BLASTX NCBI GI g2661179 BLAST score 800 1.0e-85 E value Match length 215 % identity 68 (U80984) AtZW10 [Arabidopsis thaliana] NCBI Description 10430 Seq. No. 18780 1.R1040 Contig ID 5'-most EST LIB3139-034-P1-N1-E12 Method BLASTX NCBI GI g2829918 BLAST score 153 E value 4.0e-11 Match length 59 71 % identity

NCBI Description

Seq. No. 10431

Contig ID 18780_2.R1040

5'-most EST LIB3049-004-Q1-E1-F10

[Arabidopsis thaliana]

Method BLASTX NCBI GI g2829918

(AC002291) similar to "tub" protein gp_U82468_2072162

Seq. No.

Contig ID

10438

18791 1.R1040

```
302
BLAST score
                   2.0e-27
E value
Match length
                   85
% identity
                   73
                   (AC002291) similar to "tub" protein gp U82468 2072162
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   10432
                   18780 5.R1040
Contig ID
5'-most EST
                   dpv701099903.hl
Seq. No.
                   10433
                   18783 1.R1040
Contig ID
5'-most EST
                   LIB3049-004-Q1-E1-F2
Seq. No.
                   10434
Contig ID
                   18788 1.R1040
5'-most EST
                   xpa700792484.hl
Method
                   BLASTX
NCBI GI
                   q2688824
BLAST score
                   257
E value
                   8.0e-22
Match length
                   126
% identity
                   52
                   (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                   armeniaca]
                   10435
Seq. No.
                   18788 2.R1040
Contig ID
                   g5605911
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2688824
BLAST score
                   243
                   3.0e-20
E value
Match length
                   140
% identity
                   45
NCBI Description
                   (U93273) putative auxin-repressed protein [Prunus
                   armeniaca]
                   10436
Seq. No.
                   18788 4.R1040
Contig ID
5'-most EST
                   asn701141515.hl
Method.
                   BLASTX
                   g2688824
NCBI GI
BLAST score
                   169
                   4.0e-12
E value
Match length
                   40
% identity
NCBI Description
                   (U93273) putative auxin-repressed protein [Prunus
                   armeniaca]
                   10437
Seq. No.
Contig ID
                   18789 1.R1040
5'-most EST
                   LIB3050-003-Q1-E1-D6
```

5'-most EST

```
5'-most EST
                  LIB3109-035-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  q2346986
BLAST score
                  397
                  4.0e-38
E value
                  263
Match length
% identity
                  44
NCBI Description
                   (AB006605) ZPT3-3 [Petunia x hybrida]
Seq. No.
                  10439
Contig ID
                  18798 1.R1040
5'-most EST
                  LIB3093-047-Q1-K1-G10
Method
                  BLASTX
                  g623586
NCBI GI
BLAST score
                  960
E value
                  1.0e-104
                  207
Match length
                  95
% identity
NCBI Description
                  (L29273) putative [Nicotiana tabacum]
                                                                              , :
                  10440
Seq. No.
                  18798_2.R1040
Contig ID
                  LIB3049-004-Q1-E1-D4
5'-most EST
Method
                  BLASTN
                  g435428
NCBI GI
BLAST score
                  76
E value
                  1.0e-34
                  152
Match length
                  88
% identity
                  Arabidopsis thaliana GTP-binding protein mRNA
NCBI Description
                  10441
Seq. No.
                  18798 3.R1040
Contig ID
5'-most EST
                  vwf700676648.h1
Method
                  BLASTN
NCBI GI
                  g435428
BLAST score
                  92
                  4.0e-44
E value
                  188
Match length
                  87
% identity
NCBI Description
                  Arabidopsis thaliana GTP-binding protein mRNA
                  10442
Seq. No.
Contig ID
                  18799 1.R1040
                  LIB3049-004-Q1-E1-D5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2500354
BLAST score
                  1073
E value
                  1.0e-117
Match length
                  219
                  91
% identity
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
                  10443
Seq. No.
                  18799 2.R1040
Contig ID
```

 $LIB30\overline{5}1-024-Q1-K1-F4$

Seq. No. Contig ID

```
Method
                   BLASTX
NCBI GI
                   g2500354
BLAST score
                   542
                   2.0e-55
E value
Match length
                   117
% identity
                   85
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
Seq. No.
                   18801 1.R1040
Contig ID
5'-most EST
                   g5677221
Seq. No.
                   10445
                   18801 2.R1040
Contig ID
5'-most EST
                   LIB3094-082-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   q4220534
BLAST score
                   494
E value
                   1.0e-49
Match length
                   199
% identity
NCBI Description
                   (AL035356) putative protein [Arabidopsis thaliana]
                   10446
Seq. No.
                   18814 1.R1040
Contig ID
5'-most EST
                   asn701137579.hl
                   10447
Seq. No.
                   18815 1.R1040
Contig ID
5'-most EST
                   leu70\overline{1}151423.h1
                   10448
Seq. No.
                   18816 1.R1040
Contig ID
5'-most EST
                   LIB3170-023-Q1-K1-B11
Seq. No.
                   10449
                   18817 1.R1040
Contig ID
5'-most EST
                   LIB3170-023-01-K1-B3
                   10450
Seq. No.
Contig ID
                   18820 1.R1040
5'-most EST
                   LIB3049-004-Q1-E1-C2
                   BLASTX
Method
NCBI GI
                   q2244800
BLAST score
                   326
E value
                   2.0e-30
Match length
                   106
% identity
NCBI Description
                   (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
Seq. No.
                   10451
                   18821 1.R1040
Contig ID
5'-most EST
                   LIB3170-024-Q1-K1-B7
```

18823 1.R1040

NCBI GI

```
LIB3170-024-Q1-K1-B8
5'-most EST
                   10453
Seq. No.
                   18830 1.R1040
Contig ID
                   jC-gm\overline{f}102220075b05d1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3193296
BLAST score
                   848
E value
                   5.0e-91
Match length
                   224
                   67
% identity
                  (AF069298) similar to pectinesterase [Arabidopsis thaliana]
NCBI Description
                   10454
Seq. No.
                   18831 1.R1040
Contig ID
5'-most EST
                   LIB3049-004-Q1-E1-A10
Method
                   BLASTX
NCBI GI
                   g3953479
BLAST score
                   173
E value
                   3.0e-12
Match length
                   58
                   57
% identity
NCBI Description (AC002328) F2202.24 [Arabidopsis thaliana]
                   10455
Seq. No.
                   18832 1.R1040
Contig ID
5'-most EST
                   LIB3170-023-Q1-K1-B10
                   10456
Seq. No.
                   18834 1.R1040
Contig ID
5'-most EST
                   LIB3170-023-Q1-K1-B8
                   10457
Seq. No.
                   18842 1.R1040
Contig ID
                   LIB3049-003-Q1-E1-F9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2462737
BLAST score
                   309
E value
                   2.0e-28
Match length
                   126
                   49
% identity
                    (AC002292) similar to "Mx" GTP-binding proteins
NCBI Description
                    [Arabidopsis thaliana]
                   10458
Seq. No.
                   18844 1.R1040
Contig ID
 5'-most EST
                   gsv701047810.hl
Seq. No.
                   10459
                   18844 2.R1040
Contig ID
5'-most EST
                   LIB3056-010-Q1-N1-E12
                   10460
Seq. No.
                   18849 1.R1040
Contig ID
 5'-most EST
                   uC-gmrominsoy153d04b1
Method
                   BLASTX
```

g3004549

```
358
BLAST score
E value
                   2.0e-33
                   177
Match length
                   45
% identity
                   (AC003673) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4185152 (AC005724) unknown protein [Arabidopsis
                   thaliana]
Seq. No.
                   10461
                   18849 2.R1040
Contig ID
5'-most EST
                   LIB3049-003-Q1-E1-G4
                   BLASTX
Method
                   q3004549
NCBI GI
BLAST score
                   155
E value
                   4.0e-13
                   95
Match length
                   48
% identity
NCBI Description
                   (AC003673) unknown protein [Arabidopsis thaliana]
                   >gi 4185152 (AC005724) unknown protein [Arabidopsis
                   thaliana]
                   10462
Seq. No.
                   18851_1.R1040
Contig ID
5'-most EST
                   LIB3049-003-Q1-E1-G6
Method
                   BLASTX
NCBI GI
                   g4105697
BLAST score
                   984
E value
                   1.0e-107
Match length
                   233
                   77
% identity
                   (AF049870) thaumatin-like protein [Arabidopsis thaliana]
NCBI Description
                   10463
Seq. No.
                   18851_3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy106b10b1
Method
                   BLASTX
                                             L_{\mathcal{P}_{\mathbf{q}}}
NCBI GI
                   g4105697.
BLAST score
                   369
E value
                   3.0e-35
Match length
                   86
                   74
% identity
NCBI Description
                   (AF049870) thaumatin-like protein [Arabidopsis thaliana]
                   10464
Seq. No.
Contig ID
                   18852 1.R1040
5'-most EST
                   LIB3170-024-Q1-K1-A1
Method
                   BLASTX
                   g3036840
NCBI GI
BLAST score
                   216
E value
                   1.0e-17
Match length
                   87
% identity
NCBI Description
                   (AJ222967) cystinosin [Homo sapiens]
                   >gi_3036851_emb_CAA75882_ (Y15924) cystinosin [Homo
                   sapiens]
```

10465

Seq. No.

```
18865 1.R1040
Contig ID
5'-most EST
                   LIB3049-003-Q1-E1-E8
                   BLASTX
Method
NCBI GI
                   g3228517
BLAST score
                   263
E value
                   7.0e-23
                   97
Match length
                   63
% identity
NCBI Description
                   (AF007788) ETTIN [Arabidopsis thaliana]
                   10466
Seq. No.
                   18867 1.R1040
Contig ID
                   rca701002296.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3080393
BLAST score
                   963
                   1.0e-104
E value
                   290
Match length
% identity
                   63
                   (AL022603) NADH dehydrogenase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   10467
Seq. No.
                   18867 2.R1040
Contig ID
5'-most EST
                   LIB3138-050-Q1-N1-A6
Method
                   BLASTX
                   g3080393
NCBI GI
                   289
BLAST score
                   5.0e-26
E value
                   86
Match length
                   66
% identity
NCBI Description
                   (AL022603) NADH dehydrogenase like protein [Arabidopsis
                   thaliana]
                   10468
Seq. No.
                   18875 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir070h12b1
Method
                   BLASTX
NCBI GI
                   g3927825
BLAST score
                   1660
                   0.0e + 00
E value
Match length
                   347
% identity
                   91
                   (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   10469
Seq. No.
Contig ID
                   18875 2.R1040
5'-most EST
                   LIB3139-050-P1-N1-F9
                   BLASTX
Method
                   g2351580
NCBI GI
BLAST score
                   583
E value
                   3.0e-60
Match length
                   132
                   85
% identity
NCBI Description
                   (U82433) thymidine diphospho-glucose 4-6-dehydratase
                   homolog [Prunus armeniaca]
```

NCBI GI

```
10470
Seq. No.
                   18875 3.R1040
Contig ID
5'-most EST
                   LIB3139-040-P1-N1-F6
Method
                   BLASTX
                   g2351580
NCBI GI
BLAST score
                   550
                   3.0e-56
E value
Match length
                   125
% identity
NCBI Description
                   (U82433) thymidine diphospho-glucose 4-6-dehydratase
                   homolog [Prunus armeniaca]
                   10471
Seq. No.
Contig ID
                   18875 4.R1040
                   LIB3049-003-Q1-E1-C5
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3927825
BLAST score
                   403
E value
                   2.0e-39
Match length
                   81
% identity
                   93
                   (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   10472
Seq. No.
Contig ID
                   18875 5.R1040
5'-most EST
                   ncj70\overline{0}984373.h1
Seq. No.
                   10473
Contig ID
                   18875 6.R1040
5'-most EST
                   asn70\overline{1}131968.h1
Method
                   BLASTX
NCBI GI
                   q3927825
BLAST score
                   451
E value
                   7.0e-45
Match length
                   99
% identity
                   88
NCBI Description
                   (AC005727) putative dTDP-glucose 4-6-dehydratase
                   [Arabidopsis thaliana]
                   10474
Seq. No.
Contig ID
                   18884 1.R1040
5'-most EST
                   LIB3049-003-Q1-E1-D2
Method
                   BLASTX
                   g3445201
NCBI GI
BLAST score
                   268
                   5.0e-23
E value
Match length
                   224
% identity
NCBI Description
                   (AC004786) unknown protein [Arabidopsis thaliana]
Seq. No.
                   10475
                   18885 1.R1040
Contig ID
                   LIB3170-022-Q1-K1-A8
5'-most EST
Method
                   BLASTX
```

g3176687

Method

BLASTX

```
BLAST score
                   613
E value
                   1.0e-63
Match length
                   160
% identity
                   74
NCBI Description
                   (AC003671) Strong similarity to trehalose-6-phosphate
                   synthase homolog from A. thaliana chromosome 4 contig
                   gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and
                   gb_R64855 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   18893 1.R1040
Contig ID
5'-most EST
                   fua701040501.h1
Method
                   BLASTX
NCBI GI
                   q3298536
BLAST score
                   259
E value
                   2.0e-22
Match length
                   106
                   60
% identity
                   (AC004681) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10477
Contig ID
                   18896 1.R1040
5'-most EST
                   fde700871557.hl
Method
                   BLASTX
NCBI GI
                   q3702339
BLAST score
                   990
                                                                     . .
E value
                   1.0e-107
Match length
                   321
% identity
                   60
NCBI Description
                   (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                   10478
                   18896 2.R1040
Contig ID
5'-most EST
                   zzp700830352.h1
Method
                   BLASTX
NCBI GI
                   g3702339
BLAST score
                   153
                   5.0e-10
E value
                   51
Match length
% identity
NCBI Description
                   (AC005397) unknown protein [Arabidopsis thaliana]
                   10479
Seq. No.
                   18898 1.R1040
Contig ID
                  LIB3106-011-Q1-K1-F3
5'-most EST
Method
                  BLASTN
NCBI GI
                 . g3821780
BLAST score
                   36
E value
                   2.0e-10
Match length
                   48
                   67
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
                   10480
Seq. No.
                   18899 1.R1040
Contig ID
5'-most EST
                  LIB3049-003-Q1-E1-B5
```

5'-most EST

```
. . . . . .
NCBI GI
                   q4469014
BLAST score
                   194
E value
                   1.0e-14
Match length
                   51
                   71
% identity
NCBI Description
                   (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   10481
                   18901_1.R1040
Contig ID
5'-most EST
                   LIB3170-023-Q1-J1-A7
Seq. No.
                   10482
                   18903 1.R1040
Contig ID
                   fua701039094.hl
5'-most EST
Method
                   BLASTX
                   g3157942
NCBI GI
BLAST score
                   264
E value
                   6.0e-38
Match length
                   231
% identity
NCBI Description
                   (ACO02131) Similar to style development-specific protein
                   9612 precursor gb X55193 and pectate lyase P59 precursor
                   gb X15499 from Lycopersicon esculentum. [Arabidopsis
                   thalianal
                   10483
Seq. No.
                   18903 2.R1040
Contig ID
5'-most EST
                   uC-qmrominsoy303a12b1
                   10484
Seq. No.
Contig ID
                   18905 1.R1040
5'-most EST
                   LIB3049-003-Q1-E1-C10
Seq. No.
                   10485
                   18906 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910071h05a1
                   10486
Seq. No.
                   18906 2.R1040
Contig ID
5'-most EST
                   jC-qmle01810055c08a1
Method
                   BLASTX
NCBI GI
                   q1871181
BLAST score
                   288
E value
                   2.0e-25
Match length
                   170
% identity
NCBI Description
                   (U90439) ring zinc finger protein isolog [Arabidopsis
                   thaliana]
                   10487
Seq. No.
Contig ID
                   18906 4.R1040
5'-most EST
                   LIB3052-012-Q1-N1-A12
                   10488
Seq. No.
Contig ID
                   18910 1.R1040
```

LIB3107-017-Q1-K1-H9



Seq. No. 10489

Contig ID 18915_1.R1040

5'-most EST LIB3049-002-Q1-E1-H7

Seq. No. 10490

Contig ID 18923_1.R1040

5'-most EST LIB3170-022-Q1-K1-A2

Method BLASTX
NCBI GI g1418321
BLAST score 140
E value 1.0e-08
Match length 35
% identity 40

NCBI Description (X98669) C2H2 zinc finger protein [Arabidopsis thaliana]

>gi_2317903 (U89959) C2H2 zinc finger protein [Arabidopsis

thaliana]

Seq. No. 10491

Contig ID 18926 1.R1040

5'-most EST LIB3049-003-Q1-E1-A7

Seq. No. 10492

Contig ID 18932 1.R1040

5'-most EST LIB3049-002-Q1-E1-G1

Seq. No. 10493

Contig ID 18933_1.R1040 5'-most EST seb700653121.h1

Seq. No. 10494

Contig ID 18935 1.R1040

5'-most EST LIB30 $\overline{5}1$ -002-Q1-E1-C8

Method BLASTX
NCBI GI g3193316
BLAST score 454
E value 2.0e-57
Match length 160

Match length 160 % identity 72

NCBI Description (AF069299) contains similarity to nucleotide sugar

epimerases [Arabidopsis thaliana]

Seq. No. 10495

Contig ID 18935_2.R1040 5'-most EST kl1701209745.h1

Seq. No. 10496

Contig ID 18938 1.R1040

5'-most EST LIB3138-038-Q1-N1-G5

Seq. No. 10497

Contig ID 18938_2.R1040 5'-most EST txt700732831.h1

Seq. No. 10498

Contig ID 18939_2.R1040

5'-most EST LIB3049-002-Q1-E1-G5

Method BLASTN

Method

BLASTX

```
g493019
NCBI GI
                   38
BLAST score
                   6.0e-12
E value
Match length
                   92
% identity
                   86
                   Glycine max delta-aminolevulinic acid dehydratase (Alad)
NCBI Description
                   mRNA, complete cds
                   10499
Seq. No.
Contig ID
                   18941 1.R1040
5'-most EST
                   LIB3139-122-P1-N1-E6
Method
                   BLASTX
                   q4204314
NCBI GI
BLAST score
                   284
E value
                   4.0e-25
                   176
Match length
                   38
% identity
NCBI Description
                   (AC003027) Hypothetical protein [Arabidopsis thaliana]
                   10500
Seq. No.
Contig ID
                   18949_1.R1040
5'-most EST
                   LIB3170-024-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g1684913
                   455
BLAST score
                   1.0e-45
E value
Match length
                   119
                   76
% identity
                   (U77888) receptor-like protein kinase [Ipomoea nil]
NCBI Description
                   10501
Seq. No.
                   18952 1.R1040
Contig ID
5'-most EST
                   LIB3049-002-Q1-E1-E5
                   10502
Seq. No.
                   18954 1.R1040
Contig ID
5'-most EST
                   LIB3049-002-Q1-E1-E7
                   10503
Seq. No.
                   18956 1.R1040
Contig ID
                   zhf700957433.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2598575
BLAST score
                   493
E value
                   3.0e-49
Match length
                   331
                   34
% identity
NCBI Description
                   (Y15293) MtN21 [Medicago truncatula]
                   10504
Seq. No.
                   18956_2.R1040
Contig ID
5'-most EST
                   jC-gmst02400025e02a1
                   10505
Seq. No.
                   18956_3.R1040
Contig ID
5'-most EST
                   q4291\overline{2}04
```

```
NCBI GI
                   g3355480
BLAST score
                   262
                   2.0e-22
E value.
                   118
Match length
                   42
% identity
                   (AC004218) Medicago nodulin N21-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   10506
Seq. No.
                   18956 4.R1040
Contig ID
                   LIB3107-067-Q1-K1-H1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2598575
BLAST score
                   171
                   1.0e-12
E value
                   112
Match length
% identity
                   36
                   (Y15293) MtN21 [Medicago truncatula]
NCBI Description
                   10507
Seq. No.
                   18956 6.R1040
Contig ID
5'-most EST
                   zzp700831260.hl
Method
                   BLASTX
NCBI GI
                   g3482913
BLAST score
                   172
                   2.0e-12
E value
Match length
                   108
% identity
                   33
                   (AC003970) Similar to MtN21, gi 2598575, Megicago
NCBI Description
                   truncatula nodulation induced gene [Arabidopsis thaliana]
                   10508
Seq. No.
Contig ID
                   18963 1.R1040
5'-most EST
                   LIB3049-002-Q1-E1-C4
Method
                   BLASTX
NCBI GI
                   g2827536
BLAST score
                   425
                   2.0e-41
E value
Match length
                   121
% identity
                   (AL021633) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   10509
Seq. No.
                   18964 1.R1040
Contig ID
5'-most EST
                   LIB3106-111-Q1-K1-E2
                   10510
Seq. No.
                   18964 2.R1040
Contig ID
5'-most EST
                   wrg700789867.h2
Seq. No.
                   10511
Contig ID
                   18967_1.R1040
5'-most EST
                   LIB3049-002-Q1-E1-C9
Method
                   BLASTX
NCBI GI
                   g3953461
                   303
BLAST score
```

2.0e-27

E value

```
Match length
                  101
% identity
                  56
NCBI Description
                  (AC002328) F20N2.6 [Arabidopsis thaliana]
Seq. No.
                  10512
                  18968 1.R1040
Contig ID
                  awf700838162.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q626464
BLAST score
                  181
E value
                  5.0e-13
Match length
                  68
% identity
                  43
NCBI Description
                  VPS27 protein - yeast (Saccharomyces cerevisiae)
                  >gi_496723_emb_CAA54574_ (X77395) N2038 [Saccharomyces
                  cerevisiae] >gi 1302478 emb CAA96282 (Z71620) ORF YNR006w
                   [Saccharomyces cerevisiae]
                  10513
Seq. No.
                  18968_2.R1040
Contig ID
5'-most EST
                  LIB3065-006-Q1-N1-F3
Method
                  BLASTX
NCBI GI
                  g626464
BLAST score
                  180
E value
                  2.0e-13
Match length
                  68
% identity
                  43
NCBI Description
                  VPS27 protein - yeast (Saccharomyces cerevisiae)
                  >gi_496723_emb_CAA54574_ (X77395) N2038 [Saccharomyces
                  cerevisiae] >gi 1302478 emb CAA96282 (Z71620) ORF YNR006w
                   [Saccharomyces cerevisiae]
                  10514
Seq. No.
                  18970_1.R1040
Contig ID
                  LIB3170-023-Q1-K1-H9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g732311
BLAST score
                  158
E value
                  2.0e-10
Match length
                  100
                  38
% identity
                  HYPOTHETICAL 15.7 KD PROTEIN IN PBPD-COMA INTERGENIC REGION
NCBI Description
                   (ORF2) >gi_1075880_pir__B55220 pbpD 3'-region hypothetical
                  protein - Bacillus subtilis >gi_520537 (U11882) unknown
                   [Bacillus subtilis] >gi_1934785_emb_CAB07916_ (Z93933)
                  unknown [Bacillus subtilis] >gi 2635646 emb CAB15139
                   (Z99120) alternate gene name: yugD [Bacillus subtilis]
Seq. No.
                  10515
Contig ID
                  18979 1.R1040
5'-most EST
                  LIB3170-017-Q1-K1-H9
                  BLASTX
Method
NCBI GI
                  g3831454
BLAST score
                  198
E value
                  4.0e-15
                  74
Match length
```

57

% identity

Contig ID

```
NCBI Description (AC005700) hypothetical protein [Arabidopsis thaliana]
                   10516
Seq. No.
Contig ID
                   18988 1.R1040
5'-most EST
                   LIB3051-024-Q1-K1-E3
                   10517
Seq. No.
                   18991 1.R1040
Contig ID
5'-most EST
                   LIB3170-024-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   g1001650
BLAST score
                   183
                   3.0e-13
E value
                   70
Match length
% identity
                   50
                   (D64002) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   10518
Contig ID
                   18992 1.R1040
5'-most EST
                   dpv701099639.h1
Method
                   BLASTX
                   g4539302
NCBI GI
BLAST score
                   384
E value
                   4.0e-37
                   94
Match length
                   79
% identity
NCBI Description
                   (AL049480) putative protein [Arabidopsis thaliana]
                   10519
Seq. No.
                   18995 1.R1040
Contig ID
5'-most EST
                   LIB3049-001-Q1-E1-H12
                   10520
Seq. No.
                   19001_1.R1040
Contig ID
5'-most EST
                   LIB3049-001-Q1-E1-H7
Method
                   BLASTX
NCBI GI
                   g4309732
BLAST score
                   229
E value
                   1.0e-18
Match length
                   128
                   41
% identity
NCBI Description
                   (AC006439) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   10521
Contig ID
                   19003 1.R1040
5'-most EST
                   uC-gmflminsoy059c11b1
Method
                   BLASTX
                   g3355480
NCBI GI
BLAST score
                   715
E value
                   2.0e-75
Match length
                   277
% identity
NCBI Description
                   (AC004218) Medicago nodulin N21-like protein [Arabidopsis
                   thaliana]
                   10522
Seq. No.
```

19013 1.R1040

5'-most EST

```
5'-most EST
                   LIB3106-036-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g3643606
BLAST score
                   298
E value
                   1.0e-26
                   158
Match length
                   38
% identity
NCBI Description
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   10523
                   19027 1.R1040
Contig ID
5'-most EST
                   LIB3049-001-Q1-E1-H1
Seq. No.
                   10524
Contig ID
                   19030 1.R1040
5'-most EST
                   LIB3049-001-Q1-E1-E10
Seq. No.
                   10525
Contig ID
                   19038 1.R1040
5'-most EST
                   qsv70\overline{1}053435.h1
Method
                   BLASTN
NCBI GI
                   q3204107
BLAST score
                   215
E value
                   1.0e-117
Match length
                   475
% identity
NCBI Description
                   Cicer arietinum mRNA for putative cytidine or
                   deoxycytidylate deaminase, partial
                   10526
Seq. No.
                   19038 2.R1040
Contig ID
5'-most EST
                   leu701156293.hl
Method
                   BLASTN
NCBI GI
                   q3204107
BLAST score
                   323
E value
                   0.0e + 00
Match length
                   539
% identity
                   Cicer arietinum mRNA for putative cytidine or
NCBI Description
                   deoxycytidylate deaminase, partial
Seq. No.
                   10527
Contig ID
                   19038 4.R1040
5'-most EST
                   LIB3051-038-Q1-K1-A12
Method
                   BLASTN
NCBI GI
                   g3204107
BLAST score
                   255
E value
                   1.0e-141
Match length
                   427
% identity
                   89
NCBI Description
                   Cicer arietinum mRNA for putative cytidine or
                   deoxycytidylate deaminase, partial
                   10528
Seq. No.
Contig ID
                   19045 1.R1040
```

LIB3049-001-Q1-E1-C1



Seq. No. 10529

Contig ID 19048_1.R1040 5'-most EST kl1701208113.h1

Seq. No. 10530

Contig ID 19050_1.R1040

5'-most EST LIB3049-001-Q1-E1-C4

Method BLASTX
NCBI GI g3367537
BLAST score 148
E value 8.0e-10
Match length 70
% identity 49

NCBI Description (AC004392) Contains similarity to ANK repeat region of

Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from Caenorhabditis elegans cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375.

[Arabid

Seq. No. 10531

Contig ID 19063 1.R1040

5'-most EST LIB3049-001-Q1-E1-D6

Seq. No. 10532

Contig ID 19065 1.R1040

E value 3.0e-42 Match length 124 % identity 63

NCBI Description endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG2)

- common nasturtium (fragment) >gi_311837_emb_CAA48325_

(X68255) cellulase [Tropaeolum majus]

Seq. No. 10533

Contig ID 19067_1.R1040

5'-most EST LIB3049-001-Q1-E1-A7

Seq. No. 10534

Contig ID 19069 1.R1040

5'-most EST LIB3170-020-Q1-K1-H6

Seq. No. 10535

Contig ID 19071 1.R1040

5'-most EST LIB3049-001-Q1-E1-B12

Seq. No. 10536

Contig ID 19093 1.R1040

5'-most EST LIB3050-022-Q1-K1-A7

Seq. No. 10537

Contig ID 19093 2.R1040

5'-most EST LIB3049-008-Q1-E1-A4

Seq. No. 10538

```
19094 1.R1040
Contig ID
5'-most EST
                   LIB3049-009-Q1-E1-C3
Seq. No.
                   10539
                   19095 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy058e07b1
                   BLASTX
Method
NCBI GI
                   g1944407
BLAST score
                   493
E value
                   5.0e-49
Match length
                   312
% identity
                   41
                   (D86988) KIAA0221 [Homo sapiens]
NCBI Description
Seq. No.
                   10540
                   19095 2.R1040
Contig ID
5'-most EST
                   rlr700902272.h1
Method
                   BLASTX
NCBI GI
                   g1944407
BLAST score
                   512
E value
                   5.0e-52
Match length
                   124
                   75
% identity
NCBI Description
                   (D86988) KIAA0221 [Homo sapiens]
                   10541
Seq. No.
Contig ID
                   19096 1.R1040
5'-most EST
                   LIB3049-010-Q1-E1-A7
                   10542
Seq. No.
Contig ID
                   19097 1.R1040
                   LIB3049-010-Q1-E1-H10
5'-most EST
                   10543
Seq. No.
Contig ID
                   19106_1.R1040
5'-most EST
                   g5175461
Method
                   BLASTX
                   g4006875
NCBI GI
BLAST score
                   179
E value
                   1.0e-12
                   73
Match length
                   59
% identity
NCBI Description
                   (Z99707) putative protein [Arabidopsis thaliana]
                   10544
Seq. No.
                   19106 2.R1040
Contig ID
5'-most EST
                   LIB30\overline{4}9-012-Q1-E1-H4
Seq. No.
                   10545
                   19106 3.R1040
Contig ID
5'-most EST
                   wvk700682411.h2
Seq. No.
                   10546
                   19111 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy173e11b1
Seq. No.
                   10547
```

٠.

```
19116 1.R1040
Contig ID
5'-most EST
                  LIB3170-026-Q1-K1-D1
                  BLASTX
Method
                  g2088647
NCBI GI
BLAST score
                  756
                  3.0e-80
E value
Match length
                  279
% identity
NCBI Description
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
                  >gi_3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                  10548
Seq. No.
                  19122 1.R1040
Contig ID
5'-most EST
                  LIB3170-026-01-K1-G3
                  10549
Seq. No.
                  19125 1.R1040
Contig ID
                  LIB3049-022-Q1-E1-H12
5'-most EST
Method
                  BLASTX
                  g2739369
NCBI GI
                  594
BLAST score
E value
                  1.0e-61
Match length
                  133
% identity
                  81
                   (AC002505) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                  10550
Seq. No.
                  19132 1.R1040
Contig ID
                  LIB3106-100-Q1-K1-A3
5'-most EST
Method
                  BLASTX
                   g4538929
NCBI GI
BLAST score
                   326
E value
                   6.0e-30
Match length
                   113
                   60
% identity
NCBI Description
                   (AL049483) putative nucleic acid binding protein
                   [Arabidopsis thaliana]
                  10551
Seq. No.
Contig ID
                   19139 1.R1040
5'-most EST
                  LIB3049-029-Q1-E1-C6
Seq. No.
                  10552
                   19139 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810093e08a1
                  10553
Seq. No.
Contig ID
                   19143 1.R1040
                  LIB3049-029-Q1-E1-E5
5'-most EST
                  10554
Seq. No.
Contig ID
                  19144 1.R1040
                  LIB3049-029-Q1-E1-F11
5'-most EST
                  BLASTX
Method
                   q4191783
NCBI GI
```

188

BLAST score

```
7.0e-14
E value
                ु: 55
Match length
                  60
% identity
                  (AC005917) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  10555
Seq. No.
                  19144 2.R1040
Contig ID
5'-most EST
                  uC-qmflminsoy025g03b1
Seq. No.
                   19145 1.R1040
Contig ID
5'-most EST
                  LIB3049-029-Q1-E1-F5
                  BLASTX
Method
NCBI GI
                  q3687460
BLAST score
                  127
                   6.0e-11
E value
Match length
                  99
                   49
% identity
                   (AL031798) putative leucine permease transcriptional
NCBI Description
                  regulator. [Schizosaccharomyces pombe]
                   10557
Seq. No.
Contig ID
                   19146_1.R1040
5'-most EST
                   LIB3167-077-P1-K2-A3
Method
                   BLASTX
NCBI GI
                   q3927838
BLAST score
                   416
                   1.0e-40
E value
                   117
Match length
                   68
% identity
NCBI Description
                   (AC005727) unknown protein [Arabidopsis thaliana]
                   10558
Seq. No.
                   19146 2.R1040
Contig ID
                   LIB3049-029-Q1-E1-H12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3927838
BLAST score
                   165
                   2.0e-11
E value
                   40
Match length
                   72
% identity
NCBI Description
                   (AC005727) unknown protein [Arabidopsis thaliana]
                   10559
Seq. No.
                   19148 1.R1040
Contig ID
5'-most EST
                   LIB3049-030-Q1-E1-F4
Seq. No.
                   10560
Contig ID
                   19149 1.R1040
5'-most EST
                   LIB3109-011-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   q2795806
BLAST score
                   287
                   7.0e-33
E value
Match length
                   152
% identity
                   (AC003674) unknown protein [Arabidopsis thaliana]
NCBI Description
```

450

```
10561
Seq. No.
                   19150 1.R1040
Contig ID
5'-most EST
                   uaw700666775.h1
                   BLASTX
Method
NCBI GI
                   q3297818
BLAST score
                   271
                   6.0e-24
E value
Match length
                   100
                   45
% identity
                   (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10562
                   19150 2.R1040
Contig ID
5'-most EST
                   zzp700830822.hl
Method
                   BLASTX
                   g3297818
NCBI GI
BLAST score
                   149
E value
                   3.0e-19
Match length
                   99
% identity
                   45
NCBI Description
                   (AL031032) putative protein [Arabidopsis thaliana]
                   10563
Seq. No.
Contig ID
                   19152 1.R1040
5'-most EST
                   LIB3049-033-Q1-E1-C8
                   10564
Seq. No.
                   19153 1.R1040
Contig ID
5'-most EST
                   LIB3049-033-Q1-E1-G12
Seq. No.
                   10565
Contig ID
                   19160 1.R1040
5'-most EST
                   LIB3170-031-Q1-K1-A10
                   10566
Seq. No.
Contig ID
                   19167 1.R1040
5'-most EST
                   LIB3170-085-Q1-J1-A7
                   BLASTX
Method
NCBI GI
                   q3980412
BLAST score
                   481
E value
                   2.0e-53
Match length
                   205
% identity
NCBI Description
                   (AC004561) pumilio-like protein [Arabidopsis thaliana]
Seq. No.
                   10567
Contig ID
                   19171_1.R1040
5'-most EST
                   LIB3093-022-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   g3924612
BLAST score
                   540
E value
                   5.0e-55
Match length
                   198
% identity
                   61
NCBI Description
                   (AF069442) mitochondrial elongation factor Tu [Arabidopsis
```

thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial

NCBI GI

elongation factor Tu [Arabidopsis thaliana]

```
Seq. No.
                  10568
                  19175_1.R1040
Contig ID
                  LIB3049-047-Q1-E1-G8
5'-most EST
                  BLASTX
Method
                  q1076715
NCBI GI
                  278
BLAST score
E value
                  2.0e-24
                  92
Match length
                  53
% identity
                  abscisic acid-induced protein HVA22 - barley >gi_404589
NCBI Description
                  (L19119) A22 [Hordeum vulgare]
                  10569
Seq. No.
                  19180 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy186e08b1
                  BLASTX
Method
NCBI GI
                  g3142301
BLAST score
                  295
E value
                  2.0e-26
                  101
Match length
                  63
% identity
                  (AC002411) Contains similarity to neural cell adhesion
NCBI Description
                  molecule 2, large isoform precursor gb_M76710 from Xenopus
                  laevis, and beta transducin from S. cerevisiae gb Q05946.
                  ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101,
                  gb H3630
                  10570
Seq. No.
                  19182 1.R1040
Contig ID
5'-most EST
                  LIB3049-051-Q1-E1-F5
                  BLASTX
Method
                  g2262159
NCBI GI
BLAST score
                  961
                  1.0e-104
E value
Match length
                  265
% identity
                  (ACO02329) predicted protein similar to S.pombe protein
NCBI Description
                  C5H10.03 [Arabidopsis thaliana]
                  10571
Seq. No.
Contig ID
                  19185 1.R1040
                  LIB3170-035-Q1-K1-A12
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4539351
BLAST score
                  289
E value
                  9.0e-26
Match length
                  160
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                  10572
Seq. No.
                  19201 1.R1040
Contig ID
                  LIB3106-100-Q1-K1-H11
5'-most EST
Method
                  BLASTX
```

q4105772

```
740
BLAST score
E value
                   2.0e-78
Match length
                   180
                   70
% identity
NCBI Description
                    (AF049917) PGP9B [Petunia x hybrida]
                   10573
Seq. No.
                   19203_1.R1040
Contig ID
5'-most EST
                   k1170\overline{1}214886.h1
                   10574
Seq. No.
Contig ID
                   19212 1.R1040
5'-most EST
                   g4396976
Method
                   BLASTX
NCBI GI
                   g3334230
BLAST score
                   1143
E value
                   1.0e-125
Match length
                   441
                   50
% identity
                   D-HYDANTOINASE (DIHYDROPYRIMIDINASE) (DHPASE) >qi 2828803
NCBI Description
                    (U84197) D-hydantoinase [Pseudomonas putida]
                   10575
Seq. No.
Contig ID
                   19212 2.R1040
5'-most EST
                   LIB31\overline{0}9-038-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   g3334230
BLAST score
                   450
                   9.0e-80
E value
Match length
                   315
                   51
% identity
                   D-HYDANTOINASE (DIHYDROPYRIMIDINASE) (DHPASE) >gi 2828803
NCBI Description
                    (U84197) D-hydantoinase [Pseudomonas putida]
                   10576
Seq. No.
                   19212 3.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy118d03b1
Seq. No.
                   10577
Contig ID
                   19215 1.R1040
5'-most EST
                   LIB3050-028-Q1-E1-G8
                   10578
Seq. No.
Contig ID
                   19216 1.R1040
                   LIB3139-044-P1-N1-F12
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2146775
BLAST score
                   438
                   6.0e-86
E value
Match length
                   342
                   52
% identity
NCBI Description
                   serine acetyltransferase (EC 2.3.1.30) SAT1 - Arabidopsis
                   thaliana >gi_926939 (L42212) serine acetyltransferase
                    [Arabidopsis thaliana]
                   10579
Seq. No.
```

19218 1.R1040

Contig ID

```
5'-most EST
                  LIB3050-028-Q1-E1-H10 &
Method
                  BLASTX
NCBI GI
                  q4314361
BLAST score
                  216
                  2.0e-17
E value
Match length
                   44
                   95
% identity
                   (AC006340) unknown protein [Arabidopsis thaliana]
NCBI Description
                  10580
Seq. No.
                  19218 2.R1040
Contig ID
5'-most EST
                  uC-gmropic100h07b1
Method
                  BLASTX
NCBI GI
                   g4314361
BLAST score
                   222
                   5.0e-18
E value
                   45
Match length
                   96
% identity
                   (AC006340) unknown protein [Arabidopsis thaliana]
NCBI Description
                  10581
Seq. No.
Contig ID
                  19223 1.R1040
5'-most EST
                  jC-gmle01810053c09a1
Method
                  BLASTX
                  g4006899
NCBI GI
BLAST score
                   482
E value
                   2.0e-48
Match length
                  138
% identity
                   64
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                  10582
Seq. No.
                  19223 3.R1040
Contig ID
                  rca701001718.hl
5'-most EST
                  10583
Seq. No.
                  19229 2.R1040
Contig ID
5'-most EST
                  ssr700556492.h1
Seq. No.
                  10584
                  19229 3.R1040
Contig ID
5'-most EST
                   6HC-02-Q1-B1-E8
Seq. No.
                  10585
                  19229 4.R1040
Contig ID
                  LIB3139-022-P1-N1-D5
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1665817
BLAST score
                  175
E value
                  2.0e-12
Match length
                  68
% identity
                  47
                   (D87466) Similar to S.cerevisiae hypothetical protein L3111
NCBI Description
                   (S59316) [Homo sapiens]
                  10586
Seq. No.
```

19231 1.R1040

Contig ID

5'-most EST

```
5'-most EST
                   fC-gmst700652392f1
                   10587
Seq. No.
Contig ID
                   19234 1.R1040
                   asn70\overline{1}135274.h1
5'-most EST
Method
                   BLASTX
                   q2464852
NCBI GI
                   316
BLAST score
E value
                   4.0e-29
                   124
Match length
% identity
                   (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
                   10588
Seq. No.
Contig ID
                   19235 1.R1040
                   LIB3139-041-P1-N1-F8
5'-most EST
Method
                   BLASTX
                   g3157951
NCBI GI
BLAST score
                   710
E value
                   3.0e-93
Match length
                   217
                   85
% identity
                   (AC002131) Contains similarity to vesicle trafficking
NCBI Description
                   protein gb_U91538 from Mus musculus. ESTs gb_F15494 and
                   gb F14097 come from this gene. [Arabidopsis thaliana]
                   10589
Seq. No.
                   19235 2.R1040
Contig ID
                   hrw701062691.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3157951
BLAST score
                   284
                   2.0e-25
E value
Match length
                   64
                   84
% identity
NCBI Description
                   (AC002131) Contains similarity to vesicle trafficking
                   protein gb_U91538 from Mus musculus. ESTs gb_F15494 and
                   gb F14097 come from this gene. [Arabidopsis thaliana]
                   10590
Seq. No.
                   19235 3.R1040
Contig ID
5'-most EST
                   zsg70\overline{1}117409.h1
                   10591
Seq. No.
                   19237 1.R1040
Contig ID
                   uC-gmflminsoy022d12b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4218062
BLAST score
                   374
                   1.0e-35
E value
Match length
                   172
% identity
                   42
NCBI Description
                   (AB015906) actin-related protein [Homo sapiens]
                   10592
Seq. No.
                   19240 1.R1040
Contig ID
```

LIB3072-051-Q1-E1-A9

```
BLASTX
Method
NCBI GI
                   g4539348
BLAST score
                   934
                   1.0e-101
E value
Match length
                   247
% identity
                   68
                   (AL035539) putative pollen allergen [Arabidopsis thaliana]
NCBI Description
                   10593
Seq. No.
                   19240_2.R1040
Contig ID
                   LIB3139-085-P1-N1-D11
5'-most EST
                   BLASTX
Method
                   g4539348
NCBI GI
BLAST score
                   198
                   8.0e-26
E value
                   99
Match length
% identity
                   62
                   (AL035539) putative pollen allergen [Arabidopsis thaliana]
NCBI Description
                   10594
Seq. No.
                   19240 3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy169c10b1
Method
                   BLASTX
NCBI GI
                   g4539348
                   347
BLAST score
                   1.0e-32
E value
Match length
                   86
% identity
                   (AL035539) putative pollen allergen [Arabidopsis thaliana]
NCBI Description
                   10595
Seq. No.
Contig ID
                   19242 1.R1040
5'-most EST
                   LIB3050-002-Q1-E1-D5
                   10596
Seq. No.
Contig ID
                   19242 2.R1040
                   LIB3107-061-Q1-K1-F12
5'-most EST
                   10597
Seq. No.
Contig ID
                   19246 1.R1040
                   jC-gmst02400036g10d2
5'-most EST
                   10598
Seq. No.
Contig ID
                   19247 1.R1040
                   jC-gmf102220061a10a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4006875
BLAST score
                   323
E value
                   8.0e-30
Match length
                   113
% identity
                   64
NCBI Description
                   (Z99707) putative protein [Arabidopsis thaliana]
                   10599
Seq. No.
                   19248 1.R1040
Contig ID
```

dpv701102923.h1

5'-most EST

BLAST score

E value

337

2.0e-31

```
10600
Seq. No.
                  19248 2.R1040
Contig ID
5'-most EST
                  LIB3107-036-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                   g2245060
BLAST score
                  280
E value
                   9.0e-25
Match length
                  76
% identity
                   64
NCBI Description
                   (Z97342) allergen homolog [Arabidopsis thaliana]
Seq. No.
                   10601
                   19250 1.R1040
Contig ID
                  LIB3050-028-Q1-E1-C4
5'-most EST
Seq. No.
                   10602
Contig ID
                   19252 1.R1040
5'-most EST
                  wvk700685013.hl
Method
                  BLASTX
                   g3281850
NCBI GI
BLAST score
                   788
E value
                   3.0e-84
Match length
                  175
% identity
                   (AL031004) monogalactosyldiacylglycerol synthase - like
NCBI Description
                  protein [Arabidopsis thaliana]
                   10603
Seq. No.
                   19255 1.R1040
Contig ID
                  uC-gmflminsoy080g12b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2213610
BLAST score
                   245
                   3.0e-20
E value
                  150
Match length
% identity
NCBI Description
                   (AC000103) F21J9.4 [Arabidopsis thaliana]
                   10604
Seq. No.
Contig ID
                   19257 1.R1040
5'-most EST
                  LIB3050-027-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                  q4314390
BLAST score
                   396
E value
                   4.0e-38
Match length
                  142
% identity
                   54
NCBI Description
                   (AC006232) putative calcium binding protein [Arabidopsis
                   thaliana]
                  10605
Seq. No.
Contig ID
                   19257 2.R1040
5'-most EST
                   zsg701124230.h1
Method
                  BLASTX
NCBI GI
                  g4314390
```





99 -Match length 61 % identity (AC006232) putative calcium binding protein [Arabidopsis NCBI Description thaliana] 10606 Seq. No. 19257 3.R1040 Contig ID uaw700664521.hl 5'-most EST Method BLASTX NCBI GI g4314390 BLAST score 200 2.0e-15 E value 80 Match length % identity 54 (AC006232) putative calcium binding protein [Arabidopsis NCBI Description thaliana] 10607 Seq. No. 19257 4.R1040 Contig ID uC-gmflminsoy056h10b1 5'-most EST Seq. No. Contig ID 19259 1.R1040 5'-most EST LIB3050-027-Q1-E1-H6 Seq. No. 10609 19260 1.R1040 Contig ID 5'-most EST uC-gmrominsoy299e06b1 Method BLASTX NCBI GI g1743354 BLAST score 1475 1.0e-164 E value 484 Match length 57 % identity (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum] NCBI Description Seq. No. 10610 Contig ID 19262 1.R1040 uC-gmrominsoy223a06b1 5'-most EST Method BLASTX q4063742 NCBI GI BLAST score 218 4.0e-17 E value Match length 153 % identity 38 (AC005851) putative phaseolin G-box binding protein NCBI Description [Arabidopsis thaliana] Seq. No. 10611 19262 2.R1040 Contig ID rlr700900662.h1 5'-most EST

Seq. No. 10612

Contig ID 19263_1.R1040

5'-most EST LIB30 $\overline{5}1$ -067-Q1-K1-G10

Seq. No. 10613

```
Contig ID
                   19264 1.R1040
5'-most EST
                   dpv70\overline{1}102455.h1
Seq. No.
                   10614
Contig ID
                   19266 1.R1040
                   LIB3139-017-P1-N1-C1
5'-most EST
                   10615
Seq. No.
Contig ID
                   19267 1.R1040
5'-most EST
                   zhf700952901.h1
Method
                   BLASTX
NCBI GI
                   g2654868
BLAST score
                   306
                   4.0e-52
E value
Match length
                   174
% identity
                   66
                   (AF015301) RbohAp108 [Arabidopsis thaliana]
NCBI Description
                   10616
Seq. No.
                   19268 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220097f01a1
                   10617
Seq. No.
                   19268 2.R1040
Contig ID
5'-most EST
                   LIB3051-027-Q1-K1-G5
Seq. No.
                   10618
                   19274 1.R1040
Contig ID
5'-most EST
                   LIB3050-027-Q1-E1-F3
                   BLASTN
Method
NCBI GI
                   g287563
                   77
BLAST score
E value
                   6.0e-35
Match length
                   327
                   91
% identity
NCBI Description
                 Vigna radiata arg2 mRNA
Seq. No.
                   10619
                   19274 2.R1040
Contig ID
5'-most EST
                   LIB3050-006-Q1-E1-G12
Method
                   BLASTN
NCBI GI
                   g287563
BLAST score
                   90
                   1.0e-42
E value
Match length
                   338
                   90
% identity
NCBI Description
                   Vigna radiata arg2 mRNA
                   10620
Seq. No.
                   19275 1.R1040
Contig ID
                   LIB3139-084-P1-N1-H2
5'-most EST
                   10621
Seq. No.
                   19275 2.R1040
Contig ID
5'-most EST
                   asn70\overline{1}132347.h1
```

10622

Seq. No.

Method

BLASTX

```
19278 1.R1040
Contig ID
5'-most EST
                   kmv700737840.h1
Seq. No.
                   10623
Contig ID
                   19288 1.R1040
5'-most EST
                   sat701004275.hl
Method
                   BLASTX
NCBI GI
                   q2435511
BLAST score
                   449
E value
                   3.0e-44
Match length
                   144
                   58
% identity
                   (AF024504) contains similarity to prolyl 4-hydroxylase
NCBI Description
                   alpha subunit [Arabidopsis thaliana]
                   10624
Seq. No.
                   19288 2.R1040
Contig ID
5'-most EST
                   jex70\overline{0}906632.h1
                   10625
Seq. No.
Contig ID
                   19293 1.R1040
                   hrw701058172.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4455351
BLAST score
                   653
E value
                   5.0e-68
                   183
Match length
                   68
% identity
NCBI Description
                   (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                   10626
                   19293_2.R1040
Contig ID
                   LIB30\overline{5}1-037-Q1-K1-A1
5'-most EST
Method
                   BLASTX
                   g4455351
NCBI GI
BLAST score
                   298
E value
                   8.0e-27
Match length
                   82
                   66
% identity
NCBI Description
                   (AL035524) putative protein [Arabidopsis thaliana]
                   10627
Seq. No.
                   19299 1.R1040
Contig ID
                   leu70\overline{1}148775.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1651451
BLAST score
                   517
                   2.0e-52
E value
Match length
                   137
% identity
NCBI Description
                   (D90730) Asparaginyl-tRNA synthetase (EC 6.1.1.22)
                   (asparagine-tRNA ligase) (asnRS). [Escherichia coli]
Seq. No.
                   10628
                   19305 1.R1040
Contig ID
5'-most EST
                   LIB3050-021-Q1-K1-E2
```

Match length

95

```
NCBI GI
                   g1762933
BLAST score
                   476
                   2.0e-47
E value
                  203
Match length
                   49
% identity
NCBI Description
                  (U66263) tumor-related protein [Nicotiana tabacum]
                   10629
Seq. No.
                   19305 2.R1040
Contig ID
5'-most EST
                   leu701155692.h1
                  BLASTX
Method
NCBI GI
                   g1762933
BLAST score
                   291
                   3.0e-26
E value
                   95
Match length
% identity
                   63
                  (U66263) tumor-related protein [Nicotiana tabacum]
NCBI Description
                   10630
Seq. No.
                   19306_1.R1040
Contig ID
5'-most EST
                   LIB3050-027-Q1-E1-C8
                   10631
Seq. No.
                   19308 1.R1040
Contig ID
5'-most EST
                   LIB3109-031-Q1-K1-B3
Seq. No.
                   10632
                   19311 1.R1040
Contig ID
                   LIB3170-065-Q1-K1-C8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3367522
BLAST score
                   478
E value
                   5.0e-48
Match length
                   126
% identity
NCBI Description
                   (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   10633
Contig ID
                   19313 1.R1040
5'-most EST
                   gsv701052993.hl
Method
                   BLASTX
NCBI GI
                   g1688233
BLAST score
                   366
E value
                   2.0e-34
Match length
                   176
% identity
                   62
NCBI Description
                   (U77655) DNA binding protein homolog [Solanum tuberosum]
                   10634
Seq. No.
                   19313 2.R1040
Contig ID
5'-most EST
                   LIB3050-027-Q1-E1-B7
Method
                   BLASTX
NCBI GI
                   g1688233
BLAST score
                   235
                   1.0e-19
E value
```

```
% identity
                  (U77655) DNA binding protein homolog [Solanum tuberosum]
NCBI Description
                  10635
Seq. No.
                  19314_1.R1040
Contig ID
5'-most EST
                  LIB3050-027-Q1-E1-B8
Seq. No.
                  10636
                  19321 1.R1040
Contig ID
                  LIB3051-104-Q1-K1-A3
5'-most EST
                  BLASTX
Method
                  g125722
NCBI GI
BLAST score
                  502
                  1.0e-50
E value
                  194
Match length
                  58
% identity
                  KUNITZ-TYPE TRYPSIN INHIBITOR KTI1 PRECURSOR
NCBI Description
                  >gi 81814 pir JQ1091 trypsin inhibitor KTil (Kunitz) -
                  soybean >gi 256635 bbs 115028 (S45035) Kunitz trypsin
                  inhibitor KTil [soybeans, Peptide, 203 aa] [Glycine max]
*
Seq. No.
                  10637
                  19322 1.R1040
Contig ID
5'-most EST
                  uC-gmflminsoy049c02b1
Method
                  BLASTX
NCBI GI
                  q3033386
BLAST score
                  267
E value
                   1.0e-22
Match length
                   223
% identity
                   (ACO04238) RING3-like protein [Arabidopsis thaliana]
NCBI Description
                   10638
Seq. No.
                   19322 2.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy260e09b1
Seq. No.
                   10639
                   19322 5.R1040
Contig ID
5'-most EST
                  LIB3139-011-P1-N1-G11
                  10640
Seq. No.
                   19326 1.R1040
Contig ID
5'-most EST
                   txt700735881.hl
                  10641
Seq. No.
                  19329 1.R1040
Contig ID
5'-most EST
                  g4289596
Method
                  BLASTX
NCBI GI 4
                   q1050956
BLAST score
                   314
                   2.0e-28
E value
Match length
                   242
% identity
                   36
                   (U26160) 43 kDa secreted glycoprotein precursor
NCBI Description
                   [Paracoccidioides brasiliensis] >gi_1588394_prf__2208385A
```

glycoprotein gp43 [Paracoccidioides brasiliensis]

% identity

92

```
10642
Seq. No.
Contig ID
                   19331 1.R1040
5'-most EST
                   uC-gmronoir065g05b1
Method
                   BLASTN
NCBI GI
                   q1684852
BLAST score
                   392
                   0.0e + 00
E value
                   630
Match length
                   91
% identity
NCBI Description Phaseolus vulgaris PvSR7 protein mRNA, partial cds
Seq. No.
                   10643
Contig ID
                   19331 2.R1040
5'-most EST
                   uC-gmrominsoy217b05b1
Method
                   BLASTX
NCBI GI
                   g4033469.
BLAST score
                   174
                   2.0e-12
E value
Match length
                   39
                   74
% identity
NCBI Description
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP41
                   >gi 1707370 emb_CAA67799_ (X99436) splicing factor
                   [Arabidopsis thaliana]
                   10644
Seq. No.
                   19332 1.R1040
Contig ID
5'-most EST
                  LIB30\overline{5}0-026-Q1-K1-H7
                   10645
Seq. No.
                   19333_1.R1040
Contig ID
5'-most EST
                   jex70\overline{0}905478.h1
                   10646
Seq. No.
                   19334 1.R1040
Contig ID
5'-most EST
                  LIB3050-026-Q1-K1-H9
                  10647
Seq. No.
                   19335 1.R1040
Contig ID
5'-most EST
                   uC-qmropic093d12b1
Method
                   BLASTX
NCBI GI
                   g3023961
BLAST score
                   967
E value
                   1.0e-105
Match length
                   212
% identity
                   84
NCBI Description
                  HOMEOBOX PROTEIN KNOTTED-1-LIKE >gi 1946222 emb CAA96512
                   (Z71980) knotted1-like homeobox protein [Malus domestica]
                   10648
Seq. No.
                   19335 2.R1040
Contig ID
5'-most EST
                   jC-qmle01810025e10d1
Method
                   BLASTN
                   q1946221
NCBI GI
BLAST score
                   63
E value
                   9.0e-27
                   95
Match length
```

Match length

85

```
NCBI Description M.domestica mRNA for knotted1-like homeobox protein
                  10649
Seq. No.
                  19336 1.R1040
Contig ID
5'-most EST
                  dpv701100409.h1
                  BLASTX
Method
                  g3367578
NCBI GI
BLAST score
                  260
                   3.0e-22
E value
                  107
Match length
% identity
                   45
                   (AL031135) protein kinase - like protein [Arabidopsis
NCBI Description
                  thaliana]
                   10650
Seq. No.
                   19339 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir013g04b1
Seq. No.
                  10651
                   19339 2.R1040
Contig ID
5'-most EST
                  ssr700557305.hl
Seq. No.
                   10652
                   19342 1.R1040
Contig ID
5'-most EST
                   uC-gmropic029d04b1
Method
                  BLASTX
NCBI GI
                   q1129145
BLAST score
                   1176
E value
                   1.0e-129
Match length
                   362
% identity
                   66
                   (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]
NCBI Description
                   10653
Seq. No.
Contig ID
                   19351 1.R1040
5'-most EST
                   LIB3170-057-Q1-K1-D3
                   10654
Seq. No.
                   19351 2.R1040
Contig ID
5'-most EST
                   LIB3107-082-Q1-K1-H5
Method
                   BLASTX
NCBI GI
                   q4512655
BLAST score
                   852
E value
                   2.0e-91
Match length
                   235
% identity
NCBI Description
                   (AC007048) putative protein phosphatase 2C [Arabidopsis
                   thaliana]
                   10655
Seq. No.
                   19351 3.R1040
Contig ID
5'-most EST
                   LIB3106-114-Q1-K1-D12
Method
                   BLASTX
NCBI GI
                   q2842482
BLAST score
                   274
E value
                   5.0e-24
```

Contig ID 5'-most EST

```
% identity
                   (AL021749) protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  10656
Seq. No.
Contig ID
                  19351 4.R1040
                  LIB3139-073-P1-N1-H6
5'-most EST
                  BLASTX
Method
                  q2842482
NCBI GI
                  363
BLAST score
                                · .
                   2.0e-34
E value
Match length
                  95
% identity
                   (AL021749) protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  10657
Seq. No.
                  19351 5.R1040
Contig ID
5'-most EST
                  uC-gmronoir068b05b1
Method
                  BLASTX
NCBI GI
                  g4336436
BLAST score
                  312
                   2.0e-28
E value
                  92
Match length
% identity
                  64
NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]
                   10658
Seq. No.
                   19352 1.R1040
Contig ID
                   kmv700739705.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g2244866
BLAST score
                   805
E value
                   5.0e-86
Match length
                   223
% identity
                   68
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                   10659
Seq. No.
                   19353 1.R1040
Contig ID
                   fua701043404.h1
5'-most EST
                   10660
Seq. No.
                   19354_1.R1040
Contig ID
                   LIB3050-026-Q1-K1-G5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3738332
                   195
BLAST score
                   5.0e-17
E value
Match length
                   81
% identity
                   67
NCBI Description
                   (AC005170) putative eukaryotic initiation factor
                   [Arabidopsis thaliana]
                   10661
Seq. No.
                   19354 2.R1040
```

uxk700672920.h1

```
Method
                  BLASTX
NCBI GI
                  g3738332
BLAST score
                  164
                   1.0e-11
E value
                  88
Match length
                   51
% identity
NCBI Description
                   (AC005170) putative eukaryotic initiation factor
                   [Arabidopsis thaliana]
                  10662
Seq. No.
                  19359 1.R1040
Contig ID
5'-most EST
                  LIB3050-026-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  q3928862
BLAST score
                  144
                   5.0e-09
E value
Match length
                  125
                   30
% identity
NCBI Description
                   (AF089710) disease resistance protein RPP8 (Arabidopsis
                  thaliana]
Seq. No.
                  10663
                  19360 1.R1040
Contig ID
5'-most EST
                  LIB3051-115-Q1-K1-C4
Method
                  BLASTX
                                                    14.1
NCBI GI
                  g282963
BLAST score
                  579
E value
                   9.0e-60
Match length
                  133
% identity
NCBI Description
                  transforming protein (myb) homolog (clone myb.Ph2) - garden
                  petunia >gi_20561_emb_CAA78387_ (Z13997) protein 2 [Petunia
                  x hybrida]
Seq. No.
                  10664
Contig ID
                  19362 1.R1040
5'-most EST
                  uxk700672889.h1
Seq. No.
                  10665
                  19364 1.R1040
Contig ID
5'-most EST
                  uC-gmronoir043h01b1
Method
                  BLASTX
                  g2829862
NCBI GI
BLAST score
                  773 -
E value
                  1.0e-129
Match length
                  443
% identity
NCBI Description
                   (AC002396) Similar to glucosyltransferases [Arabidopsis
                  thaliana]
Seq. No.
                  10666
Contig ID
                  19367 1.R1040
5'-most EST
                  LIB3050-026-01-K1-E7
Seq. No.
                  10667
                  19367 2.R1040
Contig ID
```

sat701009408.h1

% identity

```
10668
Seq. No.
                   19372 1.R1040
Contig ID
                   LIB31\overline{0}6-064-Q1-K1-G8
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4309728
                   836
BLAST score
                   9.0e-90
E value
                   185
Match length
                   88
% identity
                   (ACOO6439) putative ADP-ribosylation factor [Arabidopsis
NCBI Description
                   thaliana]
                   10669
Seq. No.
                   19373_1.R1040
Contig ID
5'-most EST
                   uC-gmronoir045f02b1
Method
                   BLASTX
                   q3935183
NCBI GI
BLAST score
                   358
                   8.0e-34
E value
                   222
Match length
                   38
% identity
NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]
                 . 10670
Seq. No.
                   19376 1.R1040
Contig ID
                   asn701136271.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1843462
BLAST score
                   403
E value
                   4.0e-39
Match length
                   131
% identity
                   56
                   (L10211) isoliquiritigenin 2'-O-methyltransferase [Medicago
NCBI Description
                   sativa]
                   10671
Seq. No.
                   19376 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910025a04d1
                   BLASTX
Method
NCBI GI
                   g1843462
BLAST score
                   296
                   2.0e-26
E value
                   98
Match length
% identity
NCBI Description
                   (L10211) isoliquiritigenin 2'-O-methyltransferase [Medicago
                   sativa]
                   10672
Seq. No.
                   19377 1.R1040
Contig ID
5'-most EST
                   asn701133492.hl
Method
                   BLASTX
NCBI GI
                   q4558568
BLAST score
                   467
                   1.0e-46
E value
Match length
                   177
```

```
NCBI Description
                   (AC007138) hypothetical protein [Arabidopsis thaliana]
                   10673
Seq. No.
                   19384 1.R1040
Contig ID
                   sat701006111.h1
5'-most EST
                   10674
Seq. No.
                   19385 1.R1040
Contig ID
5'-most EST
                   LIB3050-026-Q1-K1-D12
                   10675
Seq. No.
                   19391 1.R1040
Contig ID
5'-most EST
                   LIB3139-006-P1-N1-D8
Seq. No.
                   10676
                   19393 1.R1040
Contig ID
5'-most EST
                   fC-gmle700686111f1
Method
                   BLASTX
NCBI GI
                   g1723242
BLAST score
                   212
E value
                   2.0e-16
Match length
                   173
% identity
                   35
NCBI Description
                   HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I
                   >gi 1177363 emb CAA93239 (Z69240) yeast dsk2 homolog,
                   ubiquitin-like protein [Schizosaccharomyces pombe]
                   10677
Seq. No.
                   19393 2.R1040
Contig ID
5'-most EST
                   fC-gmle700686111b1
Method
                   BLASTX
NCBI GI
                   g1723242
BLAST score
                   146
E value
                   4.0e-09
Match length
                   58
% identity
NCBI Description
                   HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I
                   >gi_1177363_emb_CAA93239_ (Z69240) yeast dsk2 homolog,
                   ubiquitin-like protein [Schizosaccharomyces pombe]
                   10678
Seq. No.
Contig ID
                   19400 1.R1040
                   6HC - 0\overline{1} - Q1 - B1 - A9
5'-most EST
                   10679
Seq. No.
Contig ID
                   19402 1.R1040
5'-most EST
                   LIB30\overline{5}0-026-Q1-K1-B12
Method
                   BLASTX
                   q1706082
NCBI GI
BLAST score
                   347
E value
                   1.0e-32
Match length
                   139
% identity
                   55
NCBI Description
                   SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)
                   >gi_629787_pir__S44191 serine-type carboxypeptidase (EC
```

3.4.16.1) II-3 - barley >gi 619350 bbs 153536

CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,

```
>gi 474392 emb CAA55478 (X78877) serine carboxylase II-3
                   [Hordeum vulgare]
                  10680
Seq. No.
                  19405 1.R1040
Contig ID
5'-most EST
                  bth700847244.h1
Method
                  BLASTX
                  g1652105
NCBI GI
BLAST score
                  202
                  2.0e-15
E value
Match length
                  84
% identity
NCBI Description
                   (D90902) hypothetical protein [Synechocystis sp.]
Seq. No.
                  10681
                  19405 2.R1040
Contig ID
5'-most EST
                  LIB3050-025-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g1652105
BLAST score
                  192
E value
                  2.0e-14
Match length
                  82
% identity
                  49
NCBI Description
                  (D90902) hypothetical protein [Synechocystis sp.]
Seq. No.
                  10682
                  19408 1.R1040
Contig ID
5'-most EST
                  LIB3170-067-Q1-K1-H2
                  BLASTX
Method
NCBI GI
                  q2245007
BLAST score
                  256
E value
                  1.0e-21
Match length
                  96
                  58
% identity
NCBI Description
                   (297341) hypothetical protein [Arabidopsis thaliana]
                  10683
Seq. No.
                  19414 1.R1040
Contig ID
5'-most EST
                  LIB3050-025-Q1-K1-G8
Method
                  BLASTX
                  g1723878
NCBI GI
BLAST score
                  433
                  7.0e-43
E value
Match length
                  .143
                  50
% identity
NCBI Description
                  HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION
                  >gi_2132541_pir__S64091 probable membrane protein YGL084c -
                  yeast (Saccharomyces cerevisiae) >gi_1322607_emb_CAA96789_
                   (Z72606) ORF YGL084c [Saccharomyces cerevisiae]
                  10684
Seq. No.
Contig ID
                  19415 1.R1040
5'-most EST
                  LIB3050-025-Q1-K1-G9
                  10685
Seq. No.
```

cv. Alexis, aleurone, Peptide, 516 aa]

19417_1.R1040

Contig ID

NCBI Description

```
LIB3050-025-Q1-K1-H10
5'-most EST
Seq. No.
                  10686
Contig ID
                  19422 1.R1040
5'-most EST
                  sat701010659.hl
Method
                  BLASTX
                   q2244833
NCBI GI
                   255
BLAST score
                   2.0e-21
E value
                   328
Match length
                   29
% identity
                  (Z97337) centromere protein homolog [Arabidopsis thaliana]
NCBI Description
                   10687
Seq. No.
                   19423 1.R1040
Contig ID
5'-most EST
                  LIB31\overline{0}9-057-Q1-K1-D5
                   10688
Seq. No.
                   19424 1.R1040
Contig ID
                   k11701207370.h1
5'-most EST
                   10689
Seq. No.
                   19425 1.R1040
Contig ID
                   dpv701097982.h1
5'-most EST
                   BLASTX
Method
                   g2245093
NCBI GI
                   845
BLAST score
                   1.0e-90
E value
                   249
Match length
% identity
                   67
                  (Z97343) membrane channel protein [Arabidopsis thaliana]
NCBI Description
                   10690
Seq. No.
                   19425 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910035b05d1
Method
                   BLASTN
                   g257237
NCBI GI
BLAST score
                   69
                   2.0e-30
E value
                   201
Match length
% identity
                   84
                   TobRB7=root-specific gene regulator [Nicotiana
NCBI Description
                   tabacum=tobacco, cv Wisconsin 38, Genomic, 3426 nt]
                   >gi_1250027_gb_I15119_I15119 Sequence 1 from patent US
                   5459252 >gi 3966754 gb AR007270 AR007270 Sequence 1 from
                   patent US
                   10691
Seq. No.
                   19425 3.R1040
Contig ID
                   fua701043434.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g126959
                   348
BLAST score
E value
                   6.0e-33
Match length
                   105
% identity
                   65
                   TONOPLAST INTRINSIC PROTEIN, ROOT-SPECIFIC RB7-5A (RT-TIP)
```

>gi_82192_pir__JQ1011 TobRB7-5A protein - common tobacco
>gi_100371_pir__S13719 probable membrane channel protein common tobacco >gi_20011_emb_CAA38634_ (X54855) possible
membrane channel protein [Nicotiana tabacum]

Seq. No. 10692

Contig ID 19431_1.R1040 5'-most EST dpv701102817.h1

Method BLASTX
NCBI GI g3157943
BLAST score 295
E value 1.0e-26
Match length 146
% identity 44

NCBI Description (AC002131) Contains similarity to BAP31 protein gb_X81816

from Mus musculus. [Arabidopsis thaliana]

Seq. No. 10693

Contig ID 19434 1.R1040 5'-most EST rlr700900866.h1

Seq. No. 10694

Contig ID 19434 2.R1040

5'-most EST uC-gmrominsoy230c07b1

Seq. No. 10695

Contig ID 19440_1.R1040 5'-most EST awf700837923.h1

Method BLASTN
NCBI GI g3021356
BLAST score 108
E value 1.0e-53
Match length 164
% identity 91

NCBI Description Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,

clone GEPI48

Seq. No. 10696

Contig ID 19440_2.R1040

5'-most EST LIB3050-025-Q1-K1-G10

Method BLASTN
NCBI GI g3021356
BLAST score 76
E value 2.0e-34
Match length 116
% identity 91

NCBI Description Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,

clone GEPI48

Seq. No. 10697

Contig ID 19445_1.R1040

5'-most EST uC-qmrominsoy261h11b1

Seq. No. 10698

Contig ID 19445_2.R1040 5'-most EST hrw701060687.h1

Match length

```
Seq. No.
                   10699
                   19447 1.R1040
Contig ID
5'-most EST
                   fua701037771.h1
Method
                   BLASTX
NCBI GI
                   g477819
BLAST score
                   1102
                   1.0e-121
E value
Match length
                   268
% identity
                   78
NCBI Description
                   mitochondrial processing peptidase (EC 3.4.99.41) beta
                   chain precursor - potato >gi_410634_bbs_136741 cytochrome c
                   reductase-processing peptidase subunit II, MPP subunit II,
                   P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                   530 aa]
                   10700
Seq. No.
                   19447 2.R1040
Contig ID
5'-most EST
                   LIB3170-046-Q1-J1-D12
Method
                   BLASTX
NCBI GI
                   q477280
BLAST score
                   242
E value
                   2.0e-20
Match length
                   57
% identity
NCBI Description
                   mitochondrial processing peptidase (EC 3.4.99.41) 55K
                   protein precursor - potato >gi_410633_bbs_136740 cytochrome
                   c reductase-processing peptidase subunit I, MPP subunit I,
                   P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                   534 aal
Seq. No.
                   10701
                   19452 1.R1040
Contig ID
                   LIB30\overline{5}0-025-Q1-K1-E10
5'-most EST
Method
                   BLASTX
                   g3402709
NCBI GI
BLAST score
                   659
E value
                   3.0e-69
                                                  . . . .
Match length
                   179
% identity
                   54
NCBI Description
                   (AC004261) hypothetical protein [Arabidopsis thaliana]
                   10702
Seq. No.
                   19453 1.R1040
Contig ID
5'-most EST
                   LIB3139-116-P1-N1-F11
                   10703
Seq. No.
Contig ID
                   19455 1.R1040
                   LIB30\overline{5}0-025-Q1-K1-E6
5'-most EST
Seq. No.
                   10704
Contig ID
                   19456 1.R1040
5'-most EST
                   jC-gmf102220056b02a1
Method
                   BLASTX
NCBI GI
                   q3928543
                   1598
BLAST score
                   1.0e-178
E value
```

٠,

```
% identity
                    (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   10705
Seq. No.
Contig ID
                   19456 2.R1040
5'-most EST
                   hrw701061409.hl
Method
                   BLASTX
                   g3928543
NCBI GI
BLAST score
                   508
                   2.0e-51
E value
Match length
                   158
                   59
% identity
                    (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
                   10706
Seq. No.
                   19456 3.R1040
Contig ID
                   jC-gmf102220146c05d1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2827992
                   309
BLAST score
                   3.0e-28
E value
                   70
Match length
% identity
                    (AF034743) UDP-glucuronosyltransferase [Pisum sativum]
NCBI Description
Seq. No.
                   10707
                   19456 4.R1040
. Contig ID
5'-most EST
                   jC-gmro02800042g04d1
Method
                   BLASTN
NCBI GI
                   g2827991
BLAST score
                   107
E value
                   5.0e-53
Match length
                   239
% identity
                   86
NCBI Description
                   Pisum sativum UDP-glucuronosyltransferase gene, complete
                   cds
Seq. No.
                   10708
Contig ID
                   19459 1.R1040
5'-most EST
                   fC-qmst700605438f5
Method
                   BLASTX
NCBI GI
                   q3402751
BLAST score
                   973
E value
                   1.0e-105
Match length
                   270
% identity
NCBI Description
                   (AL031187) putative protein [Arabidopsis thaliana]
Seq. No.
                   10709
Contig ID
                   19460 1.R1040
5'-most EST
                   jsh70\overline{1}063724.h1
Seq. No.
                   10710
```

19474 1.R1040

uaw700664864.h1

Contig ID 5'-most EST

```
10711
Seq. No.
Contig ID
                   19489 1.R1040
5'-most EST
                   g4293317
Method
                  BLASTX
NCBI GI
                   q1730081
BLAST score
                  504
E value
                   9.0e-51
Match length
                  155
                   67
% identity
                  PROTEIN L1R18B (LLPR10.1B) >gi 1039336 emb CAA56299
NCBI Description
                   (X79975) L1R18B [Lupinus luteus] >gi 2183277 (AF002278)
                  LlPR10.1B [Lupinus luteus]
Seq. No.
                   10712
                   19489 2.R1040
Contig ID
                   yz1700966962.hl
5'-most EST
Method
                  BLASTX
                  g1703042
NCBI GI
BLAST score
                   367
E value
                   1.0e-34
Match length
                  157
                   42
% identity
                  ABA-RESPONSIVE PROTEIN ABR17 >gi_629631_pir__S42649
NCBI Description
                   abscisic acid-responsive protein ABR17 - garden pea
                   >gi 20631 emb CAA78829 (Z15128) ABA-responsive protein
                   [Pisum sativum]
                  10713
Seq. No.
                   19489 3.R1040
Contig ID
                   seb700650946.hl
5'-most EST
Method
                   BLASTX
                   g1730080
NCBI GI
BLAST score
                   163
E value
                   2.0e-11
                   58
Match length
                   57
% identity
NCBI Description
                  PROTEIN L1R18A (LLPR10.1A) >gi 1039334 emb CAA56298
                   (X79974) L1R18A [Lupinus luteus] >gi 2183275 (AF002277)
                  LlPR10.1A [Lupinus luteus]
                   10714
Seq. No.
Contig ID
                   19490 1.R1040
5'-most EST
                  LIB3109-029-Q1-K1-F7
                   10715
Seq. No.
                   19492 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220126c10a1
Seq. No.
                  10716
                   19492 2.R1040
Contig ID
5'-most EST
                  hrw70\overline{1}058618.h1
                  10717
Seq. No.
                  19493 1.R1040
Contig ID
5'-most EST
                  LIB3050-025-Q1-K1-B6
```

BLASTX

Method

```
g3980387
NCBI GI
BLAST score
                  379
E value
                  2.0e-36
Match length
                  112
% identity
NCBI Description
                  (AC004561) putative glutathione S-transferase [Arabidopsis
                  thaliana]
                  10718
Seq. No.
                  19499 1.R1040
Contig ID
5'-most EST
                  LIB3109-035-Q1-K3-F6
Method
                  BLASTX
NCBI GI
                  q3688181
BLAST score
                  361
E value
                  2.0e-34
                  130
Match length
% identity
                  (AL031804) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  10719
                  19508 1.R1040
Contig ID
5'-most EST
                  LIB3050-024-Q1-K1-H7
                  10720
Seq. No.
                  19509 1.R1040
Contig ID
5'-most EST
                  LIB3092-050-Q1-K1-H9
                  BLASTX
Method
NCBI GI
                  g3881189
BLAST score
                  432
E value
                  2.0e-52
Match length
                  145
% identity
                  64
NCBI Description
                  (Z99281) similar to ADP-ribosylation factor; cDNA EST
                  EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337
                  comes from this gene; cDNA EST EMBL: C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4
                  10721
Seq. No.
                  19509 2.R1040
Contig ID
5'-most EST
                  LIB3050-024-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g3881189
BLAST score
                  337
E value
                  1.0e-31
Match length
                  84
% identity
NCBI Description
                  (Z99281) similar to ADP-ribosylation factor; cDNA EST
                  EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337
                  comes from this gene; cDNA EST EMBL:C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4
                  10722
Seq. No.
                  19515 1.R1040
Contig ID
                  rca701001392.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3914996
```

```
BLAST score
                   231
E value
                   3.0e-19
Match length
                   51
                   86
% identity
                   PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
NCBI Description
                   >gi_1665831_dbj_BAA13640_ (D88541) phosphoserine
                   aminotransferase [Arabidopsis thaliana]
                   >gi 2804260 dbj BAA24441_ (AB010408) phosphoserine
                   aminotransferase [Arabidopsis thaliana]
                   >gi 3367581 emb CAA20033 (AL031135) phosphoserine
                   aminotransferase [Arabidopsis thaliana]
                   10723
Seq. No.
                   19515 2.R1040
Contig ID
5'-most EST
                   LIB3093-016-Q1-K1-C11
Method
                   BLASTN
NCBI GI
                   g2804259
BLAST score
                   150
E value
                   2.0e-78
Match length
                   446
                   83
% identity
NCBI Description
                   Arabidopsis thaliana DNA for phosphoserine
                   aminotransferase, complete cds
                   10724
Seq. No.
                   19515 3.R1040
Contig ID
                   ish70\overline{1}065269.h1
5'-most EST
                   BLASTN
Method
                   q2804259
NCBI GI
BLAST score
                   93
E value
                   1.0e-44
Match length
                   189
                   88
% identity
                   Arabidopsis thaliana DNA for phosphoserine
NCBI Description
                   aminotransferase, complete cds
Seq. No.
                   10725
                   19516 1.R1040
Contig ID
5'-most EST
                   jC-qmf102220050c05a1
                   10726
Seq. No.
Contig ID
                   19517 1.R1040
                   LIB30\overline{5}0-024-Q1-K1-F11
5'-most EST
Method
                   BLASTX
                   g2832658
NCBI GI
BLAST score
                   244
E value
                   2.0e-20
Match length
                   94
% identity
                   51
                   (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
                   10727
Seq. No.
Contig ID
                   19517 2.R1040
                   zzp700834035.hl
5'-most EST
                   BLASTX
Method
                   q2832658
NCBI GI
```

193

BLAST score

```
E value
                   4.0e-15
Match length
                   58
                   57
% identity
NCBI Description
                   (AL021710) putative protein [Arabidopsis thaliana]
                  10728
Seq. No.
                  19518 1.R1040
Contig ID
                  LIB3050-024-Q1-K1-F12
5'-most EST
Seq. No.
                   10729
                  19520 1.R1040
Contig ID
                  LIB3050-024-Q1-K1-F4
5'-most EST
Method
                  BLASTX
NCBI GI
                  q417148
                  379
BLAST score
E value
                   3.0e-39
                  138
Match length
% identity
                   61
NCBI Description
                  PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)
                   (G2-4) >gi_99912_pir__A33654 heat shock protein 26A -
                  soybean >gi 169981 (M20363) Gmhsp26-A [Glycine max]
Seq. No.
                  10730
                   19521 1.R1040
Contig ID
5'-most EST
                  wrg700788594.hl
Method
                  BLASTX
NCBI GI
                   q4335715
BLAST score
                   586
E value
                   9.0e-71
Match length
                   291
% identity
                   51
NCBI Description
                   (AC006248) putative immediate-early salicylate-induced
                  glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                   10731
Contig ID
                   19528 1.R1040
5'-most EST
                  uC-gmropic010a04b1
Seq. No.
                  10732
Contig ID
                  19530 1.R1040
5'-most EST
                  pxt700945228.h1
Method
                  BLASTX
NCBI GI
                   q4510375
BLAST score
                  207
E value
                   3.0e-16
Match length
                  123
% identity
NCBI Description
                   (AC007017) putative homeotic protein BEL1 [Arabidopsis
                  thaliana]
Seq. No.
                  10733
Contig ID
                  19533 1.R1040
5'-most EST
                  bth700843865.h1
Seq. No.
                  10734
Contig ID
                  19534 1.R1040
```

LIB3050-024-Q1-K1-D6

Method

NCBI GI

```
10735
Seq. No.
                   19536 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}0-024-Q1-K1-D8
                   10736
Seq. No.
Contig ID
                   19540 1.R1040
5'-most EST
                   LIB3050-024-Q1-K1-E11
                   10737
Seq. No.
                   19540 2.R1040
Contig ID
5'-most EST
                   jC-gmf102220052c02d1
                   10738
Seq. No.
                   19541 1.R1040
Contig ID
5'-most EST
                   zzp700832101.h1
Method
                   BLASTX
NCBI GI
                   g2651310
BLAST score
                   515
                   4.0e-52
E value
Match length
                   236
% identity
                   43
                   (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                   thaliana]
                   10739
Seq. No.
                   19543 1.R1040
Contig ID
5'-most EST
                   LIB3074-028-Q1-K1-C4
Seq. No.
                   10740
                   19544 1.R1040
Contig ID
                   fde700870563.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455225
BLAST score
                   757
E value
                   5.0e-99
Match length
                   198
% identity
NCBI Description
                  (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   10741
                   19545 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy048b10b1
Method
                   BLASTN
NCBI GI
                   g1142620
BLAST score
                   105
E value
                   6.0e-52
Match length
                   354
% identity
                   89
NCBI Description
                  Phaseolus vulgaris phaseolin G-box binding protein PG2
                   (PG2) mRNA, partial cds
                   10742
Seq. No.
                   19546 1.R1040
Contig ID
```

pmv700893028.hl

BLASTX

g3080420

Method

NCBI GI

```
BLAST score
                   534
E value
                   2.0e-54
Match length
                   144
                   67
% identity
                   (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   10743
Seq. No.
                   19548 1.R1040
Contig ID
5'-most EST
                  LIB3050-024-Q1-K1-B8
                   10744
Seq. No.
                   19553 1.R1040
Contig ID
5'-most EST
                  pxt700944431.hl
                   10745
Seq. No.
                   19565 1.R1040
Contig ID
5'-most EST
                  rca701002450.h1
                  BLASTN
Method
NCBI GI
                   g719289
BLAST score
                   33
                   7.0e-09
E value
                   85
Match length
                   85
% identity
NCBI Description
                  Arabidopsis thaliana SABRE gene, exon 14 and complete cds
                   10746
Seq. No.
                   19568 1.R1040
Contig ID
5'-most EST
                  LIB3107-013-Q1-K1-A2
Method
                  BLASTN
NCBI GI
                   g945059
BLAST score
                   536
E value
                   0.0e + 00
Match length
                   907
% identity
                   90
NCBI Description
                  Vigna unquiculata aminoimidazole ribonucleotide (AIRS)
                   synthetase (pur5) mRNA, complete cds
                   10747
Seq. No.
                   19568 2.R1040
Contig ID
5'-most EST
                  LIB3170-062-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1709925
BLAST score
                  187
E value
                   4.0e-14
Match length
                   64
% identity
NCBI Description
                   PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE PRECURSOR
                   (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR
                  SYNTHASE) >gi 945060 (U30895) aminoimidazole ribonucleotide
                   (AIRS) synthetase [Vigna unguiculata]
                  10748
Seq. No.
Contig ID
                   19569 1.R1040
```

leu701156202.hl

BLASTX

g421989

```
BLAST score
                  .999
E value
                   1.0e-108
Match length
                   387
                   55
% identity
                  serpin - barley >gi 19071 emb CAA78822 (Z15116) protein zx
NCBI Description
                   [Hordeum vulgare] >gi 444778 prf 1908213A protein Zx
                   [Hordeum vulgare]
                   10749
Seq. No.
                  19569 3.R1040
Contig ID
5'-most EST
                  wrg700787582.hl
                  BLASTX
Method
NCBI GI
                   g421989
BLAST score
                  150
                   1.0e-09
E value
Match length
                  59
                   51
% identity
                  serpin - barley >gi_19071 emb CAA78822 (Z15116) protein zx
NCBI Description
                   [Hordeum vulgare] >gi 444778 prf 1908213A protein Zx
                   [Hordeum vulgare]
                   10750
Seq. No.
                   19582 1.R1040
Contig ID
                   gbt700547938.hl
5'-most EST
Method
                  BLASTX
                   g4544409
NCBI GI
                                                                         Marie .
BLAST score
                   343
E value
                   5.0e-32
                  103
Match length
% identity
                   59
NCBI Description
                   (AC006955) putative transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   10751
Contig ID
                   19582 2.R1040
5'-most EST
                  LIB3050-023-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  q4544409
BLAST score
                  224
E value
                   2.0e-18
Match length
                  69
% identity
NCBI Description
                   (AC006955) putative transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   10752
Contig ID
                   19584 1.R1040
5'-most EST
                  LIB3050-023-Q1-K1-G6
Method
                  BLASTX
NCBI GI
                  q4567203
BLAST score
                  277
E value
                   1.0e-24
Match length
                  63
% identity
NCBI Description
                   (AC007168) putative beta-hydroxyacyl-ACP dehydratase
```

[Arabidopsis thaliana]

% identity

```
Seq. No.
                    10753
                    19586 1.R1040
Contig ID
5'-most EST
                    leu70\overline{1}150647.h1
                    10754
Seq. No.
Contig ID
                    19586 2.R1040
5'-most EST
                   jC-gmle01810011h12a1
                   10755
Seq. No.
                   19590 1.R1040
Contig ID
5'-most EST
                   LIB3050-023-Q1-K1-H12
                   10756
Seq. No.
                    19591 1.R1040
Contig ID
5'-most EST
                   LIB3050-023-Q1-K1-H2
                    10757
Seq. No.
                   19593 1.R1040
Contig ID
                   LIB31\overline{3}9-069-P1-N1-G7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1838976
BLAST score
                    289
E value
                    5.0e-50
Match length
                   243
% identity
                    49
                    (X73635) vsf-1 [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   10758
                   19593 2.R1040
Contig ID
5'-most EST
                   smc70\overline{0}750091.h1
                   10759
Seq. No.
                   19595 1.R1040
Contig ID
5'-most EST
                   rlr700901422.hl
Seq. No.
                   10760
                   19596 1.R1040
Contig ID
5'-most EST
                   zsq701128870.hl
Method
                   BLASTX
NCBI GI
                   q2129915
BLAST score
                   493
E value
                   2.0e-49
Match length
                   148
% identity
                    66
NCBI Description
                   ferredoxin precursor - sweet orange
                   >gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic
                   ferredoxin [Citrus sinensis]
                   10761
Seq. No.
Contig ID
                   19599 1.R1040
5'-most EST
                   fC-gmse700660496f5
Method
                   BLASTX
NCBI GI
                   q3193332
BLAST score
                   304
E value
                   1.0e-27
Match length
                   164
```

NCBI Description

```
NCBI Description
                   (AF069299) similar to Arabidopsis AT-hook protein 1
                   (GB:AJ222585) [Arabidopsis thaliana]
                  10762
Seq. No.
                  19607 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy316d05b1
Method
                  BLASTX
NCBI GI
                  g1002796
BLAST score
                  602
                  1.0e-62
E value
                  140
Match length
                  78
% identity
NCBI Description
                  (U33915) Cpm10 [Craterostigma plantagineum]
                  10763
Seq. No.
                  19607 2.R1040
Contig ID
                  LIB30\overline{5}0-023-Q1-K1-F5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1002796
BLAST score
                  291
E value
                  2.0e-38
Match length
                  157
% identity
                   57
                   (U33915) Cpm10 [Craterostigma plantagineum]
NCBI Description
Seq. No.
                  10764
                  19611 1.R1040
Contig ID
                  LIB3139-095-P1-N1-B11
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4006829
BLAST score
                  1516
E value
                   1.0e-169
Match length
                   429
% identity
                  70
NCBI Description
                   (AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  10765
                  19612 1.R1040
Contig ID
5'-most EST
                  LIB3106-065-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q4490702
BLAST score
                  213
E value
                   7.0e-17
Match length
                   63
% identity
NCBI Description
                   (AL035680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  10766
Contig ID
                  19615 1.R1040
5'-most EST
                  LIB3050-023-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2759999
BLAST score
                   466
E value
                  2.0e-46
Match length
                  179
% identity
```

(AJ003141) peroxidase [Hordeum vulgare]

```
10767
Seq. No.
                  19619 1.R1040
Contig ID
                  uC-gmflminsoy042g05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2244792
BLAST score
                  2456
                  0.0e + 00
E value
                  601
Match length
                  76
% identity
                  (Z97336) ankyrin homolog [Arabidopsis thaliana]
NCBI Description
                  10768
Seq. No.
                   19619 2.R1040
Contig ID
                  uC-gmrominsoy061a01b1
5'-most EST
Seq. No.
                  10769
                  19619 4.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy044a02b1
                  10770
Seq. No.
                  19622 1.R1040
Contig ID
5'-most EST
                  LIB3106-091-Q1-K1-G4
                  BLASTX
Method
                  g1749676
NCBI GI
                                                       200
BLAST score
                   361
                   1.0e-33
E value
Match length
                   247
                   37
% identity
                   (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
NCBI Description
                   EMBL Accession Number Z72990 [Schizosaccharomyces pombe]
                   10771
Seq. No.
                   19622 2.R1040
Contig ID
                   fde700874652.hl
5'-most EST
                   10772
Seq. No.
                   19625 1.R1040
Contig ID
                   LIB3109-033-Q1-K1-F3
5'-most EST
                   10773
Seq. No.
                   19625 2.R1040
Contig ID
                   LIB3139-046-P1-N1-E1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4544409
BLAST score
                   716
                   1.0e-75
E value
                   186
Match length
                   70
% identity
                   (AC006955) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   10774
Seq. No.
                   19625 3.R1040
Contig ID
                   jC-gmst02400009h01a1
5'-most EST
```

10775

Seq. No.

Seq. No.

```
19625 4.R1040
Contig ID
                   uC-gmrominsoy231b03b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4544409
BLAST score
                   259
E value
                   2.0e-22
                   88
Match length
                   53
% identity
                   (AC006955) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   10776
Seq. No.
                   19626 1.R1040
Contig ID
                   ejt70\overline{0}606274.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1730560
BLAST score
                   2686
                   0.0e + 00
E value
Match length
                   557
                   91
% identity
                  ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                   H) >gi_510932_emb_CAA84494_ (Z35117) alpha 1,4-glucan
                   phosphorylase type H [Vicia faba]
                   10777
Seq. No.
                   19627 1.R1040
Contig ID
                   LIB30\overline{5}0-023-Q1-K1-E3
5'-most EST
                   10778
Seq. No.
                   19633 1.R1040
Contig ID
                   crh70\overline{0}851363.h1
5'-most EST
                   BLASTX
Method
                   q4455251
NCBI GI
BLAST score
                   625
E value
                   8.0e-77
Match length
                   206
                   75
% identity
                   (AL035523) magnesium-protoporphyrin IX
NCBI Description
                   methyltransferase-like protein [Arabidopsis thaliana]
                   10779
Seq. No.
                   19640 1.R1040
Contig ID
5'-most EST
                   LIB3050-023-Q1-K1-C7
                   10780
Seq. No.
                   19644_1.R1040
Contig ID
                   taw700659052.hl
5'-most EST
Method
                   BLASTX
                   g4093157
NCBI GI
BLAST score
                   734
                   2.0e-77
E value
Match length
                   274
% identity
                   62
                   (AF087936) phytochrome-associated protein 2 [Arabidopsis
NCBI Description
                   thaliana]
```

```
Contig ID
                   19644 2.R1040
                   taw700657766.hl
5'-most EST
Method
                   BLASTX
                   g4093157
NCBI GI
BLAST score
                   412
                   3.0e-40
E value
                   118
Match length
                   77
% identity
                   (AF087936) phytochrome-associated protein 2 [Arabidopsis
NCBI Description
                   thaliana]
                   10782
Seq. No.
                   19648 1.R1040
Contig ID
5'-most EST
                   LIB3050-023-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   g3157933
BLAST score
                   343
E value
                   6.0e-33
Match length
                   106
% identity
                   61
                   (AC002131) Contains similarity to box helicases gb U29097
NCBI Description
                   from C. elegans and to the ENBP1 gene product gb \overline{X95995}
                   from Vicia sativa. [Arabidopsis thaliana]
Seq. No.
                   10783
                   19648 2.R1040
Contig ID
                   fde700876682.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2781345
BLAST score
                   427
E value
                   4.0e-42
Match length
                   96
% identity
NCBI Description
                   (AC003113) F2401.2 [Arabidopsis thaliana]
Seq. No.
Contig ID
                   19652 1.R1040
                   taw700660047.hl
5'-most EST
                   10785
Seq. No.
Contig ID
                   19653 1.R1040
5'-most EST
                   LIB3107-030-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   q4220527
BLAST score
                   896
E value
                   2.0e-96
Match length
                   315
% identity
NCBI Description
                   (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                   10786
                   19653 2.R1040
Contig ID
5'-most EST
                   pxt700941158.h1
Seq. No.
                   10787
Contig ID
                   19654 1.R1040
```

LIB3093-005-Q1-K1-E7

```
10788
Seq. No.
                   19654 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy306b07b1
                   10789
Seq. No.
Contig ID
                   19662 1.R1040
5'-most EST
                   LIB31\overline{3}9-065-P1-N1-H3
                   BLASTX
Method
                   g3297817
NCBI GI
BLAST score
                   153
                   1.0e-09
E value
                   79
Match length
                   39
% identity
                   (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
                   10790
Seq. No.
                   19662 2.R1040
Contig ID
5'-most EST
                   LIB3050-014-Q1-E1-B10
                   10791
Seq. No.
                   19662 3.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy189h09b1
Seq. No.
                   10792
                   19663 1.R1040
Contig ID
                   LIB3051-036-Q1-K1-H5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3004556
BLAST score
                   355
E value
                   4.0e-33
Match length
                   236
% identity
                   38
NCBI Description
                   (AC003673) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   10793
                   19665 1.R1040
Contig ID
5'-most EST
                   LIB3109-006-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   q2649424
BLAST score
                   157
E value
                   2.0e-10
Match length
                   100
% identity
                   39
NCBI Description
                   (AE001023) A. fulgidus predicted coding region AF1178
                   [Archaeoglobus fulgidus]
Seq. No.
                   10794
Contig ID
                   19667 1.R1040
5'-most EST
                   uC-gmronoir031d10b1
Method
                   BLASTX
NCBI GI
                   q4263507
BLAST score
                   735
E value
                   2.0e-77
Match length
                   588
% identity
NCBI Description
                   (AC004044) hypothetical protein [Arabidopsis thaliana]
```

NCBI Description

10803

Seq. No.

```
10795
Seq. No.
                   19667_2.R1040
Contig ID
5'-most EST
                   uC-gmropic101b12b1
                   10796
Seq. No.
Contig ID
                   19669 1.R1040
5'-most EST
                   LIB3050-022-Q1-K1-G7
                   10797
Seq. No.
                   19671 1.R1040
Contig ID
5'-most EST
                   LIB3074-036-Q1-K1-G12
                   10798
Seq. No.
                   19671 2.R1040
Contig ID
5'-most EST
                   pxt700944051.hl
Seq. No.
                   10799
                   19680 1.R1040
Contig ID
5'-most EST
                   LIB3107-063-Q1-K1-E11
Seq. No.
                   10800
                   19682 1.R1040
Contig ID
5'-most EST
                   LIB3073-019-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   g2245001
BLAST score
                   459
                   1.0e-45
E value
                   101
Match length
% identity
                   85
                   (Z97341) similarity to NADH dehydrogenase (ubiquinone)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   10801
Contig ID
                   19685 1.R1040
5'-most EST
                   wrg700791916.hl
Method
                   BLASTX
NCBI GI
                   q3617741
BLAST score
                   906
E value
                   5.0e-98
Match length
                   213
% identity
                   79
NCBI Description
                   (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis
                   thaliana]
Seq. No.
                   10802
Contig ID
                   19686 1.R1040
5'-most EST
                   uC-gmrominsoy056g12b1
Method
                   BLASTX
NCBI GI
                   q3128172
BLAST score
                   251
E value
                   3.0e-21
Match length
                   88
% identity
```

(AC004521) hypothetical protein [Arabidopsis thaliana]

Match length

```
Contig ID
                   19686 2.R1040
5'-most EST
                   uC-gmropic010c03b1
Method
                   BLASTX
NCBI GI
                   g3128172
BLAST score
                   695
E value
                   2.0e-73
Match length
                   188
                   65
% identity
                   (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   10804
Seq. No.
Contig ID
                   19689 1.R1040
5'-most EST
                   zpv700756991.h1
Method
                   BLASTX
                   g4335763
NCBI GI
BLAST score
                   404
E value
                   3.0e-39
Match length
                   159
% identity
                   48
NCBI Description
                   (AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.
                   10805
                   19689 2.R1040
Contig ID
                   LIB3139-082-P1-N1-D4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4335763
                   222
BLAST score
                   4.0e-18
E value
                   96
Match length
% identity
                   42
                   (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
                   10806
Seq. No.
                   19693 1.R1040
Contig ID
5'-most EST
                   zsg701118870.hl
Method
                   BLASTX
NCBI GI
                   g3249066
BLAST score
                   284
E value
                   3.0e-25
Match length
                   117
% identity
                   56
NCBI Description
                   (AC004473) Similar to S. cerevisiae SIK1P protein
                   gb 984964. ESTs gb_F15433 and gb_AA395158 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   10807
Contig ID
                   19696 1.R1040
                   LIB3050-025-Q1-K1-C12
5'-most EST
Seq. No.
                   10808
                   19697 1.R1040
Contig ID
5'-most EST
                   ncj70\overline{0}975670.h1
Method
                   BLASTX
NCBI GI
                   g1420936
BLAST score
                   1820
E value
                   0.0e+00
```

% identity NCBI Description (U61396) Vigna unguiculata aspartic proteinase mRNA, complete cds. [Vigna unguiculata] Seq. No. 10809 Contig ID 19703 1.R1040 5'-most EST LIB3050-022-Q1-K1-E1 Method ' BLASTX NCBI GI q2583123 BLAST score 205 E value 4.0e-16 Match length 47 % identity (AC002387) putative nucleotide sugar epimerase [Arabidopsis NCBI Description thaliana] Seq. No. 10810 Contig ID 19706 1.R1040 LIB3109-005-Q1-K1-B6 5'-most EST Method BLASTX NCBI GI g3023625 BLAST score 324 E value 2.0e-29 148 Match length 44 % identity POLYPEPTIDE DEFORMYLASE (PDF) (FORMYLMETHIONINE NCBI Description DEFORMYLASE) >gi 1772503 emb CAA71353 (Y10305) polypeptide deformylase [Calothrix PCC7601] Seq. No. 10811 19713 1.R1040 Contig ID 5'-most EST jC-gmf102220073d11a1 10812 Seq. No. 19713 2.R1040 Contig ID 5'-most EST LIB3050-022-Q1-K1-E8 Seq. No. 10813 19714 1.R1040 Contig ID 5'-most EST LIB3050-022-Q1-K1-D1 Method BLASTX NCBI GI g4512659 BLAST score 369 2.0e-35 E value Match length 99 % identity NCBI Description (AC006931) putative protein kinase [Arabidopsis thaliana] >gi 4544465 gb AAD22372.1 AC006580 4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No. 10814

Contig ID 19715_1.R1040

5'-most EST LIB30 $\overline{5}$ 0-019-Q1-K1-H7

Seq. No. 10815

Contig ID 19720_1.R1040

5'-most EST LIB3050-022-Q1-K1-C3

```
Seq. No.
                  10816
                  19724 1.R1040
Contig ID
                  fua701038254.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2245060
BLAST score
                  686
                  5.0e-72
E value
                  204
Match length
% identity
                   61
                  (Z97342) allergen homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  10817
                  19728 1.R1040
Contig ID
5'-most EST
                  LIB3050-022-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3386620
                  592
BLAST score
                  2.0e-61
E value
Match length
                  134
                   46
% identity
NCBI Description
                   (AC004665) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  10818
                  19729 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy048d04b1
Method
                  BLASTX
NCBI GI
                  g3335376
BLAST score
                  1170
E value
                  1.0e-131
Match length
                  313
                  75
% identity
NCBI Description
                   (AC003028) putative ammonium transporter [Arabidopsis
                  thaliana]
Seq. No.
                  10819
                  19729 2.R1040
Contig ID
5'-most EST
                  uC-gmropic115g04b1
Method
                  BLASTX
NCBI GI
                  q3335376
BLAST score
                  271
E value
                  8.0e-24
Match length
                  58
% identity
NCBI Description
                   (AC003028) putative ammonium transporter [Arabidopsis
                  thaliana]
Seq. No.
                  10820
Contig ID
                  19733 1.R1040
5'-most EST
                  LIB3050-022-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q3643608
BLAST score
                  372
E value
                  9.0e-36
Match length
                  129
% identity
NCBI Description
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
```

```
Contig ID
                   19737 1.R1040
5'-most EST
                   LIB3050-022-Q1-K1-A9
Method
                   BLASTX
NCBI GI
                   q3461846
BLAST score
                   312
E value
                   2.0e-28
Match length
                   91
                   33
% identity
NCBI Description
                   (AC005315) putative zinc-finger protein [Arabidopsis
                   thaliana]
                   10822
Seq. No.
                   19739 1.R1040
Contig ID
5'-most EST
                   fde700875824.h1
Method
                   BLASTX
                   g2829910
NCBI GI
BLAST score
                   793
E value
                   9.0e-85
Match length
                   166
                   19
% identity
NCBI Description
                   (AC002291) Unknown protein, contains regulator of
                   chromosome condensation motifs [Arabidopsis thaliana]
                   10823
Seq. No.
                   19739 2.R1040
Contig ID
5'-most EST
                   rlr700896417.hl
                   BLASTX
Method
                   g2829910
NCBI GI
BLAST score
                   757
E value
                   1.0e-80
Match length
                   191
                   76
% identity
NCBI Description
                   (AC002291) Unknown protein, contains regulator of
                   chromosome condensation motifs [Arabidopsis thaliana]
                   10824
Seq. No.
                   19744 1.R1040·
Contig ID
                   LIB30\overline{5}0-022-Q1-K1-B4
5'-most EST
                   10825
Seq. No.
                   19746_1.R1040
Contig ID
5'-most EST
                   pcp700989286.hl
Seq. No.
                   10826
                   19756 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy183d12b1
Method
                   BLASTX
NCBI GI
                   g4510345
BLAST score
                   460
E value
                   2.0e-45
Match length
                   160
% identity
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10827
```

10821

Seq. No.

Match length

% identity

164

```
19756 2.R1040
Contig ID
5'-most EST
                   LIB3170-078-Q1-K1-E5
Method
                   BLASTX.
                   q4510345
NCBI GI
BLAST score
                   244
E value
                   2.0e-20
Match length
                   93
                   77
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   10828
Seq. No.
Contig ID
                   19756 3.R1040
                   LIB3139-085-P1-N1-H5
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4510345
BLAST score
                   232
                   3.0e-19
E value
Match length
                   57
                   70
% identity
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                   10829
                   19756 4.R1040
Contig ID
5'-most EST
                   fua701039811.hl
Method
                   BLASTX
NCBI GI
                   g4510345
BLAST score
                   170
E value
                   3.0e-12
Match length
                   33
% identity
                   88
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
                   10830
Seq. No.
Contig ID
                   19760 1.R1040
5'-most EST
                   hyd700726331.h1
Method
                   BLASTX
NCBI GI
                   g2827141
BLAST score
                   1633
E value
                   0.0e + 00
Match length
                   371
% identity
                   81
NCBI Description
                   (AF027173) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
                   10831
Seq. No.
Contig ID
                   19764 1.R1040
5'-most EST
                   LIB3109-001-Q1-K4-E2
Seq. No.
                   10832
                   19767 1.R1040
Contig ID
5'-most EST
                   LIB3093-018-Q1-K2-D3
Method
                   BLASTX
NCBI GI
                   q1703143
BLAST score
                   568
E value
                   3.0e-58
```

Seq. No.

```
NCBI Description ACTIN-LIKE PROTEIN 3 >gi 881635 (U29610) Arp3 [Acanthamoeba
                   castellanii]
Seq. No.
                   10833
                   19767 2.R1040
Contig ID
5'-most EST
                   jC-gmst02400023b08a1
Method
                   BLASTX
NCBI GI
                   q1168329
BLAST score
                   498
E value
                   3.0e-50
Match length
                   175
                   54
% identity
                   ACTIN-LIKE PROTEIN 3 (ACTIN-LIKE PROTEIN 66B) (ACTIN-2)
NCBI Description
                   >gi_558568_emb_CAA50674_ (X71789) actin related protein
[Drosophila melanogaster] >gi_1096138_prf__2111232A
                   actin-related protein [Drosophila melanogaster]
Seq. No.
                   10834
Contig ID
                   19768 1.R1040
5'-most EST
                   LIB3107-053-Q1-K1-A5
Method
                   BLASTX
NCBI GI
                   g2760834
BLAST score
                   948
E value
                   1.0e-103
Match length
                   278
% identity
                   70
NCBI Description
                    (AC003105) putative nitrate transporter [Arabidopsis
                   thalianal
Seq. No.
                   10835
                   19768 2.R1040
Contig ID
5'-most EST
                   k11701205306.h1
Method
                   BLASTX
NCBI GI
                   q3912921
BLAST score
                   148
E value
                   3.0e-09
Match length
                   59
% identity
NCBI Description
                    (AF001308) G/T DNA mismatch repair enzyme [Arabidopsis
                   thalianal
Seq. No.
                   10836
                   19768 3.R1040
Contig ID
5'-most EST
                   taw700657702.h1
Seq. No.
                   10837
Contig ID
                   19769 1.R1040
5'-most EST
                   LIB3050-021-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   q4454567
BLAST score
                   235
E value
                   2.0e-19
Match length
                   123
% identity
NCBI Description
                   (AF128407) lipase homolog [Arabidopsis thaliana]
```

```
19774 1.R1040
Contig ID
5'-most EST
                  LIB3050-021-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                   g2147328
BLAST score
                  202
                   5.0e-16
E value
Match length
                  90
% identity
                   52
NCBI Description dioscorin class B - Dioscorea cayenensis (fragment)
                   10839
Seq. No.
                   19775 1.R1040
Contig ID
                  LIB3109-045-Q1-K1-D6
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2160184
BLAST score
                  143
                   7.0e-09
E value
Match length
                   107
% identity
                   41
                   (AC000132) ESTs gb_H37208,gb_H36853 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   10840
                   19790 1.R1040
Contig ID
5'-most EST
                   LIB3107-006-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                   q2501448
BLAST score
                   450
E value
                   9.0e-45
Match length
                   93
% identity
                   92
NCBI Description
                  UBIQUITIN-LIKE PROTEIN SMT3 >gi_1707372_emb_CAA67923
                   (X99609) ubiquitin-like protein [Arabidopsis thaliana]
Seq. No.
                   10841
Contig ID
                   19791 1.R1040
5'-most EST
                   q5677872
Seq. No.
                   10842
                   19791 2.R1040
Contig ID
5'-most EST
                  LIB3050-021-01-K1-E12
Seq. No.
                   10843
Contig ID
                   19794 1.R1040
5'-most EST
                  LIB3139-040-P1-N1-A3
Method
                  BLASTX
NCBI GI
                   q4558591
BLAST score
                  588
E value
                   2.0e-60
Match length
                   178
% identity
NCBI Description
                   (AC006555) putative beta-1,3-glucanase [Arabidopsis
                   thalianal
Seq. No.
                   10844
                   19794 2.R1040
Contig ID
```

sat701004908.hl

```
Method
                   BLASTX
NCBI GI
                   q4455206
BLAST score
                  1230
                   1.0e-136
E value
Match length
                   324
                   72
% identity
                   (AL035440) putative beta-1, 3-glucanase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   10845
                   19794 3.R1040
Contig ID
5'-most EST
                   LIB3092-045-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                   q4455206
BLAST score
                   351
E value
                   3.0e-33
                   99
Match length
% identity
NCBI Description
                   (AL035440) putative beta-1, 3-glucanase [Arabidopsis
                   thaliana]
                   10846
Seq. No.
Contig ID
                   19794 4.R1040
5'-most EST
                   LIB3092-030-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   q4455206
BLAST score
                   251
E value
                   2.0e-21
Match length
                   77
% identity
NCBI Description
                   (AL035440) putative beta-1, 3-glucanase [Arabidopsis
                   thaliana]
                   10847
Seq. No.
                   19794_5.R1040
Contig ID
5'-most EST
                   jC-gmro02910043a11d1
Method
                   BLASTX
NCBI GI
                   q4558591
BLAST score
                   242
E value
                   2.0e-20
Match length
                   62
% identity
NCBI Description
                   (ACO06555) putative beta-1,3-glucanase [Arabidopsis
                   thaliana]
                   10848
Seq. No.
Contig ID
                   19794 6.R1040
5'-most EST
                   jC-gmro02800026b05d1
Seq. No.
Contig ID
                   19795 1.R1040
5'-most EST
                  LIB3050-020-01-K1-H4
Seq. No.
                   10850
                   19797 1.R1040
Contig ID
```

LIB3050-020-Q1-K1-H6

Method

BLASTX

```
10851
Seq. No.
                   19801 1.R1040
Contig ID
5'-most EST
                   hyd700727614.h1
                   10852
Seq. No.
                   19803 1.R1040
Contig ID
                   pmv700888283.hl
5'-most EST
Seq. No.
                   10853
                   19804 1.R1040
Contig ID
5'-most EST
                   g4283486
Method
                   BLASTX
NCBI GI
                   g2104816
BLAST score
                   220
E value
                   2.0e-17
Match length
                   174
                   28
% identity
NCBI Description
                   (Y13092) alpha-adaptin [Drosophila melanogaster]
Seq. No.
                   10854
                   19807 1.R1040
Contig ID
5'-most EST
                   LIB3050-021-Q1-K1-A6
Method
                   BLASTX
NCBI GI
                   g2342682
BLAST score
                   290
E value
                   6.0e-26
Match length
                   76
                   72
% identity
                   (AC000106) Contains similarity to Rattus AMP-activated
NCBI Description
                   protein kinase (gb_X95577). [Arabidopsis thaliana]
                   10855
Seq. No.
                   19820 1.R1040
Contig ID
5'-most EST
                   LIB3050-015-Q1-E1-D10
Method
                   BLASTX
NCBI GI
                   g1871577
BLAST score
                   433
                   1.0e-42
E value
Match length
                   158
% identity
                   (Y11553) putative 21kD protein precursor [Medicago sativa]
NCBI Description
                   10856
Seq. No.
                   19824 1.R1040
Contig ID
                   LIB30\overline{5}0-020-Q1-K1-F2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4508069
BLAST score
                   385
E value
                   5.0e-37
Match length
                   149
                   48
% identity
NCBI Description
                   (AC005882) 12246 [Arabidopsis thaliana]
Seq. No.
                   10857
                   19838 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy244f07b1
```

Method

BLASTN

```
g3785983
NCBI GI
                   320
BLAST score
                   3.0e-29
E value
                   153
Match length
                   43
% identity
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10858
                   19838 2.R1040
Contig ID
                   LIB3073-017-Q1-K1-E3
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3785983
BLAST score
                   253
                   1.0e-21
E value
                   119
Match length
% identity
                   43
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10859
                   19838 3.R1040
Contig ID
5'-most EST
                   leu701149924.hl
Seq. No.
                   10860
                   19842 1.R1040
Contig ID
5'-most EST
                   LIB3092-062-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   g1931638
BLAST score
                   706
E value
                   2.0e-74
Match length
                   277
% identity
                   58
NCBI Description
                   (U95973) transcription factor RUSH-lalpha isolog
                   [Arabidopsis thaliana]
Seq. No.
                   10861
Contig ID
                   19844 1.R1040
5'-most EST
                   q4292527
Seq. No.
                   10862
                   19846 1.R1040
Contig ID
5'-most EST
                   LIB3050-020-Q1-K1-C6
Seq. No.
                   10863
Contig ID
                   19852 1.R1040
5'-most EST
                   LIB3051-107-Q1-K1-E10
Method
                   BLASTN
NCBI GI
                   q1209887
BLAST score
                   279
E value
                   1.0e-155
Match length
                   703
% identity
                   99
NCBI Description
                  Glycine max nonsymbiotic hemoglobin gene, complete cds
                   10864
Seq. No.
                   19852 2.R1040
Contig ID
                   LIB3170-074-Q1-K1-E2
5'-most EST
```

Match length

```
NCBI GI
                   g1209887
BLAST score
                   404
E value
                   0.0e+00
Match length
                   420
                   99
% identity
                   Glycine max nonsymbiotic hemoglobin gene, complete cds
NCBI Description
                   10865
Seq. No.
                   19854 1.R1040
Contig ID
                   epx70\overline{1}103941.h1
5'-most EST
Method
                   BLASTX
                   g2832717
NCBI GI
                   325
BLAST score
E value
                   4.0e-30
                   99
Match length
% identity
                   67
                   (AJ003114) alkaline/neutral invertase [Lolium temulentum]
NCBI Description
Seq. No.
                   10866
                   19855 1.R1040
Contig ID
5'-most EST
                   LIB3050-025-Q1-K1-G12
                   BLASTX
Method
NCBI GI
                   q2982456
BLAST score
                   328
E value
                   3.0e-30
Match length
                   101
                   69
% identity
NCBI Description
                   (AL022223) putative protein [Arabidopsis thaliana]
                   10867
Seq. No.
                   19857 1.R1040
Contig ID
5'-most EST
                   LIB3170-051-Q1-J1-D10
                   10868
Seq. No.
                   19858 1.R1040
Contig ID
5'-most EST
                   sat701010221.h2
                   10869
Seq. No.
                   19859 1.R1040
Contig ID
5'-most EST
                   uxk70\overline{0}671202.h1
Method
                   BLASTX
                   g4337207
NCBI GI
BLAST score
                   786
                   9.0e-84
E value
Match length
                   268
% identity
NCBI Description
                   (AC006403) putative zinc-finger protein [Arabidopsis
                   thaliana]
                   10870
Seq. No.
                   19868 1.R1040
Contig ID
5'-most EST
                   trc700564095.hl
Method
                   BLASTX
NCBI GI
                   q1871185
BLAST score
                   300
E value
                   4.0e-27
```

```
% identity
NCBI Description
                   (U90439) seven in absentia isolog [Arabidopsis thaliana]
Seq. No.
                   10871
                   19873 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910007d04a1
                   BLASTX
Method
NCBI GI
                   q3928084
BLAST score
                   394
E value
                   3.0e-38
Match length
                   140
                   59
% identity
                   (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   10872
Seq. No.
                   19878 1.R1040
Contig ID
                   pcp700988751.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2388580
BLAST score
                   549
E value
                   1.0e-56
Match length
                   112
% identity
NCBI Description
                   (AC000098) Similar to Sequence 10 from patent 5477002
                   (gb 1253956). [Arabidopsis thaliana]
Seq. No.
Contig ID
                   19884 1.R1040
5'-most EST
                   g5666<del>6</del>94
                   10874
Seq. No.
Contig ID
                   19888 1.R1040
5'-most EST
                   gsv701049390.h1
Method
                   BLASTX
NCBI GI
                   q4204304
BLAST score
                   252
E value
                   2.0e-21
Match length
                   97
% identity
NCBI Description
                   (AC003027) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   10875
Contig ID
                   19892 1.R1040
5'-most EST
                   LIB3050-019-Q1-K1-E6
Method
                   BLASTX
                   g3461820
NCBI GI
BLAST score
                   190
E value
                   2.0e-14
Match length
                   58
% identity
NCBI Description
                   (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   10876
Contig ID
                   19894 1.R1040
```

 $ncj70\overline{0}983051.h1$

NCBI GI

```
Seq. No.
                   10877
Contig ID
                   19897 1.R1040
5'-most EST
                   uC-gmflminsoy058b03b1
Seq. No.
                   19897 2.R1040
Contig ID
5'-most EST
                   LIB3093-058-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   q3142290
BLAST score
                   295
E value
                   3.0e-26
Match length
                   91
% identity
NCBI Description
                   (AC002411) Contains similarity to gb Z69902 from C.
                   elegans. [Arabidopsis thaliana]
                   10879
Seq. No.
                   19899 1.R1040
Contig ID
5'-most EST
                   r1r70\overline{0}901811.h1
Method
                   BLASTX
NCBI GI
                   g3184098
BLAST score
                   1118
E value
                   1.0e-122
Match length
                   510·
% identity
NCBI Description
                   (AL023777) coenzyme a synthetase [Schizosaccharomyces
                   pombe]
                   10880
Seq. No.
Contig ID
                   19899 2.R1040
                   LIB3092-008-Q1-K1-F12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3184098
BLAST score
                   368
E value
                   4.0e-35
Match length
                   181
% identity
NCBI Description
                   (AL023777) coenzyme a synthetase [Schizosaccharomyces
                   pombe]
                   10881
Seq. No.
Contig ID
                   19905 1.R1040
5'-most EST
                   uC-gmrominsoy047e11b1
Method
                   BLASTX
                   g4580517
NCBI GI
BLAST score
                   662
E value
                   2.0e-69
Match length
                   213
% identity
NCBI Description
                   (AF036302) scarecrow-like 5 [Arabidopsis thaliana]
Seq. No.
                   10882
Contig ID
                   19913 1.R1040
                   LIB3050-019-Q1-K1-B4
5'-most EST
Method
                   BLASTX
```

g2281098

Match length

144

```
412
BLAST score
E value
                   3.0e-40
Match length
                   125
% identity
                   58
NCBI Description
                   (AC002333) hypothetical protein [Arabidopsis thaliana]
                   10883
Seq. No.
Contig ID
                   19916 1.R1040
                   rca70\overline{0}998019.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4530126
BLAST score
                   680
E value
                   4.0e-71
Match length
                   326
% identity
                   45
NCBI Description
                   (AF078082) receptor-like protein kinase homolog RK20-1
                   [Phaseolus vulgaris]
                   10884
Seq. No.
                   19916 3.R1040
Contig ID
                   smc700745880.h1
5'-most EST
Seq. No.
                   10885
Contig ID
                   19918 1.R1040
5'-most EST
                   LIB3050-019-Q1-K1-C1
                   10886
Seq. No.
                   19927 1.R1040
Contig ID
                   LIB3109-035-Q1-K2-H6
5'-most EST
Seq. No.
                   10887
                   19930 1.R1040
Contig ID
                   LIB30\overline{5}0-019-Q1-K1-E1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3164115
BLAST score
                   337
E value
                   3.0e-31
Match length
                   153
% identity
                   45
NCBI Description
                   (AJ224145) major latex-like protein [Rubus idaeus]
                   10888
Seq. No.
Contig ID
                   19932 1.R1040
5'-most EST
                   LIB3050-019-Q1-K1-B12
Seq. No.
                   10889
Contig ID
                   19932 2.R1040
5'-most EST
                   zsg701117871.h2
Seq. No.
                   10890
Contig ID
                   19935_1.R1040
5'-most EST
                   LIB3051-035-Q1-K1-B3
Method
                   BLASTX
NCBI GI
                   g3924596
BLAST score
                   632
                   8.0e-66
E value
```

% identity

76

```
% identity
NCBI Description
                    (AF069442) putative phospho-ser/thr phosphatase
                    [Arabidopsis thaliana]
                    10891
Seq. No.
                    19938 1.R1040
Contig ID
 5'-most EST
                    jC-gmf102220069b05d1
Method
                    BLASTX
NCBI GI
                    g1706082
BLAST score
                    144
E value
                    7.0e-09
Match length
                    46
% identity
                    63
                    SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)
NCBI Description
                    >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536
                    CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,
                    cv. Alexis, aleurone, Peptide, 516 aa]
                    >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3
                    [Hordeum vulgare]
Seq. No.
                    10892
                    19939 1.R1040
Contig ID
                    LIB3050-018-Q1-E1-H7
5'-most EST
                    10893
Seq. No.
                    19943 1.R1040
Contig ID
5'-most EST
                    uC-gmflminsoy023d08b1
Method
                    BLASTX
NCBI GI
                    g3935165
BLAST score
                    294
E value
                    2.0e-26
Match length
                    132
% identity
NCBI Description (AC004557) F17L21.8 [Arabidopsis thaliana]
Seq. No.
                    10894
                    19943 2.R1040
Contig ID
5'-most EST
                    LIB3167-077-P1-K2-H4
Method
                    BLASTN
NCBI GI
                    g3228389
BLAST score
                    38
E value
                    6.0e-12
Match length
                    74
% identity
                    88
NCBI Description
                    Genomic sequence for Arabidopsis thaliana BAC F17L21,
                    complete sequence [Arabidopsis thaliana]
Seq. No.
                    10895
                    19958 1.R1040
Contig ID
                    bth700845494.h1
5'-most EST
Method
                    BLASTX
NCBI GI
                    q3367536
BLAST score
                    435
E value
                    7.0e-43
Match length
                    117
```

NCBI Description (AC004392) Contains similarity to symbiosis-related like protein F1N20.80 gi 2961343 from A. thaliana BAC gb AL022140. EST $g\overline{b}$ T04695 comes from this gene. [Arabidopsis thaliana] 10896 Seq. No. Contig ID 19958 2.R1040 5'-most EST asn701138380.hl Method BLASTX NCBI GI q3367536 BLAST score 432 E value 2.0e-42 Match length 117 % identity 75 (AC004392) Contains similarity to symbiosis-related like NCBI Description protein F1N20.80 gi_2961343 from A. thaliana BAC gb AL022140. EST \overline{gb} T04695 comes from this gene. [Arabidopsis thaliana] Seq. No. 10897 19958 3.R1040 Contig ID 5'-most EST LIB3106-023-Q1-K1-B5 Seq. No. 10898 Contig ID 19958 4.R1040 LIB3093-017-Q1-K1-F10 5'-most EST Seq. No. 10899 Contig ID 19963 1.R1040 5'-most EST LIB3050-018-Q1-E1-G12 Seq. No. 10900 19978 1.R1040 Contig ID 5'-most EST $uxk70\overline{0}672945.h1$

Seq. No. 10901

Contig ID 19986 1.R1040 5'-most EST pxt700943425.h1

Seq. No. 10902

Contig ID 19995_1.R1040 5'-most EST hyd700729446.h1

Method BLASTX
NCBI GI g3033377
BLAST score 1123
E value 1.0e-123
Match length 501
% identity 47

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No. 10903

Contig ID 19995_2.R1040 5'-most EST fua701037134.h1

Method BLASTX NCBI GI g3033377 BLAST score 314

```
E value
                   8.0e-29
Match length
                   131
% identity
NCBI Description
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
                   thaliana]
                   10904
Seq. No.
                   19997 1.R1040
Contig ID
5'-most EST
                   zsg701120155.h1
                   BLASTX
Method
NCBI GI
                   g1931647
BLAST score
                   2216
                   0.0e + 00
E value
Match length
                   564
% identity
                   74
                   (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                   [Arabidopsis thaliana]
                   10905
Seq. No.
Contig ID
                   19997 2.R1040
                  LIB3051-087-Q1-K1-A6
5'-most EST
                   10906
Seq. No.
                   19997_3.R1040
Contig ID
5'-most EST
                   LIB3170-059-Q1-K1-A9
                   BLASTX
Method
                   g1931647
NCBI GI
BLAST score
                   231
E value
                   4.0e-24
Match length
                   90
                   59
% identity
NCBI Description
                   (U95973) endomembrane protein EMP70 precusor isolog
                   [Arabidopsis thaliana]
                   10907
Seq. No.
                   20000_1.R1040
Contig ID
5'-most EST
                   LIB3050-018-Q1-E1-C3
                   10908
Seq. No.
                   20003 1.R1040
Contig ID
5'-most EST
                  LIB3109-032-Q1-K1-G2
                  BLASTX
Method
                   g3695392
NCBI GI
BLAST score
                   424
E value
                   4.0e-41
Match length
                   201
                   47
% identity
NCBI Description
                  (AF096371) No definition line found [Arabidopsis thaliana]
                   10909
Seq. No.
                   20013 1.R1040
Contig ID
5'-most EST
                  LIB3050-018-Q1-E1-A2
Seq. No.
                   10910
Contig ID
                   20016 1.R1040
                   crh70\overline{0}852015.h1
5'-most EST
```

BLASTX

Method

```
q3721540
NCBI GI
BLAST score
                   2338
E value
                   0.0e + 00
Match length
                   519
% identity
                   82
NCBI Description
                   (D83583) Sulfite Reductase [Nicotiana tabacum]
                   >gi_3738234_dbj BAA33796_ (AB010717) sulfite reductase
                   [Nicotiana tabacum] .
Seq. No.
                   10911
                   20017 1.R1040
Contig ID
                   LIB3050-015-Q1-E1-G5
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1922242
BLAST score
                   250
E value
                   3.0e-21
Match length
                   122
% identity
NCBI Description
                   (Y10084) hypothetical protein [Arabidopsis thaliana]
                   10912
Seq. No.
                   20017 2.R1040
Contig ID
5'-most EST
                   LIB3050-018-Q1-E1-A6
Method
                   BLASTX
NCBI GI
                   q1922242
BLAST score
                   223
E value
                   5.0e-18
Match length
                   76
                   59
% identity
NCBI Description
                   (Y10084) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   10913
                   20017 3.R1040
Contig ID
5'-most EST
                   wrg700787203.h2
Seq. No.
                   10914
Contig ID
                   20017 4.R1040
5'-most EST
                   LIB3055-012-01-N1-G8
                   10915
Seq. No.
                   20021 1.R1040
Contig ID
5'-most EST
                   LIB3050-018-Q1-E1-B1
Method
                   BLASTX
NCBI GI
                   q4063750
BLAST score
                   140
E value
                   1.0e-08
Match length
                   90
% identity
NCBI Description
                   (AC005851) putative indole-3-acetate
                   beta-glucosyltransferase synthetase [Arabidopsis thaliana]
                   10916
Seq. No.
Contig ID
                   20024 1.R1040
5'-most EST
                   LIB3050-018-Q1-E1-B12
```

20025 1.R1040

Seq. No. Contig ID

```
uC-gmropic042c12b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2842485
BLAST score
                  211
E value
                  3.0e-16
Match length
                  118
% identity
                  38
NCBI Description
                   (AL021749) hypothetical protein [Arabidopsis thaliana]
                  10918
Seq. No.
                  20030 1.R1040
Contig ID
                  LIB3050-017-Q1-E1-G2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q282963
BLAST score
                  629
E value
                  1.0e-65
Match length
                  176
                  70
% identity
NCBI Description
                  transforming protein (myb) homolog (clone myb.Ph2) - garden
                  petunia >gi_20561_emb_CAA78387_ (Z13997) protein 2 [Petunia
                  x hybrida]
Seq. No.
                  10919
Contig ID
                  20038 1.R1040
                  uC-qmrominsoy282f05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2275214
BLAST score
                  232
                  3.0e-19
E value
Match length
                  91
% identity
                   (AC002337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  10920
Seq. No.
                  20040 1.R1040
Contig ID
5'-most EST
                  vzy700754715.hl
Method
                  BLASTX
NCBI GI
                  q3646451
BLAST score
                  204
                  8.0e-16
E value
Match length
                  112
% identity
                   (AL031603) mRNA cap methyltransferase [Schizosaccharomyces
NCBI Description
                  pombe]
                  10921
Seq. No.
Contig ID
                  20043 1.R1040
5'-most EST
                  zsg701124088.h1
Method
                  BLASTX
NCBI GI
                  q2828147
BLAST score
                  537
                  2.0e-54
E value
Match length
                  222
% identity
                   (AF042384) BC-2 protein [Homo sapiens]
NCBI Description
```

Seq. No.

BLAST score

480

```
20043 2.R1040
Contig ID
5'-most EST
                   LIB3139-097-P1-N1-A11
Method
                   BLASTX
NCBI GI
                   g3021268
BLAST score
                   114
                   3.0e-11
E value
                   193
Match length
% identity
                   36
NCBI Description
                   (AL022347) putative protein [Arabidopsis thaliana]
                   10923
Seq. No.
                   20043 7.R1040
Contig ID
5'-most EST
                   eep700865965.hl
                   10924
Seq. No.
                   20047 1.R1040
Contig ID
5'-most EST
                   g4313881
Seq. No.
                   10925
Contig ID
                   20051 1.R1040
5'-most EST
                   trc700562631.h1
Method
                   BLASTX
NCBI GI
                   g1732247
BLAST score
                   329
E value
                   3.0e-37
Match length
                   121
% identity
                   64
NCBI Description
                   (U72762) transcription factor Mybl [Nicotiana tabacum]
                   10926
Seq. No.
                   20051 2.R1040
Contig ID
5'-most EST
                   trc700566792.h1
Method
                   BLASTX
NCBI GI
                   g1945279
BLAST score
                   368
E value
                   2.0e-35
Match length
                   96
% identity
NCBI Description
                   (Y11350) myb factor [Oryza sativa]
Seq. No.
                   10927
                   20051 3.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy043b11b1
Method
                   BLASTX
NCBI GI
                   q1946267
BLAST score
                   247
E value
                   2.0e-21
Match length
                   61
% identity
                   70
NCBI Description
                   (Y11415) myb [Oryza sativa]
Seq. No.
                   10928
                   20056 1.R1040
Contig ID
5'-most EST
                   r1r70\overline{0}898958.h1
Method
                   BLASTX
NCBI GI
                   g1168940
```

```
5.0e-48
E value
Match length
                  175
% identity
                  51
NCBI Description
                  CHORISMATE MUTASE PRECURSOR (CM-1) >gi 629509 pir S38958
                  chorismate mutase precursor - Arabidopsis thaliana
                  >gi_429153_emb_CAA81286_ (Z26519) chorismate mutase
                  precursor [Arabidopsis thaliana]
Seq. No.
                  10929
                  20056_2.R1040
Contig ID
5'-most EST
                  qsv701047857.hl
Method
                  BLASTX
NCBI GI
                  q1168940
BLAST score
                  157
E value
                  2.0e-10
Match length
                  96
                  39
% identity
                  CHORISMATE MUTASE PRECURSOR (CM-1) >gi 629509 pir S38958
NCBI Description
                  chorismate mutase precursor - Arabidopsis thaliana
                  >gi_429153_emb_CAA81286 (Z26519) chorismate mutase
                  precursor [Arabidopsis thaliana]
Seq. No.
                  10930
Contig ID
                  20063 1.R1040
                  LIB3050-017-Q1-E1-F6
5'-most EST
Method
                  BLASTX
                  q1730502
NCBI GI
                  271
BLAST score
                  1.0e-23
E value
Match length
                  116
% identity
                  47
                  TRANSMEMBRANE PROTEIN PFT27 >gi 110903 pir A31351 probable
NCBI Description
                  transmembrane protein FT27 - mouse >gi_535682 (M23568)
                  transmembrane protein [Mus musculus]
Seq. No.
                  10931
Contig ID
                  20065 1.R1040
                  LIB3050-017-Q1-E1-F9
5'-most EST
Method
                  BLASTX
                  q1362019
NCBI GI
BLAST score
                  166
E value
                  2.0e-11
Match length
                  68
% identity
                  zinc finger protein 6 - Arabidopsis thaliana >gi_790683
NCBI Description
                   (L39649) zinc finger protein [Arabidopsis thaliana]
Seq. No.
                  10932
Contig ID
                  20067 1.R1040
5'-most EST
                  wrg70\overline{0}787082.h2
Method
                  BLASTX
NCBI GI
                  q3757527
BLAST score
                  472
E value
                  4.0e-47
Match length
                  116
% identity
                  (AC005167) putative ribosomal protein L27 [Arabidopsis
NCBI Description
```

```
10933
Seq. No.
                   20067 3.R1040
Contig ID
                   wrg700787493.h2
5'-most EST
                   10934
Seq. No.
                   20068 1.R1040
Contig ID
                   LIB30\overline{5}0-012-Q1-E1-C3
5'-most EST
                   10935
Seq. No.
                   20070_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy309h05b1
Method
                   BLASTX
NCBI GI
                   g2642158
                   739
BLAST score
                   3.0e-78
E value
Match length
                   236
% identity
                   (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   10936
Seq. No.
                   20072 1.R1040
Contig ID
5'-most EST
                   LIB3109-016-Q1-K1-F10
Method
                   BLASTX
NCBI GI
                   g3128173
BLAST score
                   415
E value
                   7.0e-41
Match length
                   97
% identity
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   10937
                   20081 1.R1040
Contig ID
                   LIB3139-006-P1-N1-A11
5'-most EST
Method
                   BLASTX
                   g4220476
NCBI GI
BLAST score
                   310
                   5.0e-48
E value
Match length
                   140
% identity
NCBI Description
                  (AC006069) ribophorin I-like protein [Arabidopsis thaliana]
                   10938
Seq. No.
Contig ID
                   20085 1.R1040
5'-most EST
                   jC-gmst02400056c10d1
                   10939
Seq. No.
                   20085 2.R1040
Contig ID
5'-most EST
                   zsg70\overline{1}127688.h1
Method
                   BLASTX
NCBI GI
                   g2832658
                   300
BLAST score
                   1.0e-26
E value
```

thaliana]

1901

NCBI Description (ALO21710) putative protein [Arabidopsis thaliana]

120

Match length % identity

NCBI GI

```
10940
Seq. No.
                   20085 3.R1040
Contig ID
5'-most EST
                  hrw701062022.h1
                   10941
Seq. No.
                   20085 4.R1040
Contig ID
5'-most EST
                   hyd700727277.hl
Method
                   BLASTX
                   g4432845
NCBI GI
                   195
BLAST score
                   3.0e-15
E value
                   98
Match length
                   43
% identity
NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
                   10942
Seq. No.
                   20085 6.R1040
Contig ID
                   zsg701129657.h1
5'-most EST
Seq. No.
                   10943
Contig ID
                   20086 1.R1040
5'-most EST
                   LIB3050-017-Q1-E1-A10
                   10944
Seq. No.
Contig ID
                   20090 2.R1040
5'-most EST
                   awf70\overline{0}836953.h1
                   10945
Seq. No.
Contig ID
                   20091 1.R1040
5'-most EST
                   g5126401
Method
                   BLASTX
NCBI GI
                   q2160182
                   273
BLAST score
                   1.0e-23
E value
Match length
                   148
                   46
% identity
                   (AC000132) ESTs gb_ATTS1236, gb_T43334, gb_N97019, gb_AA395203
NCBI Description
                   come from this gene. [Arabidopsis thaliana]
                   10946
Seq. No.
                   20091 2.R1040
Contig ID
5'-most EST
                   LIB3051-006-Q1-K1-D4
Method
                   BLASTX
                   g2160182
NCBI GI
BLAST score
                   156
E value
                   2.0e-10
Match length
                   114
                   39
% identity
                   (AC000132) ESTs gb ATTS1236, gb T43334, gb N97019, gb AA395203
NCBI Description
                   come from this gene. [Arabidopsis thaliana]
                   10947
Seq. No.
                   20096 1.R1040
Contig ID
5'-most EST
                   LIB3055-011-Q1-N1-H7
Method
                   BLASTX
```

g4056438

```
BLAST score
                    248
E value
                    8.0e-21
Match length
                    144
                    41
% identity
NCBI Description
                    (AC005990) F508.11 [Arabidopsis thaliana]
Seq. No.
                    10948
                    20096 2.R1040
Contig ID
                    uxk70\overline{0}670789.h1
5'-most EST
                    10949
Seq. No.
Contig ID
                    20097 1.R1040
5'-most EST
                    LIB3050-017-Q1-E1-B12
                    10950
Seq. No.
                    20097 2.R1040
Contig ID
5'-most EST
                    bth700846843.h1
                    10951
Seq. No.
                    20105 1.R1040
Contig ID
5'-most EST
                    LIB3050-016-Q1-E1-G9
                    10952
Seq. No.
                    20106 1.R1040
Contig ID
5'-most EST
                    LIB3050-016-Q1-E1-G1
                    10953
Seq. No.
                    20109 1.R1040
Contig ID
5'-most EST
                    pxt700943385.h1
                    10954
Seq. No.
Contig ID
                    20115 1.R1040
5'-most EST
                    LIB3109-042-Q1-K1-A1
Method
                    BLASTX
NCBI GI
                    q1351365
BLAST score
                    153
E value
                    5.0e-10 ···
Match length
                    48
% identity
                    60
NCBI Description
                    UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 6.7 KD PROTEIN
                    (CR6) >gi_2130002_pir__S68969 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) - potato >gi_633683_emb_CAA57768
                    (X82325) cytochrome c reductase subunit [Solanum tuberosum]
Seq. No.
                    10955
                    20122 1.R1040
Contig ID
5'-most EST
                    q4289641
Method
                    BLASTX
NCBI GI
                    g2864615
BLAST score
                    241
E value
                    3.0e-20
Match length
                    156
% identity
NCBI Description
                    (AL021811) putative protein [Arabidopsis thaliana]
```

20127_1.R1040

Seq. No.

Contig ID

Contig ID

```
5'-most EST
                  g5677300
Method
                  BLASTX
NCBI GI
                  q4454452
BLAST score
                   406
                   2.0e-39
E value
Match length
                   91
% identity
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  10957
Seq. No.
                   20127 2.R1040
Contig ID
                  ASG3244V4L-01-Q1-E1-H2
5'-most EST
                   10958
Seq. No.
Contig ID
                   20145 1.R1040
5'-most EST
                   vwf700676069.hl
Method
                  BLASTX
                  g3702332
NCBI GI
BLAST score
                   179
E value
                   8.0e-13
                   98
Match length
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  10959
Seq. No.
                  20147 1.R1040
Contig ID
5'-most EST
                   zsg701126402.h1
Method
                  BLASTX
NCBI GI
                  g3850108
BLAST score
                   437
E value
                   3.0e-43
Match length
                  147
% identity
                   56
NCBI Description
                   (AL033388) putative calcium-transporting atpase
                   [Schizosaccharomyces pombe]
                  10960
Seq. No.
                  20155 1.R1040
Contig ID
5'-most EST
                  LIB3050-016-Q1-E1-B1
Method
                  BLASTX
                  g1853968
NCBI GI
BLAST score
                  568
E value
                  2.0e-58
Match length
                  154
                  71
% identity
NCBI Description (D88121) CPRD12 protein [Vigna unguiculata]
                  10961
Seq. No.
                  20163 1.R1040
Contig ID
5'-most EST
                  LIB3093-031-Q1-K1-F2
Seq. No.
                  10962
                  20167 1.R1040
Contig ID
5'-most EST
                  jC-gmro02910054f07d1
Seq. No.
                  10963
```

20168_1.R1040

Method

BLASTX

```
5'-most EST
                   LIB3109-054-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   q1730502
BLAST score
                   163
E value
                   8.0e-11
Match length
                   81
                   47
% identity
NCBI Description
                   TRANSMEMBRANE PROTEIN PFT27 >gi 110903 pir A31351 probable
                   transmembrane protein FT27 - mouse >gi 535682 (M23568)
                   transmembrane protein [Mus musculus]
                   10964
Seq. No.
Contig ID
                   20168 2.R1040
5'-most EST
                   jC-gmle01810082f07a1
Seq. No.
                   10965
Contig ID
                   20180 1.R1040
5'-most EST
                   dpv70\overline{1}098046.h1
                   10966
Seq. No.
Contig ID
                   20182 1.R1040
5'-most EST
                   uC-gmrominsoy293b01b1
Method
                   BLASTX
NCBI GI
                   g4558678
BLAST score
                   256
E value
                   2.0e-21
Match length
                   119
                   49
% identity
NCBI Description (AC006586) unknown protein [Arabidopsis thaliana]
                   10967
Seq. No.
                   20183 1.R1040
Contig ID
                   LIB30\overline{5}0-016-Q1-E1-A3
5'-most EST
Seq. No.
                   10968
                   20184 1.R1040
Contig ID
5'-most EST
                   LIB3050-010-Q1-E1-H4
Seq. No.
                   10969
                   20185 1.R1040
Contig ID
5'-most EST
                   LIB3050-016-Q1-E1-A5
                   10970
Seq. No.
                   20188 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy021e02b1
Method
                   BLASTX
NCBI GI
                   q2369766
BLAST score
                   1153
E value
                   1.0e-126
Match length
                   303
% identity
                   74
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
Seq. No.
                   10971
                   20188 2.R1040
Contig ID
5'-most EST
                   LIB3106-026-Q1-K1-E1
```

Contig ID

5'-most EST

```
NCBI GI
                   g2369766
BLAST score
                   217
E value
                   2.0e-17
Match length
                   130
% identity
                   50
                   (AJ001304) hypothetical protein [Citrus x paradisi]
NCBI Description
                   10972
Seq. No.
                   20188 5.R1040
Contig ID
5'-most EST
                   kl1701210213.h1
Seq. No.
                   10973
Contig ID
                   20194 1.R1040
5'-most EST
                   LIB3050-015-Q1-E1-F7
Method
                   BLASTX
NCBI GI
                   g642134
BLAST score
                   431
E value
                   2.0e-42
Match length
                   138
% identity
                   62
                   (D45355) protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi 3063704 emb CAA18595.1 (AL022537) protein kinase AME3
                   [Arabidopsis thaliana]
                   10974
Seq. No.
                   20194 4.R1040
Contig ID
5'-most EST
                   gsv701054279.h1
                   10975
Seq. No.
                   20202 1.R1040
Contig ID
5'-most EST
                   fua701038834.hl
Method
                   BLASTX
NCBI GI
                   g452593
BLAST score
                   1056
E value
                   1.0e-115
Match length
                   291
                   67
% identity
NCBI Description
                   (D21814) ORF [Lilium longiflorum]
                   10976
Seq. No.
                   20209 1.R1040
Contig ID
5'-most EST
                   g4295899
Seq. No.
                   10977
                   20211 1.R1040
Contig ID
5'-most EST
                   smc70\overline{0}746358.h1
Method
                   BLASTX
NCBI GI
                   q3550519
BLAST score
                   1317
E value
                   1.0e-151
Match length
                   335
% identity
NCBI Description
                   (AJ007630) oxygenase [Nicotiana tabacum]
                   10978
Seq. No.
```

20213 1.R1040

 $vzy70\overline{0}756512.h1$

```
Method
                   BLASTX
NCBI GI
                   g3335335
BLAST score
                   472
                   3.0e-47
E value
                   121
Match length
                   73
% identity
NCBI Description
                   (ACO04512) ESTs gb F14113 and gb T42122 come from this
                   region. [Arabidopsis thaliana]
                   10979
Seq. No.
                   20215 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy208b07b1
Method
                   BLASTX
NCBI GI
                   g121345
BLAST score
                   1683
                   0.0e+00
E value
                   341
Match length
                   91
% identity
NCBI Description
                   GLUTAMINE SYNTHETASE PR-2 (ISOZYME ALPHA)
                   (GLUTAMATE--AMMONIA LIGASE) >gi_68593_pir__AJFBQA glutamate--ammonia ligase (EC 6.3.1.2) alpha, cytosolic -
                   kidney bean >gi_21013_emb_CAA27632_ (X04002) glutamine
                   synthetase subunit (aa 1-356) [Phaseolus vulgaris]
                   >gi 225068 prf 1208270B synthetase R2,Gln [Phaseolus
                   vulgaris]
                   10980
Seq. No.
                   20215 2.R1040
Contig ID
5'-most EST
                   LIB3087-013-Q1-K1-C5
Method
                   BLASTN
NCBI GI
                   g21012
BLAST score
                   366
E value
                   0.0e+00
Match length
                   762
                   93
% identity
NCBI Description
                   Phaseolus vulgaris mRNA (pR-2) for glutamine synthetase
                   (GS, EC 6.3.1.2)
Seq. No.
                   10981
                   20217 1.R1040
Contig ID
5'-most EST
                   LIB3050-015-Q1-E1-E12
Method
                   BLASTX
NCBI GI
                   q1491776
BLAST score
                   336
                   1.0e-31
E value
Match length
                   87
% identity
                   78
NCBI Description
                   (M37636) cationic peroxidase [Arachis hypogaea]
Seq. No.
                   10982
                   20228 1.R1040
Contig ID
5'-most EST
                   rca701001008.hl
Method
                   BLASTX
NCBI GI
                   q4567226
BLAST score
                   195
E value
                   1.0e-14
```

Match length

```
% identity
                  (AC007119) unknown protein [Arabidopsis thaliana]
NCBI Description
                   10983
Seq. No.
                   20230 1.R1040
Contig ID
5'-most EST
                   zhf700954844.h1
Method
                   BLASTX
                   g3688174
NCBI GI
BLAST score
                   537
                   8.0e-55
E value
                   148
Match length
                   68
% identity
                   (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                   10984
Seq. No.
                   20239 1.R1040
Contig ID
                   pxt700946086.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3064039
BLAST score
                   323
                   1.0e-29
E value
Match length
                   142
% identity
                   41
                   (AF054445) major latex protein homolog [Mesembryanthemum
NCBI Description
                   crystallinum]
                   10985
Seq. No.
                   20242 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy155d05b1
                   10986
Seq. No.
                   20243 1.R1040
Contig ID
                   LIB3051-048-Q1-K1-E9
5'-most EST
Seq. No.
                   10987
Contig ID
                   20249 1.R1040
5'-most EST
                   vwf700676351.h1
Method
                   BLASTX
NCBI GI
                   q3860250
BLAST score
                   400
E value
                   7.0e-39
Match length
                   163
                   53
% identity
NCBI Description
                   (AC005824) putative chloroplast prephenate dehydratase
                   [Arabidopsis thaliana]
Seq. No.
                   10988
Contig ID
                   20254 1.R1040
5'-most EST
                   zzp700833517.hl
                   BLASTX
Method
NCBI GI
                   q4103635
BLAST score
                   432
E value
                   2.0e-42
Match length
                   162
                   56
% identity
```

NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]

```
10989
Seq. No.
                   20262 1.R1040
Contig ID
                   LIB30\overline{5}0-015-Q1-E1-A1
5'-most EST
                   BLASTX
Method
                   g2460188
NCBI GI
BLAST score
                   1082
E value
                   1.0e-118
                   320
Match length
% identity
                   (AF020785) polygalacturonase inhibiting protein [Prunus
NCBI Description
                   armeniaca]
                   10990
Seq. No.
                   20268 1.R1040
Contig ID
                   LIB3050-014-Q1-E1-G6
5'-most EST
Method
                   BLASTX
                   g3618214
NCBI GI
BLAST score
                   203
E value
                   2.0e-15
Match length
                   186
% identity
                   31
                   (AL031579) dihydrofolate reductase [Schizosaccharomyces
NCBI Description
                   pombe]
                   10991
Seq. No.
                   20273 1.R1040
Contig ID
                   asn701142539.hl
5'-most EST
                   10992
Seq. No.
                   20275 1.R1040
Contig ID
5'-most EST
                   fC-gmse700839629a5
Method
                   BLASTX
NCBI GI
                   g3152608
BLAST score
                   488
E value
                   3.0e-49
Match length
                   96
% identity
                   (AC004482) putative BEL1-like homeotic protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   10993
                   20278 1.R1040
Contig ID
5'-most EST
                   sat701010383.h1
Method
                   BLASTX
NCBI GI
                   q3193287
BLAST score
                   770
E value
                   3.0e-82
Match length
                   156
% identity
NCBI Description
                   (AF069298) Arabidopsis predicted protein of unknown
                   function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]
Seq. No.
                   10994
                   20281 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810035g12a2
```

Seq. No.

5'-most EST

```
Contig ID
                   20281 2.R1040
5'-most EST
                   seb70\overline{0}653544.h1
                   10996
Seq. No.
Contig ID
                   20288 1.R1040
5'-most EST
                   LIB3170-055-Q1-K1-A3
                   BLASTX
Method
NCBI GI
                   q4469009
BLAST score
                   491
E value
                   3.0e-49
Match length
                   137
                   75
% identity
                   (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   10997
Contig ID
                   20293 1.R1040
5'-most EST
                   fde700871956.h1
                   10998
Seq. No.
Contig ID
                   20296 1.R1040
                   LIB30\overline{5}0-014-Q1-E1-F8
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1015315
BLAST score
                   66
E value
                   9.0e-29
                                                                · . .
Match length
                   82
                   95
% identity
                   Pisum sativum (clone PsRCI35-2) ribosomal protein L41 mRNA,
NCBI Description
                   complete cds
                   10999
Seq. No.
                   20297 1.R1040
Contig ID
5'-most EST
                   LIB3050-014-Q1-E1-F9
Seq. No.
                   11000
                   20300 1.R1040
Contig ID
5'-most EST
                   uC-gmropic030b10b1
                   11001
Seq. No.
                   20300 2.R1040
Contig ID
                   LIB30\overline{5}1-018-Q1-E1-H2
5'-most EST
Seq. No.
                   11002
                   20305 1.R1040
Contig ID
5'-most EST
                   uC-gmropic102d02b1
Method
                   BLASTX
NCBI GI
                   g4538939
BLAST score
                   1181
E value
                   1.0e-130
Match length
                   254
% identity
                   87
NCBI Description
                   (AL049483) Col-0 casein kinase I-like protein [Arabidopsis
                   thaliana]
                   11003
Seq. No.
                   20308 1.R1040
Contig ID
```

LIB3050-014-Q1-E1-D12

NCBI GI

BLAST score

```
Method
                   BLASTX
                   g2642215
NCBI GI
                   304
BLAST score
E value
                   2.0e-27
                   79
Match length
                   70
% identity
                   (AF030386) NOI protein [Arabidopsis thaliana]
NCBI Description
                   11004
Seq. No.
                   20312 1.R1040
Contig ID
5'-most EST
                   LIB3092-016-Q1-K1-G8
                   11005
Seq. No.
                   20313 1.R1040
Contig ID
5'-most EST
                   LIB3050-003-Q1-E1-F3
                   11006
Seq. No.
                   20313 2.R1040
Contig ID
5'-most EST
                   LIB3050-014-Q1-E1-D7
Seq. No.
                   11007
                   20316_1.R1040
Contig ID
5'-most EST
                   LIB3050-014-Q1-E1-E11
                   11008
Seq. No.
                   20317 1.R1040
Contig ID
5'-most EST
                   LIB3050-014-Q1-E1-C3
                   BLASTX
Method
                   g3335376
NCBI GI
BLAST score
                   300
                   2.0e-27
E value
Match length
                   73
                   73
% identity
                   (AC003028) putative ammonium transporter [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   11009
Contig ID
                   20319 1.R1040
                  LIB30\overline{9}3-009-Q1-K1-E5
5'-most EST
Method
                   BLASTX
                   g3281848
NCBI GI
BLAST score
                   467
E value
                   4.0e-46
                   251
Match length
                   49
% identity
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   11010
Seq. No.
                   20319 2.R1040
Contig ID
5'-most EST
                   LIB3050-014-Q1-E1-A6
                   11011
Seq. No.
Contig ID
                   20319_3.R1040
5'-most EST
                   LIB3053-014-Q1-N1-H2
Method
                   BLASTX
```

g4559352

148



E value 3.0e-09 Match length 83 % identity NCBI Description (AC006585) putative DNA binding protein [Arabidopsis thaliana] Seq. No. 11012 20319 5.R1040

Contig ID $smc70\overline{0}749977.h1$ 5'-most EST

11013 Seq. No. 20319 6.R1040 Contig ID g5677508 5'-most EST BLASTX Method g3281848 NCBI GI BLAST score 331 2.0e-30

E value Match length 182 % identity 44

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 11014

Contig ID 20319 7.R1040

5'-most EST · LIB3050-007-Q1-E1-E1

11015 Seq. No.

20319 8.R1040 Contig ID rca701002460.h1 5'-most EST

Seq. No. 11016

20319 9.R1040 Contig ID

LIB3139-054-P1-N1-A7 5'-most EST

BLASTX Method NCBI GI g2130024 BLAST score 216 E value 7.0e-30 Match length 151

49

% identity

NCBI Description DNA-binding protein ABF2 - wild oat

>gi 1159879 emb CAA88331 (Z48431) DNA-binding protein

et.

[Avena fatua]

11017 Seq. No.

20319 11.R1040 Contig ID pmv700891060.hl 5'-most EST

Seq. No. 11018

20330 1.R1040 Contig ID 5'-most EST fjg700968365.hl

Seq. No. 11019

20330 2.R1040 Contig ID 5'-most EST jsh701070124.h1

11020 Seq. No.

20333 1.R1040 Contig ID

5'-most EST uC-gmflminsoy046e07b1

BLAST score

% identity

E value Match length 214 3.0e-17

128

45

```
Method
                  BLASTX
NCBI GI
                  g3152559
                  591
BLAST score
                  8.0e-61
E value
                  165
Match length
                  66
% identity
NCBI Description
                  (AC002986) Similarity to A. thaliana gene product
                  F21M12.20, gb_AC000132. EST gb_Z25651 comes from this gene.
                  [Arabidopsis thaliana]
                  11021
Seq. No.
                  20333 2.R1040
Contig ID
5'-most EST
                  sat701011980.hl
                  11022
Seq. No.
                  20334 1.R1040
Contig ID
5'-most EST
                  LIB3050-014-Q1-E1-C12
Method
                  BLASTX
                  g2270994
NCBI GI
BLAST score
                  159
E value
                  8.0e-11
Match length
                  57
                  53
% identity
NCBI Description
                 (AF004809) Ca+2-binding EF hand protein [Glycine max]
Seq. No.
                  11023
                  20340 1.R1040
Contig ID
5'-most EST
                  LIB3050-012-Q1-E1-E5
Seq. No.
                  11024
                  20344_1.R1040
Contig ID
                  gsv701045374.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3420056
BLAST score
                  220
E value
                  9.0e-18
                  85
Match length
% identity
                  (AC004680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  11025
                  20346 1.R1040
Contig ID
5'-most EST
                  LIB3050-013-Q1-E1-H6
                  11026
Seq. No.
Contig ID
                  20348 1.R1040
5'-most EST
                  dpv701098552.h1
                  11027
Seq. No.
                  20351 1.R1040
Contig ID
                  LIB3050-014-Q1-E1-A11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3885339
```

5'-most EST

```
NCBI Description
                   (AC005623) putative bzip protein [Arabidopsis thaliana]
                   11028
Seq. No.
                   20360 1.R1040
Contig ID
5'-most EST
                   LIB3139-075-P1-N1-C2
                   11029
Seq. No.
                   20360 2.R1040
Contig ID
                   zhf700963712.h1
5'-most EST
                   11030
Seq. No.
Contig ID
                   20361 1.R1040
5'-most EST
                   jC-qmst02400069e10a1
                   BLASTX
Method
NCBI GI
                   g4454033
BLAST score
                   487
                   6.0e-49
E value
Match length
                   213
                   47
% identity
NCBI Description
                   (AL035394) putative potassium transport protein
                   [Arabidopsis thaliana]
Seq. No.
                   11031
                   20362 1.R1040
Contig ID
5'-most EST
                   LIB3050-013-Q1-E1-F10
Seq. No.
                   11032
                   20365 1.R1040
Contig ID
5'-most EST
                   LIB3050-013-Q1-E1-F2
Seq. No.
                   11033
                   20368 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy298f07b1
Seq. No.
                   11034
                   20370 1.R1040
Contig ID
5'-most EST
                   dpv701097078.h1
                   11035
Seq. No.
                   20371 1.R1040
Contig ID
5'-most EST
                   jC-qmle01810093c07d1
Method
                   BLASTX
NCBI GI
                   g3426048
BLAST score
                   239
E value
                   4.0e-20
Match length
                   63
% identity
                   78
NCBI Description
                   (AC005168) putative hydroxymethylglutaryl-CoA lyase
                   precursor [Arabidopsis thaliana]
Seq. No.
                   11036
                   20373 1.R1040
Contig ID
5'-most EST
                   LIB3139-069-P1-N1-F4
                   11037
Seq. No.
                   20374 1.R1040
Contig ID
```

LIB3138-029-Q1-N1-F7

% identity

```
Method
                   BLASTX
NCBI GI
                   g1922242
BLAST score
                   200
                   5.0e-15
E value
                   68
Match length
                   56
% identity
NCBI Description
                  (Y10084) hypothetical protein [Arabidopsis thaliana]
                   11038
Seq. No.
                   20377 1.R1040
Contig ID
5'-most EST
                   LIB3050-013-Q1-E1-C7
Method
                   BLASTX
NCBI GI
                   g2500572
BLAST score
                   176
E value
                   1.0e-12
Match length
                   139
                   37
% identity
                  RIBONUCLEASE S-2 PRECURSOR (STYLAR GLYCOPROTEIN 2)
NCBI Description
                   (S2-RNASE) >gi_1405424_emb_CAA65319_ (X96465) S2-RNase
                   [Antirrhinum hispanicum]
Seq. No.
                   11039
                   20385 1.R1040
Contig ID
5'-most EST
                   sat701002746.h2
Method
                   BLASTX
NCBI GI
                   g4467156
BLAST score
                   730
E value
                   3.0e-77
                   218
Match length
% identity
                   69
NCBI Description
                   (AL035540) putative protein [Arabidopsis thaliana]
                   11040
Seq. No.
                   20387 1.R1040
Contig ID
5'-most EST
                   LIB3139-076-P1-N1-E11
                   11041
Seq. No.
                   20388 1.R1040
Contig ID
5'-most EST
                   LIB3051-048-Q1-K1-H11
Method
                   BLASTX
NCBI GI
                   g2832629
BLAST score
                   838
E value
                   9.0e-90
Match length
                   314
% identity
                   49
NCBI Description
                   (ALO21711) 4-coumarate-CoA ligase - like [Arabidopsis
                   thaliana]
                   11042
Seq. No.
                   20391 1.R1040
Contig ID
5'-most EST
                   LIB3050-013-Q1-E1-E1
Method
                  BLASTX
NCBI GI
                   q1363482
BLAST score
                   211
                   9.0e-17
E value
                  101
Match length
                   50
```

```
NCBI Description IAA11 protein - Arabidopsis thaliana >gi_972925 (U18413)
                  IAA11 [Arabidopsis thaliana]
                  11043
Seq. No.
                  20398 1.R1040
Contig ID
5'-most EST
                  LIB3050-013-Q1-E1-B12
Method
                  BLASTX
                  q1706282
NCBI GI
BLAST score
                  314
                  6.0e-29
E value
Match length
                  112
% identity
                  54
                  DISEASE RESISTANCE RESPONSE PROTEIN 206 >gi 508844 (U11716)
NCBI Description
                  disease resistance response protein 206-d [Pisum sativum]
                  11044
Seq. No.
Contig ID
                  20401 1.R1040
5'-most EST
                  gsv701049038.h1
Seq. No.
                  11045
                  20410 1.R1040
Contig ID
                  trc700565029.h1
5'-most EST
Seq. No.
                  11046
                  20410 2.R1040
Contig ID
                  LIB3074-033-Q1-K1-G12
5'-most EST
                  11047
Seq. No.
                  20412 1.R1040
Contig ID
5'-most EST
                  uC-gmrominsoy106e08b1
Method
                  BLASTX
NCBI GI
                  g481002
BLAST score
                  1406
E value
                  1.0e-156
Match length
                  338
% identity
                  78
NCBI Description protein kinase - common ice plant >gi 407057 emb CAA81443
                   (Z26846) protein kinase [Mesembryanthemum crystallinum]
                  11048
Seq. No.
                  20412_2.R1040
Contig ID
5'-most EST
                  fC-gmse700842846d3
                  11049
Seq. No.
                  20412_3.R1040
Contig ID
5'-most EST
                  LIB3051-051-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q2055374
BLAST score
                  381
E value
                  6.0e-37
Match length
                  87
% identity
                  (U29095) serine-threonine protein kinase [Triticum
NCBI Description
                  aestivum]
                  11050
Seq. No.
```

20414 1.R1040

Contig ID

5'-most EST

```
5'-most EST
                   LIB3139-101-P1-N1-D5
                   11051
Seq. No.
                   20421 1.R1040
Contig ID
5'-most EST
                   LIB3051-020-Q1-E1-A11
Method
                   BLASTX
NCBI GI
                   g3738285
BLAST score
                   482
                   4.0e-48
E value
                   159
Match length
                   59
% identity
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   11052
Seq. No.
                   20421 2.R1040
Contig ID
                   g4314028
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3738285
BLAST score
                   313
                   1.0e-28
E value
Match length
                   102
% identity
                   57
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11053
                   20421 3.R1040
Contig ID
                   r1r70\overline{0}900790.h1
5'-most EST
                   BLASTX
Method
                   g3738285
NCBI GI
BLAST score
                   181
E value
                   3.0e-13
                   57
Match length
% identity
NCBI Description
                   (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                   11054
                   20421 4.R1040
Contig ID
                   LIB3093-030-Q1-K1-H10
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3738285
BLAST score
                   173
E value
                   3.0e-12
Match length
                   87
% identity
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11055
                   20427 1.R1040
Contig ID
5'-most EST
                   LIB3106-010-Q1-K1-D12
                   11056
Seq. No.
Contig ID
                   20431 1.R1040
5'-most EST
                   LIB3050-012-Q1-E1-F4
                   11057
Seq. No.
                   20433 1.R1040
Contig ID
```

uC-gmrominsoy185f05b1

Method

NCBI GI

BLASTX

g3341697

 \mathfrak{T}'

```
Seq. No.
                   11058
Contig ID
                   20435 1.R1040
                   gsv701045964.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2708747
BLAST score
                   154
                   6.0e-10
E value
Match length
                   74
                   12
% identity
                   (AC003952) putative glycine-rich, zinc-finger DNA-binding
NCBI Description
                   protein [Arabidopsis thaliana]
                   11059
Seq. No.
                   20436 1.R1040
Contig ID
5'-most EST
                   LIB3050-012-Q1-E1-G1
Seq. No.
                   11060
                   20440 1.R1040
Contig ID
                   LIB3050-012-Q1-E1-G2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3885334
BLAST score
                   281
E value
                   1.0e-35
Match length
                   105
                   70
% identity
                   (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   11061
                   20441 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400065g01d1
Method
                   BLASTX
NCBI GI
                   g3309583
BLAST score
                   540
E value
                   3.0e-55
Match length
                   112
% identity
                   93
NCBI Description
                   (AF073830) fructose-6-phosphate
                   2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]
Seq. No.
                   11062
                   20445 1.R1040
Contig ID
                   LIB31\overline{0}9-007-Q1-K1-G4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2760317
BLAST score
                   258
E value
                   5.0e-27
                   106
Match length
% identity
NCBI Description
                   (AC002130) F1N21.1 [Arabidopsis thaliana]
Seq. No.
                   11063
                   20445 2.R1040
Contig ID
                   leu70\overline{1}155845.h1
5'-most EST
```

5'-most EST

```
BLAST score
                   237
                   1.0e-19
E value
                   58
Match length
                   69
% identity
                   (AC003672) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11064
                   20445 3.R1040
Contig ID
                   LIB3170-052-Q1-K1-F10
5'-most EST
                   11065
Seq. No.
                   20445 4.R1040
Contig ID
                   bth70\overline{0}847369.h1
5'-most EST
                   11066
Seq. No.
                   20446_1.R1040
Contig ID
                   LIB3050-005-Q1-K1-E2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2981475
BLAST score
                   1301
E value
                   1.0e-144
                   325
Match length
% identity
                   74
                   (AF053084) putative cinnamyl alcohol dehydrogenase [Malus
NCBI Description
                   domestica]
Seq. No.
                   11067
                   20447 1.R1040
Contig ID
5'-most EST
                   LIB3050-012-Q1-E1-D6
Seq. No.
                   11068
                   20450 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy042b07b1
Seq. No.
                   11069
                   20452 1.R1040
Contig ID
5'-most EST
                   LIB3139-036-P1-N1-G10
Seq. No.
                   11070
Contig ID
                   20453 1.R1040
5'-most EST
                   LIB3139-096-P1-N1-H4
Seq. No.
                   11071
                   20453 2.R1040
Contig ID
5'-most EST
                   LIB3072-024-Q1-E1-F2
Seq. No.
                   11072
                   20453 5.R1040
Contig ID
5'-most EST
                   LIB3073-001-Q1-K1-H3
Seq. No.
                   11073
Contig ID
                   20453 6.R1040
5'-most EST
                   uC-gmropic004e03b1
Seq. No.
                   11074
                   20458 1.R1040
Contig ID
```

LIB3051-083-Q1-K1-A4

```
Seq. No.
                   11075
                   20458 2.R1040 ·
Contig ID
                   LIB30\overline{5}1-031-Q1-K1-C2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g285741
BLAST score
                   720
                   9.0e-76
E value
                   405
Match length
                   42
% identity
                   (D14550) EDGP precursor [Daucus carota]
NCBI Description
Seq. No.
                   11076
                   20458 3.R1040
Contig ID
5'-most EST
                   LIB3051-086-Q1-K1-B6
                   11077
Seq. No.
Contig ID
                   20461 1.R1040
                   LIB30\overline{5}0-012-Q1-E1-B6
5'-most EST
                   11078
Seq. No.
                   20464 1.R1040
Contig ID
                   LIB3092-033-Q1-K1-A12
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4490736
BLAST score
                   257
E value
                   3.0e-22
                   80
Match length
% identity
                   34
NCBI Description
                   (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   1.1079
                   20464 2.R1040
Contig ID
5'-most EST
                   gsv701048836.hl
Method
                   BLASTX
NCBI GI
                   g4490736
BLAST score
                   416
E value
                   9.0e-41
                   166
Match length
% identity
                   34
NCBI Description
                   (AL035708) putative protein [Arabidopsis thaliana]
                   11080
Seq. No.
                   20466 1.R1040
Contig ID
5'-most EST
                   LIB3050-012-Q1-E1-C10
Seq. No.
                   11081
                   20470 1.R1040
Contig ID
                   fua701039064.hl
5'-most EST
Method
                   BLASTX
                   g4567228
NCBI GI
BLAST score
                   480
E value
                   5.0e-48
                   143
Match length
% identity
                   65
```

NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

5'-most EST

```
11082
Seq. No.
                   20479 1.R1040
Contig ID
                  LIB3050-011-Q1-E1-H9
5'-most EST
                  BLASTX
Method
                   g2832623
NCBI GI
BLAST score
                   703
E value
                   5.0e-74
                   207
Match length
                   65
% identity
                   (AL021711) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   11083
Seq. No.
                   20481 1.R1040
Contig ID
                   gsv701056625.h1
5'-most EST
                   BLASTX
Method
                   g3953458
NCBI GI
BLAST score
                   948
E value
                   1.0e-103
                   215
Match length
% identity
                   88
                   (AC002328) F20N2.3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11084
                   20482 1.R1040
Contig ID
                  kl1701213506.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4539301
                   822
BLAST score
E value
                   8.0e-88
Match length
                   355
% identity
                   47
                   (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   11085
                   20487 1.R1040
Contig ID
5'-most EST
                   jsh701063973.hl
                   11086
Seq. No.
Contig ID
                   20488 1.R1040
5'-most EST
                   LIB3107-014-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   g4049350
BLAST score
                   538
E value
                   1.0e-54
Match length
                   220
% identity
NCBI Description
                   (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                   11087
Contig ID
                   20497 1.R1040
5'-most EST
                   LIB3109-038-Q1-K1-G8
Seq. No.
                   11088
Contig ID
                   20500 1.R1040
```

LIB3139-047-P1-N1-B4

```
BLASTX
Method
NCBI GI
                  g3309082
BLAST score
                  656
                  1.0e-68
E value
                  164
Match length
                   77
% identity
NCBI Description
                   (AF076251) calcineurin B-like protein 1 [Arabidopsis
                  thaliana]
                   11089
Seq. No.
                   20501 1.R1040
Contig ID
                  dpv701102737.h1
5'-most EST
Method
                  BLASTX
                  q2598589
NCBI GI
BLAST score
                  853
                   1.0e-109
E value
Match length
                  275
% identity
                   69
NCBI Description
                  (Y15367) MtN19 [Medicago truncatula]
                   11090
Seq. No.
                   20501 2.R1040
Contig ID
5'-most EST
                  LIB3050-011-Q1-E1-D7
Method
                  BLASTX
NCBI GI
                   q2598589
BLAST score
                  590
E value
                   5.0e-61
Match length
                  177
% identity
                   64
NCBI Description
                  (Y15367) MtN19 [Medicago truncatula]
                   11091
Seq. No.
Contig ID
                   20511 1.R1040
5'-most EST
                   LIB3050-011-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                   q4406789
BLAST score
                   433
E value
                   9.0e-43
Match length
                   114
% identity
NCBI Description
                   (AC006532) putative glutamate decarboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   11092
Contig ID
                   20513 1.R1040
5'-most EST
                  LIB3050-011-Q1-E1-G10
Seq. No.
                   11093
Contig ID
                   20522 1.R1040
5'-most EST
                  LIB3107-049-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                   q2244924
BLAST score
                   335
E value
                   2.0e-31
Match length
                  87
% identity
```

NCBI Description (Z97339) glutaredoxin [Arabidopsis thaliana]

Seq. No.

```
Seq. No.
                   11094
Contig ID
                  20522 2.R1040
5'-most EST
                  LIB3050-011-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                  g2244924
BLAST score
                  291
E value
                   3.0e-26
Match length
                  75
% identity
                   71
NCBI Description (Z97339) glutaredoxin [Arabidopsis thaliana]
                   11095
Seq. No.
Contig ID
                   20529 1.R1040
5'-most EST
                  LIB3051-017-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                   g4538913
BLAST score
                   490
E value
                   4.0e-49
Match length
                  207
% identity
                   56
                   (AL049482) putative protein [Arabidopsis thaliana]
NCBI Description
                   11096
Seq. No.
                   20532 1.R1040
Contig ID
                   g4293043
5'-most EST
Method
                   BLASTX
                   q417148
NCBI GI
                   695
BLAST score
                   5.0e-73
E value
Match length
                   215
% identity
                   63
                   PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)
NCBI Description
                   (G2-4) >gi_99912_pir__A33654 heat shock protein 26A -
                   soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]
Seq. No.
                   11097
                   20538_1.R1040
Contig ID
                  LIB3050-011-Q1-E1-D12
5'-most EST
                   BLASTX
Method
                   g2275204
NCBI GI
BLAST score
                   371
E value
                   4.0e-35
Match length
                  104
                   72
% identity
                   (AC002337) DNA binding protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   11098
Seq. No.
Contig ID
                   20539 1.R1040
                   LIB3050-011-Q1-E1-D4
5'-most EST
                   11099
Seq. No.
                   20539 2.R1040
Contig ID
5'-most EST
                   jC-qmro02800032c01a1
                   11100
```

```
20540 1.R1040
Contig ID 1
                  LIB3050-011-Q1-E1-D5
5'-most EST
                  11101
Seq. No.
                  20543 1.R1040
Contig ID
5'-most EST
                  jC-qmle01810037b02a2
Method
                  BLASTX
                  g112925
NCBI GI
BLAST score
                  335
                  6.0e-31
E value
                  177
Match length
                  45
% identity
                  41-2 PROTEIN ANTIGEN PRECURSOR >gi_320938_pir A45503 41-2
NCBI Description
                  protein antigen precursor - Plasmodium falciparum
                  >gi 160039 (J04656) 41-2 protein antigen [Plasmodium
                  falciparum]
Seq. No.
                  11102
                  20544 1.R1040
Contig ID
                  LIB3050-011-Q1-E1-D9
5'-most EST
Method
                  BLASTX
                  g2580584
NCBI GI
BLAST score
                  625
                  4.0e-65
E value
                  208
Match length
                  59
% identity
NCBI Description (AF000976) 7-0-methyltransferase [Medicago sativa]
                  11103
Seq. No.
                  20545 1.R1040
Contig ID
                  LIB3092-047-Q1-K1-C3
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1170620
BLAST score
                  701
E value
                  6.0e-74
                  186
Match length
                  73
% identity
                  KINESIN-LIKE PROTEIN B >gi 1084341 pir__S48019
NCBI Description
                  kinesin-related protein katB - Arabidopsis thaliana
                  >gi 1438842 dbj BAA04673_ (D21137) heavy chain polypeptide
                  of kinesin-like protein [Arabidopsis thaliana]
                  11104
Seq. No.
                 20545 2.R1040
Contig ID
5'-most EST
                  LIB3050-011-Q1-E1-E11
Method
                  BLASTX
NCBI GI
                  g1170619
BLAST score
                  557
                  2.0e-57
E value
Match length
                  149
                  76
% identity
                  KINESIN-LIKE PROTEIN A >gi_479594_pir__S34830
NCBI Description
                  kinesin-related protein katA - Arabidopsis thaliana
                  >gi_303502_dbj_BAA01972_ (D11371) kinesin-like motor
                  protein heavy chain [Arabidopsis thaliana]
                  >gi_2911084_emb_CAA17546_ (AL021960) kinesin-related
```

protein katA [Arabidopsis thaliana]

Contig ID

```
11105
Seq. No.
                   20562 1 R1040 -
Contig ID
5'-most EST
                   jC-qmst02400016e09a1
Method
                   BLASTX
NCBI GI
                   q4309698
BLAST score
                   227
                   3.0e-18
E value
Match length
                   63
                   78
% identity.
                   (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                   11106
Seq. No.
Contig ID
                   20563 1.R1040
5'-most EST
                   LIB3050-011-Q1-E1-A8
Method
                   BLASTX
NCBI GI
                   g1362018
BLAST score
                   189
E value
                   4.0e-14
                   88
Match length
                   53
% identity
NCBI Description
                   zinc finger protein 5 - Arabidopsis thaliana >gi_790681
                   (L39648) zinc finger protein [Arabidopsis thaliana]
Seq. No.
                   11107
                   20564 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810031f07d1
Seq. No.
                   11108
Contig ID
                   20565 1.R1040
5'-most EST
                   LIB3051-015-Q1-E1-G1
Method
                   BLASTX
NCBI GI
                   g1762933
BLAST score
                   267
E value
                   3.0e-23
Match length
                   132
% identity
                   48
                   (U66263) tumor-related protein [Nicotiana tabacum]
NCBI Description
                   11109
Seq. No.
                   20570 1.R1040
Contig ID
5'-most EST
                   LIB3109-055-Q1-K1-E11
                   11110
Seq. No.
                   20572 1.R1040
Contig ID
5'-most EST
                   uC-gmropic073f05b1
Method
                   BLASTX
NCBI GI
                   q4432841
BLAST score
                   555
E value
                   1.0e-68
Match length
                   384
                   48
% identity
NCBI Description
                   (AC006283) hypothetical protein [Arabidopsis thaliana]
                   11111
Seq. No.
```

- 7,7

20572 2.R1040

```
5'-most EST
                   zsq701117769.h2
 Method
                   BLASTX
 NCBI GI
                   q4432841
 BLAST score
                   296
 E value
                   2.0e-26
Match length
                   97
 % identity
 NCBI Description
                    (AC006283) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                   11112
 Contig ID
                   20580 1.R1040
 5'-most EST
                   uC-gmropic009b03b1
 Method
                   BLASTX
 NCBI GI
                   q3695389
 BLAST score
                   351
 E value
                   4.0e-33
Match length
                   127
                   27
% identity
 NCBI Description
                    (AF096371) contains similarity to D-isomer specific
                   2-hydroxyacid dehydrogenases (Pfam: 2-Hacid DH.hmm, score:
                   19.11) [Arabidopsis thaliana]
Seq. No.
                   11113
 Contig ID
                   20580 2.R1040
 5'-most EST
                   uC-gmronoir015e07b1
 Seq. No.
                   11114
 Contig ID
                   20581 1.R1040
 5'-most EST
                   q5753648
Method
                   BLASTX
 NCBI GI
                   g1732556
                   198
 BLAST score
                   3.0e-15
 E value
Match length
                   91
 % identity
                   59
NCBI Description
                   (U66316) desiccation protective protein LEA5 [Glycine max]
 Seq. No.
                   11115
 Contig ID
                   20581 2.R1040
 5'-most EST
                   LIB3050-010-Q1-E1-H12
Method
                   BLASTX
NCBI GI
                   g1084390
BLAST score
                   202
                   1.0e-15
E value
Match length
                   88
 % identity
NCBI Description
                   late-embryogenesis protein lea5 - sweet orange
                   >gi_599726_emb_CAA86851_ (Z46824) Lea5 protein [Citrus
                   sinensis]
Seq. No.
                   11116
 Contig ID
                   20588 1.R1040
 5'-most EST
                   LIB3050-010-Q1-E1-G12
Seq. No.
                   11117
                   20591 1.R1040
 Contig ID
                   jC-gmle01810068b12d1
 5'-most EST
```

```
11118
Seq. No.
                   20591 2.R1040
Contig ID
5'-most EST
                   jC-gmle01810071b09a1
                   11119
Seq. No.
                   20595 1.R1040
Contig ID
                   pmv70\overline{0}889116.h1
5'-most EST
Method
                   BLASTX
                   q4490342
NCBI GI
BLAST score
                   617
                   4.0e-64
E value
                   216
Match length
                   64
% identity
                   (AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
                   11120
Seq. No.
                   20597 1.R1040
Contig ID
                   trc700565580.h1
5'-most EST
                   11121
Seq. No.
                   20599 1.R1040
Contig ID
                   hyd70\overline{0}724906.h1
5'-most EST
                   BLASTX
Method
                   g4056490
NCBI GI
BLAST score
                   512
E value
                   1.0e-51
                   276
Match length
% identity
                   42
                   (AC005896) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   11122
Seq. No.
                   20599 2.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy075c06b1
                   11123
Seq. No.
                   20599 4.R1040
Contig ID
                   kmv70\overline{0}741926.h1
5'-most EST
                   BLASTX
Method
                   g4056490
NCBI GI
                   712
BLAST score
                   3.0e-75
E value
Match length
                   264
                   56
% identity
                   (AC005896) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   11124
Seq. No.
                   20599 6.R1040
Contig ID
                   vwf700675878.h1
5'-most EST
                   11125
Seq. No.
                   20602 1.R1040
Contig ID
5'-most EST
                   LIB3050-010-Q1-E1-D9
                   11126
Seq. No.
                   20605 1.R1040
Contig ID
                   LIB3107-069-Q1-K1-A8
5'-most EST
```

5'-most EST

```
Seq. No.
                   11127
Contig ID
                  20609 1.R1040
                   g5677800
5'-most EST
                  BLASTX
Method
                   g1146165
NCBI GI
BLAST score
                  626
E value
                   6.0e-65
Match length
                  154
% identity
                   81
                  (L47479) urophorphyrin III methylase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11128
Contig ID
                   20610 1.R1040
                  ncj700985028.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3122858
BLAST score
                   1283
E value
                   1.0e-142
Match length
                   307
                   83
% identity
NCBI Description
                  D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR
                  >gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate
                  dehydrogenase [Arabidopsis thaliana]
                   >gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate
                   dehydrogenase [Arabidopsis thaliana]
                   11129
Seq. No.
                   20622 1.R1040
Contig ID
5'-most EST
                   zsq701117761.h2
Method
                   BLASTX
NCBI GI
                   q3132696
BLAST score
                   2115
                   0.0e + 00
E value
Match length
                   462
% identity
NCBI Description
                   (AF061962) SAR DNA-binding protein-1 [Pisum sativum]
                   11130
Seq. No.
                   20628 1.R1040
Contig ID
5'-most EST
                   LIB3093-046-01-K1-B5
                   11131
Seq. No.
                   20628 2.R1040
Contig ID
5'-most EST
                   LIB3087-002-Q1-K1-F10
Seq. No.
                   11132
                   20628 3.R1040
Contig ID
5'-most EST
                   LIB3139-113-P1-N1-D4
                   11133
Seq. No.
                   20633 1.R1040
Contig ID
5'-most EST
                   V4R-01-Q1-E1-E1
                   11134
Seq. No.
                   20636 1.R1040
Contig ID
```

pmv700891688.h1

% identity

```
Method
                  BLASTX
NCBI GI
                  q1707021
BLAST score
                  450
E value
                  5.0e-45
Match length
                  109
                  72
% identity
                   (U78721) Ubiquitin-conjugating enzyme, E2-16kD isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  11135
                  20642 1.R1040
Contig ID
                  LIB3050-010-Q1-E1-A2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4510398
BLAST score
                  231
E value
                  5.0e-19
Match length
                  111
                  52
% identity
NCBI Description
                  (AC006587) hypothetical protein [Arabidopsis thaliana]
                  11136
Seq. No.
                  20643 1.R1040
Contig ID
5'-most EST
                  LIB3050-010-Q1-E1-A3
Method
                  BLASTX
NCBI GI
                  q2565010
BLAST score
                  472
E value
                   3.0e-47
Match length
                   108
                   76
% identity
                   (AC002983) putative microfibril-associated protein
NCBI Description
                   [Arabidopsis thaliana] >gi_3377811 (AF076275) contains
                   similarity to ATP synthase B/B' (Pfam: ATP-synt_B.hmm,
                   score: 11.71) [Arabidopsis thaliana]
                   11137
Seq. No.
Contig ID
                   20645 1.R1040
5'-most EST
                  hrw701062847.hl
Method
                  BLASTX
NCBI GI
                   q2129597
BLAST score
                  1954
E value
                   0.0e + 00
Match length
                   411
                  89
% identity
                  glutamate dehydrogenase 1 - Arabidopsis thaliana
NCBI Description
                  >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis
                   thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1
                   [Arabidopsis thaliana]
Seq. No.
                   11138
                   20645 2.R1040
Contig ID
5'-most EST
                  fC-gmf1700906513f4
Method
                  BLASTX
NCBI GI
                   q2129597
BLAST score
                   678
E value
                   2.0e-71
Match length
                  152
```

```
NCBI Description glutamate dehydrogenase 1 - Arabidopsis thaliana
                  >gi 1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis
                  thaliana] >gi 1293095 (U53527) glutamate dehydrogenase 1
                  [Arabidopsis thaliana]
                  11139
Seq. No.
                  20645 3.R1040
Contig ID
                  LIB3109-035-Q1-K6-D10
5'-most EST
                  BLASTX
Method
                  g2129597
NCBI GI
                  332
BLAST score
                  1.0e-30
E value
Match length
                  72
                  90
% identity
                  glutamate dehydrogenase 1 - Arabidopsis thaliana
NCBI Description
                  >gi 1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis
                  thaliana] >gi 1293095 (U53527) glutamate dehydrogenase 1
                  [Arabidopsis thaliana]
Seq. No.
                  11140
                  20655 1.R1040
Contig ID
5'-most EST
                  leu701149415.hl
Method
                  BLASTX
NCBI GI
                  g3157934
BLAST score
                  611
E value
                  1.0e-63
Match length
                  164
% identity
                  72
                  (AC002131) Similar to hypothetical protein F09E5.8
NCBI Description
                  gb U37429 from C. elegans. ESTs gb T42019 and gb N97000
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  11141
                  20670 1.R1040
Contig ID
5'-most EST
                  LIB3094-073-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4454457
BLAST score
                  466
E value
                  2.0e-46
Match length
                  116
% identity
                  78
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  11142
Seq. No.
                  20670 2.R1040
Contig ID
5'-most EST
                  pmv700892880.h1
Method
                  BLASTX
NCBI GI
                  q4454457
BLAST score
                  370
E value
                  2.0e-35
Match length
                  84
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                  11143
```

20670 5.R1040

LIB3094-031-Q1-K1-C5

Contig ID 5'-most EST

% identity

```
BLASTN
Method
NCBI GI
                   q4454447
BLAST score
                   5.2
                   3.0e-20
E value
Match length
                   100
% identity
                   88
                   Arabidopsis thaliana chromosome II BAC F5H14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   11144
                   20672 1.R1040
Contig ID
                   LIB3050-009-Q1-E1-H5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1707016
BLAST score
                   144
                   5.0e-09
E value
Match length
                   111
% identity
                   33
NCBI Description
                   (U78721) cadmium-induced protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                   11145
                   20673 1.R1040
Contig ID
5'-most EST
                   zzp700832934.h1
Seq. No.
                   11146
Contig ID
                   20679 1.R1040
5'-most EST
                   LIB3050-009-01-E1-E2
                   11147
Seq. No.
                   20679 2.R1040
Contig ID
5'-most EST
                   pmv700890721.h1
                   11148
Seq. No.
Contig ID
                   20684 1.R1040
5'-most EST
                   epx701103717.h1
Method
                   BLASTX
NCBI GI
                   q3004565
BLAST score
                   207
E value
                   7.0e-16
Match length
                   193
% identity
NCBI Description
                   (AC003673) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   11149
Contig ID
                   20685 1.R1040
5'-most EST
                   ssr70\overline{0}556138.h1
Seq. No.
                   11150
Contig ID
                   20694 1.R1040
5'-most EST
                   jC-gmle01810055b11a1
Method
                   BLASTX
NCBI GI
                   q3068717
BLAST score
                   698
E value
                   1.0e-81
Match length
                   220
```

Match length

```
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
                  11151
Seq. No.
Contig ID ...
                  20695 1.R1040
5'-most EST
                  LIB3050-009-Q1-E1-C4
Method
                  BLASTX
NCBI GI
                  g4580393
BLAST score
                  412
E value
                  3.0e-40
Match length
                  155
% identity
                   51
                   (AC007171) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  11152
Seq. No.
                  20712 1.R1040
Contig ID
5'-most EST
                  jC-gmst02400050g04a1
Method
                  BLASTX
NCBI GI
                  g3786011
BLAST score
                  1069
E value
                   1.0e-117
Match length
                  239
% identity
NCBI Description
                   (AC005499) putative elongation factor [Arabidopsis
                  thaliana]
Seq. No.
                   11153
                   20712 2.R1040
Contig ID
5'-most EST
                  LIB3050-009-Q1-E1-A3
Method
                  BLASTX
NCBI GI
                  q3786011
BLAST score
                   423
E value
                   1.0e-41
Match length
                   98
% identity
                   (AC005499) putative elongation factor [Arabidopsis
NCBI Description
                   thaliana]
                  11154
Seq. No.
                   20712 3.R1040
Contig ID
5'-most EST
                   jC-gmro02800030d09a1
Method
                  BLASTX
NCBI GI
                  q3786011
BLAST score
                  264
E value
                   5.0e-33
Match length
                   94
% identity
NCBI Description
                   (AC005499) putative elongation factor [Arabidopsis
                  thalianal
                   11155
Seq. No.
                  20712 4.R1040
Contig ID
5'-most EST
                  ncj700978495.hl
Method
                  BLASTX
NCBI GI
                  g3786011
BLAST score
                  264
E value
                   2.0e-23
```

Match length

```
% identity
                   83
                   (AC005499) putative elongation factor [Arabidopsis
NCBI Description
                   thalianal
                   11156
Seq. No.
                   20713 1.R1040
Contig ID
                   jC-gmle01810006g11a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3482979
BLAST score
                   149.
E value
                   6.0e-09
                   206
Match length
                   28
% identity
                   (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070)
                   hypothetical protein [Arabidopsis thaliana]
                   11157
Seq. No.
                   20713 2.R1040
Contig ID
5'-most EST
                   LIB3170-062-Q1-J1-E3
Seq. No.
                   11158
Contig ID
                   20713 3.R1040
5'-most EST
                   epx70\overline{1}108675.h1
Seq. No.
                   11159
Contig ID
                   20715 1.R1040
5'-most EST
                   uC-gmropic091h07b1
                   11160
Seq. No.
                   20738 1.R1040
Contig ID
                   pmv700894377.h1
5'-most EST
                   BLASTX
Method
                   g2289006
NCBI GI
BLAST score
                   703
                   6.0e-74
E value
Match length
                   180
% identity
                   (AC002335) glutathione perosidase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   11161
Seq. No.
Contig ID
                   20738 2.R1040
5'-most EST
                   pxt700946407.hl
                   11162
Seq. No.
Contig ID
                   20738_3.R1040
5'-most EST
                   LIB3170-049-Q1-K2-E6
Seq. No.
                   11163
Contig ID
                   20738 4.R1040
5'-most EST
                   jC-gm\overline{f}102220108d04a1
Method
                   BLASTX
NCBI GI
                   q1946690
                   526
BLAST score
E value
                   1.0e-53
```

Contig ID

```
% identity
NCBI Description (U94495) glutathione peroxidase [Arabidopsis thaliana]
                   11164
Seq. No.
                   20739 1.R1040
Contig ID
                   LIB3050-008-Q1-E1-H4
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1699024
                   727
BLAST score
E value
                   9.0e-77
                   233
Match length
                   58
% identity
                   (U78866) gene1000 [Arabidopsis thaliana] >gi 1699057
NCBI Description
                   (U78870) unknown [Arabidopsis thaliana]
Seq. No.
                   11165
                   20739 2.R1040
Contig ID
                   leu70\overline{1}146127.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1699024
BLAST score
                   350
E value
                   4.0e-33
Match length
                   100
% identity
NCBI Description
                   (U78866) gene1000 [Arabidopsis thaliana] >gi 1699057
                   (U78870) unknown [Arabidopsis thaliana]
                  . 11166
Seq. No.
                   20739 3.R1040
Contig ID
5'-most EST
                   jC-qmst02400039a04a1
Method
                   BLASTX
NCBI GI
                   q1699024
BLAST score
                   269
E value
                   2.0e-23
Match length
                   150
% identity
                   (U78866) gene1000 [Arabidopsis thaliana] >gi 1699057
NCBI Description
                   (U78870) unknown [Arabidopsis thaliana]
Seq. No.
                   11167
Contig ID
                   20739 5.R1040
                   eep70\overline{0}863855.h1
5'-most EST
Seq. No.
                   11168
                   20740 1.R1040
Contig ID
5'-most EST
                   trc70\overline{0}565610.h1
Method
                   BLASTX
NCBI GI
                   q1708424
BLAST score
                   1036
E value
                   1.0e-113
Match length
                   262
% identity
                   ISOFLAVONE REDUCTASE HOMOLOG >gi 1230614 (U48590)
NCBI Description
                   isoflavone reductase-like protein [Lupinus albus]
Seq. No.
                   11169
```

20741 1.R1040

```
jC-qmf102220114a10d1
5'-most EST
                  11170
Seq. No.
                  20749 1.R1040
Contig ID
5'-most EST
                  LIB3050-008-Q1-E1-F11
                  BLASTN
Method
NCBI GI
                  g4432811
BLAST score
                  61
E value
                  3.0e-25
Match length
                  125
                  87
% identity
                  Arabidopsis thaliana chromosome II BAC F16D14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  11171
                  20754 1.R1040
Contig ID
                  LIB3050-008-Q1-E1-F6
5'-most EST
                  11172
Seq. No.
                  20758 1.R1040
Contig ID
5'-most EST
                  jC-qmst02400049c04a1
                  11173
Seq. No.
                   20758 3.R1040
Contig ID
                  LIB3050-008-Q1-E1-G1
5'-most EST
                   11174
Seq. No.
                   20760 1.R1040
Contig ID
                  LIB3107-041-Q1-K1-F4
5'-most EST
                  BLASTN
Method
NCBI GI
                   q667048
BLAST score
                   377
                   0.0e + 00
E value
                   536
Match length
                   93
% identity
NCBI Description
                  P.vulgaris mRNA for protein phosphatase 1 (PP1)
                   11175
Seq. No.
                   20760 2.R1040
Contig ID
                   LIB3167-013-P1-K1-D11
5'-most EST
                   BLASTN
Method
NCBI GI
                   q667048
                   178
BLAST score
                   2.0e-95
E value
                   266
Match length
% identity
NCBI Description P.vulgaris mRNA for protein phosphatase 1 (PP1)
Seq. No.
                   11176
                   20760 3.R1040
Contig ID
                   fua701038292.h1
5'-most EST
                   BLASTN
Method
                   q667048
NCBI GI
BLAST score
                   109
                   3.0e-54
E value
Match length
                   181
```

90

% identity

```
NCBI Description P.vulgaris mRNA for protein phosphatase 1 (PP1)
                  11177
Seq. No.
Contig ID
                  20763 1.R1040
5'-most EST
                  LIB3050-008-Q1-E1-E7
Method
                  BLASTX
NCBI GI
                  q1729938
BLAST score
                  321
E value
                   3.0e-29
Match length
                  101
% identity
                  56
NCBI Description
                  THIOREDOXIN-LIKE PROTEIN SLR0233 >gi_1001610_dbj_BAA10238
                   (D64000) thioredoxin M [Synechocystis sp.]
Seq. No.
                  11178
                  20763 2.R1040
Contig ID
5'-most EST
                  LIB3170-002-Q1-K1-A2
                  11179
Seq. No.
Contig ID
                  20765 1.R1040
5'-most EST
                  jC-gmro02910034a10d1
Seq. No.
                  11180
Contig ID
                  20770 1.R1040
5'-most EST
                  pxt700945188.h1
Seq. No.
                  11181
Contig ID
                  20772 1.R1040
5'-most EST
                  LIB3094-006-Q1-K1-C1
Method
                  BLASTX
                  g4039014
NCBI GI
BLAST score
                  783
                  1.0e-106
E value
Match length
                  372
% identity
                  51
NCBI Description
                   (AF037338) cleft lip and palate transmembrane protein 1
                   [Homo sapiens] >gi_4063033 (AF037339) cleft lip and palate
                  transmembrane protein 1 [Homo sapiens]
                  >gi_4502897_ref_NP_001285.1_pCLPTM1_ cleft lip and palate
                  associated transmembrane protein
                  11182
Seq. No.
                  20787 1.R1040
Contig ID
5'-most EST
                  LIB3050-008-Q1-E1-C5
Seq. No.
                  11183
Contig ID
                  20790 1.R1040
                  ncj70\overline{0}980962.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3123295
BLAST score
                  248
                  1.0e-20
E value
Match length
                  136
% identity
NCBI Description
                  CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi 2583169
```

thalianal

(AF026473) calmodulin-related protein [Arabidopsis

BLAST score

```
Seq. No.
                   11184
                   20790 2.R1040
Contig ID
5'-most EST
                   zzp700832902.h1
Seq. No.
                   11185
                   20794 1.R1040
Contig ID
5'-most EST
                   jC-gmst02400069d05a1
Method
                   BLASTX
NCBI GI
                   g4206196
BLAST score
                   316
E value
                   1.0e-28
Match length
                   153
% identity
                   42
NCBI Description
                   (AF071527) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   11186
Contig ID
                   20795 1.R1040
5'-most EST
                   uxk700667764.h1
Method
                   BLASTX
NCBI GI
                   g2827621
BLAST score
                   157
E value
                   3.0e-10
Match length
                   143
                   30
% identity
NCBI Description
                   (AL021636) putative protein [Arabidopsis thaliana]
Seq. No.
                   11187
                   20804_1.R1040
Contig ID
5'-most EST
                   uC-gmropic057b03b1
Method
                   BLASTX
NCBI GI
                   g3738320
BLAST score
                   672
                   3.0e-70
E value
Match length
                   282
% identity
NCBI Description
                   (AC005170) putative cinnamoyl CoA reductase [Arabidopsis
                   thaliana]
                   11188
Seq. No.
                   20804 2.R1040
Contig ID
5'-most EST
                   fua701041128.hl
Method
                   BLASTX
NCBI GI
                   g3738320
BLAST score
                   184
                   2.0e-13
E value
Match length
                   95
% identity
NCBI Description
                   (AC005170) putative cinnamoyl CoA reductase [Arabidopsis
                   thaliana]
                   11189
Seq. No.
Contig ID
                   20814 1.R1040
5'-most EST
                   sat701012928.h1
Method
                  BLASTN
NCBI GI
                   q4530125
```

NCBI Description

```
1.0e-108
E value
Match length
                   384
% identity
                   88
NCBI Description
                   Phaseolus vulgaris receptor-like protein kinase homolog
                   RK20-1 mRNA, complete cds
                   11190
Seq. No.
Contig ID
                   20817 1.R1040
5'-most EST
                   LIB3050-007-Q1-E1-G4
                   BLASTX
Method
NCBI GI
                   g3004556
BLAST score
                   246
E value
                   6.0e-21
Match length
                   93
% identity
                   53
NCBI Description
                   (AC003673) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   11191
                   20825 1.R1040
Contig ID
5'-most EST
                   sat701011326.hl
Method
                   BLASTX
NCBI GI
                   g3549679
BLAST score
                   752
E value
                   1.0e-79
Match length
                   259
% identity
                   62
                   (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
                   11192
Seq. No.
                   20825 2.R1040
Contig ID
5'-most EST
                   LIB3092-030-Q1-K1-D4
                   11193
Seq. No.
                   20825_3.R1040
Contig ID
                   epx70\overline{1}105311.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3549679
BLAST score
                   398
                   3.0e-38
E value
Match length
                   176
% identity
                   (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11194
                   20825 5.R1040
Contig ID
5'-most EST
                   LIB3056-014-Q1-N1-F2
Seq. No.
                   11195
Contig ID
                   20825 6.R1040
5'-most EST
                   uC-gmrominsoy097g08b1
Method
                   BLASTX
NCBI GI
                   g3549679
BLAST score
                   360
E value
                   3.0e - 34
Match length
                   132
% identity
```

(AL031394) putative protein [Arabidopsis thaliana]

```
11196
Seq. No.
Contig ID
                   20825 7.R1040
5'-most EST
                   ssr700560602.h1
                   BLASTX
Method
                   g3549679
NCBI GI
BLAST score
                   170
                   7.0e-12
E value
Match length
                   61
                   57
% identity
NCBI Description
                   (AL031394) putative protein [Arabidopsis thaliana]
                   11197
Seq. No.
                   20825 8.R1040
Contig ID
5'-most EST
                   LIB3051-003-Q1-E1-G7
Method
                   BLASTX
NCBI GI
                   q3549679
BLAST score
                   167
                   1.0e-11
E value
Match length
                   86
% identity
                   60
                   (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
                   11198
Seq. No.
Contig ID
                   20828 1.R1040
                                                 : · ·
5'-most EST
                   LIB3050-007-Q1-E1-F7
Method
                   BLASTX
                   g2781355
NCBI GI
BLAST score
                   284
E value
                   2.0e-25
Match length
                   106
% identity
                   56
NCBI Description
                   (AC003113) F2401.11 [Arabidopsis thaliana]
                   11199
Seq. No.
                   20832 1.R1040
Contig ID
5'-most EST
                  LIB3050-005-Q1-K1-E4
                   11200
Seq. No.
                   20833_1.R1040
Contig ID
5'-most EST
                   zzp700831448.h1
Method
                   BLASTX
                   g2244806
NCBI GI
BLAST score
                   568
E value
                   6.0e-58
Match length
                   296
% identity
                   46
NCBI Description
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
                   11201
Seq. No.
                   20833 2.R1040
Contig ID
5'-most EST
                   LIB3139-107-P1-N1-C1
Method
                   BLASTX
NCBI GI
                   g2244806
                   355
BLAST score
                   3.0e-33
E value
```

113

Match length

Contig ID

```
% identity
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11202
                   20833 3.R1040
Contig ID
                   g5342\overline{5}37
5'-most EST
Seq. No.
                   11203
                   20857 1.R1040
Contig ID
5'-most EST
                   fC-gmle700685573f1
Method
                   BLASTX
                   g3859603
NCBI GI
BLAST score
                   311
E value
                   4.0e-32
Match length
                   188
% identity
                   47
NCBI Description
                   (AF104919) contains similarity to wild oat DNA-binding
                   protein ABF2 (GB:Z48431) [Arabidopsis thaliana]
Seq. No.
                   11204
                   20860 1.R1040
Contig ID
5'-most EST
                   dpv70\overline{1}097008.h1
Method
                   BLASTX
NCBI GI
                   q3123295
BLAST score
                   203
E value
                   1.0e-15
Match length
                   145
% identity
                   CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi 2583169
NCBI Description
                   (AF026473) calmodulin-related protein [Arabidopsis
                   thaliana]
                   11205
Seq. No.
                   20862 1.R1040
Contig ID
                   LIB3170-037-Q1-K1-E12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1707017
BLAST score
                   1332
                   1.0e-148
E value
Match length
                   284
                   89
% identity
NCBI Description
                   (U78721) RNA helicase isolog [Arabidopsis thaliana]
                   11206
Seq. No.
                   20866_1.R1040
Contig ID
5'-most EST
                   jC-gmro02910024g10a1
Method
                   BLASTX
NCBI GI
                   q4309759
BLAST score
                   1578
                   1.0e-176
E value
Match length
                   431
% identity
NCBI Description
                   (AC006217) unknown protein with Src homology 3 (SH3) domain
                   profile (PDOC50002) [Arabidopsis thaliana]
Seq. No.
```

20883 1.R1040

NCBI GI

BLAST score

```
5'-most EST
                   q5057935
Method
                   BLASTX
NCBI GI
                   q3193296
BLAST score
                   959
E value
                   1.0e-104
Match length
                   230
                   77
% identity
NCBI Description
                   (AF069298) similar to pectinesterase [Arabidopsis thaliana]
Seq. No.
                   11208
                   20885 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir044d01b1
Seq. No.
                   11209
Contig ID
                   20886 1.R1040
5'-most EST
                   zhf700952345.hl
Method
                   BLASTX
NCBI GI
                   g3335341
BLAST score
                   287
E value
                   2.0e-25
                   77
Match length
% identity
NCBI Description
                   (AC004512) T8F5.10 [Arabidopsis thaliana]
                   11210
Seq. No.
Contig ID
                   20887 1.R1040
5'-most EST
                   LIB3050-007-01-E1-A10
                   11211
Seq. No.
                   20894 1.R1040
Contig ID
5'-most EST
                   zhf70\overline{0}963376.h1
Method
                   BLASTX
NCBI GI
                   q2647949
BLAST score
                   516
E value
                   6.0e-57
Match length
                   130
% identity
                   73
NCBI Description
                   (AJ001369) cytochrome b5 [Olea europaea]
Seq. No.
                   11212
                   20898 1.R1040
Contig ID
5'-most EST
                   LIB3050-006-Q1-E1-H4
Method
                   BLASTX
NCBI GI
                   g3142290
BLAST score
                   633
E value
                   6.0e-66
Match length
                   196
% identity
NCBI Description
                   (AC002411) Contains similarity to gb Z69902 from C.
                   elegans. [Arabidopsis thaliana]
Seq. No.
                   11213
Contig ID
                   20908 1.R1040
5'-most EST
                   LIB3139-106-P1-N1-F8
Method
                  BLASTX
```

q2130073

Contig ID

```
1.0e-173
E value
Match length
                     358
% identity
                    84
                    fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
NCBI Description
                    C-1 [Oryza sativa] > \overline{gi} 790970 dbj BAA088\overline{30} (D50301)
                    aldolase C-1 [Oryza sativa]
Seq. No.
                    11214
                    20911 1.R1040
Contig ID
5'-most EST
                    LIB3050-006-Q1-E1-H10
                    11215
Seq. No.
                    20912 1.R1040
Contig ID
                    leu701146187.hl
5'-most EST
Method
                    BLASTX
NCBI GI
                    q2245136
BLAST score
                    1349
E value
                     1.0e-150
Match length
                     333
% identity
                    73
NCBI Description
                     (Z97344) trehalose-6-phosphate synthase homolog
                     [Arabidopsis thaliana]
Seq. No.
                    11216
                    20917 1.R1040
Contig ID
5'-most EST
                    jC-qmro02910067f09d1
Seq. No.
                    11217
Contig ID
                    20919 1.R1040
5'-most EST
                    fC-gmse700851501a3
Seq. No.
                    11218
Contig ID
                    20921 1.R1040
5'-most EST
                    LIB3109-012-Q1-K1-H4
Method
                    BLASTN
                    q3319883
NCBI GI
                                                                                      4.5
BLAST score
                    35
E value
                    6.0e-10
Match length
                    77
% identity
                    95
NCBI Description
                    Arabidopsis thaliana PRT1 gene
Seq. No.
                    11219
                    20922 1.R1040
Contig ID
5'-most EST
                    jex70\overline{0}908390.h1
Seq. No.
                    11220
Contig ID
                    20931 1.R1040
5'-most EST
                    LIB3050-006-01-E1-F8
Seq. No.
                    11221
Contig ID
                    20941 1.R1040
5'-most EST
                    LIB3050-006-Q1-E1-D7
Seq. No.
                    11222
```

20943_1.R1040

```
5'-most EST
                   wvk700684733.h1
                   11223
Seq. No.
Contig ID
                   20947 1.R1040
                   LIB3050-006-Q1-E1-E12
5'-most EST
Method
                   BLASTX
                   q4006881
NCBI GI
BLAST score
                   654
E value
                   4.0e-68
                   194
Match length
                   66
% identity
NCBI Description
                   (Z99707) putative protein [Arabidopsis thaliana]
                   11224
Seq. No.
Contig ID
                   20947 2.R1040
                   LIB31\overline{0}6-040-Q1-K1-D6
5'-most EST
                   11225
Seq. No.
                   20950 1.R1040
Contig ID
5'-most EST
                   seb70\overline{0}653241.h1
Method
                   BLASTX
NCBI GI
                   g2104681
                   495
BLAST score
                   1.0e-49
E value
Match length
                   153
% identity
                   64
NCBI Description
                  (X97907) transcription factor [Vicia faba]
                   11226
Seq. No.
                   20950 2.R1040
Contig ID
                   LIB3050-006-Q1-E1-B4
5'-most EST
                   BLASTN
Method
                   g2104680
NCBI GI
BLAST score
                   65
E value
                   9.0e-28
                   214
Match length
                   87
% identity
NCBI Description V.faba mRNA for putative transciption factor (1556bp)
Seq. No.
                   11227
                   20950 3.R1040
Contig ID
5'-most EST
                   LIB3051-045-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                   g2104681
BLAST score
                   287
                   2.0e-25
E value
                   180
Match length
% identity
                   41
                   (X97907) transcription factor [Vicia faba]
NCBI Description
Seq. No.
                   11228
Contig ID
                   20952 1.R1040
                   jC-gmst02400047e11a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q627468
BLAST score
                   382
```

2.0e-56

E value

Method

BLASTN

```
348
Match length
% identity
                    40
NCBI Description
                    hypothetical protein 1 - human >gi 285983 dbj BAA02799
                    (D13635) KIAA0010 [Homo sapiens]
Seq. No.
                    11229
                    20952 2.R1040
Contig ID
5'-most EST
                    LIB30\overline{5}0-006-Q1-E1-B6
Method
                    BLASTX
NCBI GI
                    q627468
BLAST score
                    324
                    2.0e-35
E value
                    159
Match length
% identity
                    49
                    hypothetical protein 1 - human >gi 285983 dbj BAA02799
NCBI Description
                    (D13635) KIAA0010 [Homo sapiens]
Seq. No.
                    11230
Contig ID
                    20953 1.R1040
5'-most EST
                    awf700836982.h1
Method
                    BLASTX
NCBI GI
                    q462567
BLAST score
                    638
E value
                    3.0e-75
Match length
                    388
% identity
                    45
NCBI Description
                    MANNOSE-6-PHOSPHATE ISOMERASE (PHOSPHOMANNOSE ISOMERASE)
                    (PMI) (PHOSPHOHEXOMUTASE) >gi_631328_pir_S41122 mannose-6-phosphate isomerase (EC 5.3.1.8) - human
                    >gi_416017_emb_CAA53657 (X76057) phosphomannose isomerase
[Homo sapiens] >gi_740967_prf__2006245A phosphomannose
                    isomerase [Homo sapiens] >gi_4505235_ref_NP_002426.1_pMPI_
                    mannose phosphate isomerase
Seq. No.
                    11231
Contig ID
                    20955 1.R1040
5'-most EST
                    bth700848304.h1
Seq. No.
                    11232
                    20955 2.R1040
Contig ID
5'-most EST
                    LIB3107-054-01-K1-H10
Seq. No.
                    11233
                    20956 1.R1040 ·
Contig ID
5'-most EST
                    LIB3050-006-Q1-E1-C1
Method
                    BLASTX
NCBI GI
                    q2245060
BLAST score
                    273
E value
                    4.0e-24
Match length
                    93
% identity
NCBI Description
                    (Z97342) allergen homolog [Arabidopsis thaliana]
                    11234
Seq. No.
Contig ID
                    20960 1.R1040
5'-most EST
                    g5676902
```

NCBI GI

NCBI GI

```
q4530125
BLAST score
                   120
E value
                   1.0e-60
Match length
                   466
                   83
% identity
                   Phaseolus vulgaris receptor-like protein kinase homolog
NCBI Description
                   RK20-1 mRNA, complete cds
Seq. No.
                   11235
                   20960 2.R1040
Contig ID
5'-most EST
                   q5605743
                   BLASTN
Method
NCBI GI
                   q4530125
BLAST score
                   111
E value
                   2.0e-55
Match length
                   367
                   86
% identity
                   Phaseolus vulgaris receptor-like protein kinase homolog
NCBI Description
                   RK20-1 mRNA, complete cds
Seq. No.
                   11236
Contig ID
                   20966_1.R1040
5'-most EST
                   asj70\overline{0}967487.h1
Method
                   BLASTX
                   g4185143
NCBI GI
                                                                   . .
BLAST score
                   856
E value
                   6.0e-92
Match length
                   258
                   64
% identity
NCBI Description
                   (AC005724) putative signal recognition particle receptor
                   beta subunit [Arabidopsis thaliana]
                   11237
Seq. No.
                   20966_2.R1040
Contig ID
                   zhf700962435.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4185143
BLAST score
                   322
E value
                   1.0e-29
Match length
                   100
                  61
% identity
NCBI Description
                   (AC005724) putative signal recognition particle receptor
                  beta subunit [Arabidopsis thaliana]
                   11238
Seq. No.
                   20968 1.R1040
Contig ID
5'-most EST
                   g4301715
                   11239
Seq. No.
Contig ID
                   20968 2.R1040
5'-most EST
                   LIB3050-006-Q1-E1-A12
                   11240
Seq. No.
Contig ID
                   20970 1.R1040
5'-most EST
                   LIB3051-015-Q1-E1-B6
Method
                   BLASTX
```

g2829870

```
BLAST score
                   336
E value
                   3.0e - 31
Match length
                   151
% identity
                   49
NCBI Description
                   (AC002396) Hypothetical protein [Arabidopsis thaliana]
                   11241
Seq. No.
Contig ID
                   20975 1.R1040
5'-most EST
                   LIB3087-012-Q1-K1-B10
Method
                   BLASTX
                   q480618
NCBI GI
                   650
BLAST score
E value
                   1.0e-67
Match length
                   234
% identity
                   61
NCBI Description
                   ATAF1 protein - Arabidopsis thaliana (fragment)
                   >qi 1345506 emb CAA52771 (X74755) ATAF1 [Arabidopsis
                   thaliana]
Seq. No.
                   11242
                   20975 2.R1040
Contig ID
5'-most EST
                   pcp700989592.h1
Seq. No.
                   11243
                   20996 1.R1040
Contig ID
5'-most EST
                   LIB3050-005-01-K1-G6
Seq. No.
                   11244
                   20996 2.R1040
Contig ID
5'-most EST
                   LIB3094-040-Q1-K1-H1
Method
                   BLASTN
NCBI GI
                   q3510336
BLAST score
                   73
                   9.0e-33
E value
Match length
                   77
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K18J17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   11245
Contig ID
                   20996 3.R1040
5'-most EST
                   leu70\overline{1}148232.h1
                   11246
Seq. No.
                   21005 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}0-005-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   g1169017
BLAST score
                   571
E value
                   8.0e-59
Match length
                   181
                   27
% identity
NCBI Description
                   COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
                   >gi_1078361_pir__B55123 coatomer complex beta' chain -
                   yeast (Saccharomyces cerevisiae) >gi 595415 (U11237)
                   betaprime COP [Saccharomyces cerevisiae]
```

>gi_1246841_emb_CAA63359_ (X92670) see also U11237; yeast

```
[Saccharomyces cerevisiae]
                   11247
Seq. No.
                   21027 1.R1040
Contig ID
5'-most EST
                  LIB3050-004-Q1-E1-H3
Seq. No.
                   11248
                   21030 1.R1040
Contig ID
5'-most EST
                   LIB3050-004-Q1-E1-H6
                  BLASTX
Method
NCBI GI
                  q3851214
BLAST score
                   145
E value
                   8.0e-09
Match length
                   103
% identity
                   8
                   (AJ012449) NS1-binding protein [Homo sapiens]
NCBI Description
                   11249
Seq. No.
                   21032 1.R1040
Contig ID
5'-most EST
                   gsv701044272.h1
                   11250
Seq. No.
                   21032 2.R1040
Contig ID
5'-most EST
                  hrw701063207.h1
Seq. No.
                   11251
Contig ID
                   21036 1.R1040
5'-most EST
                   jC-gmle01810092g02d1
Method
                   BLASTX
                   g4185599
NCBI GI
BLAST score
                   216
E value
                   2.0e-17
Match length
                  137
% identity
NCBI Description
                   (AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana
                   triflora]
                   11252
Seq. No.
Contig ID
                   21044 1.R1040
5'-most EST
                  LIB3050-004-Q1-E1-H2
Method
                  BLASTX
                  g4056438
NCBI GI
BLAST score
                   247
E value
                   7.0e-21
Match length
                  120
% identity
NCBI Description
                   (AC005990) F508.11 [Arabidopsis thaliana]
                   11253
Seq. No.
                   21050 1.R1040
Contig ID
5'-most EST
                   jC-gmf102220103a11d1
```

coatomer subunit [Saccharomyces cerevisiae]
>gi 1322710 emb CAA96848 (Z72659) ORF YGL137w

11254

21051 1.R1040

LIB3139-094-P1-N1-E1

Seq. No.

Contig ID

5'-most EST

NCBI Description

```
Method
                   BLASTX
NCBI GI
                   q1066447
BLAST score
                   177
E value
                   3.0e-12
Match length
                   182
                   31
% identity
                   (Z67980) Chalcone isomerase [Callistephus chinensis]
NCBI Description
Seq. No.
                   11255
                   21051 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy212e01b1
                   11256
Seq. No.
                   21057 1.R1040
Contig ID
5'-most EST
                   leu701149634.h1
                   BLASTX
Method
NCBI GI
                   g1168940
BLAST score
                   483
E value
                   3.0e-50
Match length
                   146
                   70
% identity
NCBI Description
                   CHORISMATE MUTASE PRECURSOR (CM-1) >gi_629509_pir__S38958
                   chorismate mutase precursor - Arabidopsis thaliana
                   >gi_429153_emb_CAA81286_ (Z26519) chorismate mutase
                   precursor [Arabidopsis thaliana]
Seq. No.
                   11257
Contig ID
                   21071 1.R1040
5'-most EST
                   uC-gmropic066e01b1
Method
                   BLASTX
NCBI GI
                   g3901012
BLAST score
                   913
E value
                   9.0e-99
Match length
                   223
% identity
                   73
NCBI Description
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
                   sylvatica]
                   11258
Seq. No.
                   21072 1.R1040
Contig ID
5'-most EST
                   g5753493
                   11259
Seq. No.
                   21076 2.R1040
Contig ID
5'-most EST
                   pmv700889252.hl
Seq. No.
                   11260
                   21084_1.R1040
Contig ID
5'-most EST
                   ssr700556809.hl
Method
                   BLASTX
NCBI GI
                   q3757520
BLAST score
                   211
E value
                   3.0e-16
Match length
                   169
                   33
% identity
```

(AC005167) unknown protein [Arabidopsis thaliana]

```
Seq. No.
                   11261
                   21102 1.R1040
Contig ID
                   LIB3139-002-Q1-N1-C12
5'-most EST
Seq. No.
                   11262
                   21102 2.R1040
Contig ID
                   jC-gmst02400037c03a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2827528
                   178
BLAST score
E value
                   6.0e-13
                   105
Match length
% identity
                   36
                   (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                   11263
Seq. No.
                   21103 1.R1040
Contig ID
                  bth700847330.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4539456
BLAST score
                   710
E value
                   2.0e-79
Match length
                   215
% identity
                   62
NCBI Description
                   (AL049500) osmotin precursor [Arabidopsis thaliana]
Seq. No.
                   11264
                   21103 2.R1040
Contig ID
                   jC-gmro02910008h01a1
5'-most EST
                   BLASTX
Method
                   g129320
NCBI GI
BLAST score
                   235
E value
                   9.0e-20
Match length
                   55
                   71
% identity
NCBI Description
                  P21 PROTEIN >gi_99943_pir__A33176 P21 protein - soybean
Seq. No.
                   11265
                   21104 1.R1040
Contig ID
5'-most EST
                   uC-gmropic058b10b1
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   11266
Seq. No.
Contig ID
                   21104 2.R1040
5'-most EST
                   uC-gmrominsoy257a10b1
                   11267
Seq. No.
                   21108 1.R1040
Contig ID
                   gsv701054978.hl
5'-most EST
Method
                   BLASTX
```

g3874563

NCBI GI

Match length

```
BLAST score
                    589
E value
                    1.0e-60
Match length
                    253
% identity
                    49
NCBI Description
                    (Z81042) similar to Yeast hypothetical protein YEY6 like;
                    cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5
                    comes from this gene; cDNA EST yk303h1.3 comes from this
                    gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...
                    >gi_3924825_emb_CAB05549 (Z83113) similar to Yeast
hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes
                    from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5
                    comes from this gene; cDNA
                    11268
Seq. No.
                    21114 1.R1040
Contig ID
5'-most EST
                    LIB3107-009-Q1-K1-F9
Seq. No.
                    11269
                    21118 1.R1040
Contig ID
5'-most EST
                    leu701144831.hl
Seq. No.
                    11270
Contig ID
                    21122 1.R1040
5'-most EST
                    LIB3109-036-Q1-K1-E1
                    11271
Seq. No.
                    21130 1.R1040
Contig ID
5'-most EST
                    uC-gmrominsoy211e11b1
Seq. No.
                    11272
                    21136 1.R1040
Contig ID
5'-most EST
                    eep700868362.hl
Method
                    BLASTX
NCBI GI
                    g3080418
BLAST score
                    212
E value
                    1.0e-16
Match length
                    68
                    53
% identity
                    (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    11273
Contig ID
                    21139 1.R1040
5'-most EST
                    uC-gmflminsoy024f01b1
Seq. No.
                    11274
Contig ID
                    21139 2.R1040
5'-most EST
                    kl1701203774.h2
                    11275
Seq. No.
Contig ID
                    21141 1.R1040
5'-most EST
                    uC-gmronoir048f04b1
Method
                    BLASTN
NCBI GI
                    g4566613
BLAST score
                    153
E value
                    3.0e-80
```

Method

BLASTX

```
% identity
                   85
NCBI Description
                   Populus alba x Populus tremula actin depolymerizing factor
                   mRNA, partial cds
                   11276
Seq. No.
                   21141 3.R1040
Contig ID
                   LIB3107-039-Q1-K1-C6
5'-most EST
Method
                   BLASTN
NCBI GI
                   q4566613
BLAST score
                   86
E value
                   2.0e-40
Match length
                   270
                   83
% identity
                   Populus alba x Populus tremula actin depolymerizing factor
NCBI Description
                   mRNA, partial cds
                   11277
Seq. No.
                   21144 1.R1040
Contig ID
                   LIB3170-080-Q1-K1-D5
5'-most EST
Method
                   BLASTX
                   g3786008
NCBI GI
BLAST score
                   363
E value
                   3.0e-34
Match length
                   201
% identity
                   45
                   (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11278
Contig ID
                   21149 1.R1040
                   LIB3050-003-Q1-E1-E7
5'-most EST
Seq. No.
                   11279
Contig ID
                   21153 1.R1040
5'-most EST
                   fjg700968328.hl
                   BLASTX
Method
NCBI GI
                   g2245087
BLAST score
                   547
E value
                   5.0e-57
Match length
                   268
% identity
                   46
NCBI Description
                   (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   11280
                   21153 2.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-026-Q1-K1-H1
Method
                   BLASTX
NCBI GI
                   g2245087
BLAST score
                   176
E value
                   2.0e-12
Match length
                   42
                   69
% identity
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   11281
Contig ID
                   21154 1.R1040
                   LIB3050-003-Q1-E1-D3
5'-most EST
```

```
g3176708
NCBI GI
                   149
BLAST score
                   6.0e-14
E value
Match length
                   90
% identity
                   45
                   (AC002392) putative proline-rich protein APG [Arabidopsis
NCBI Description
                   thaliana]
                   11282
Seq. No.
Contig ID
                   21162 1.R1040
5'-most EST
                   kl1701206442.hl
Method
                   BLASTX
                   q2982301
NCBI GI
BLAST score
                   285
E value
                   2.0e-25
                   108
Match length
% identity
                   53
                   (AF051235) YGL010w-like protein [Picea mariana]
NCBI Description
                   11283
Seq. No.
Contig ID
                   21164 1.R1040
5'-most EST
                  LIB3050-003-Q1-E1-E2
Method
                   BLASTX
NCBI GI
                   g2252824
BLAST score
                   600
E value
                  2.0e-62
Match length
                   144
                   76
% identity
                   (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
                   11284
Seq. No.
Contig ID
                   21165 1.R1040
5'-most EST
                   g5678094
                   BLASTN
Method
NCBI GI
                   g3582780
BLAST score
                   152
E value
                   1.0e-79
Match length
                   440
                   84
% identity
                  Nicotiana tabacum clone 354 peroxisomal targeting sequence
NCBI Description
                   1 receptor (PEX5) mRNA, partial cds
Seq. No.
                   11285
                   21165 2.R1040
Contig ID
5'-most EST
                   pmv700891870.h1
Method
                   BLASTX
NCBI GI
                   g3582779
BLAST score
                   260
E value
                   2.0e-22
Match length
                   51
                   96
% identity
NCBI Description
                   (AF056282) peroxisomal targeting sequence 1 receptor
                   [Nicotiana tabacum]
                   11286
Seq. No.
                   21165 3.R1040
Contig ID
```

 $jex70\overline{0}904785.h1$

5'-most EST

```
Method
                   BLASTX
NCBI GI
                   g3582779
BLAST score
                   216
E value
                   8.0e-18
Match length
                   42
                   95
% identity
                   (AF056282) peroxisomal targeting sequence 1 receptor
NCBI Description
                   [Nicotiana tabacum]
                   11287
Seq. No.
Contig ID
                   21167 1.R1040
5'-most EST
                   jC-gmst02400003d04d1
                   11288
Seq. No.
Contig ID
                   21169 1.R1040
                  bth700846963.h1
5'-most EST
                   11289
Seq. No.
                   21171 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910068d03a1
Method
                   BLASTX
NCBI GI
                   g3395439
BLAST score
                   330
                   2.0e-30
E value
Match length
                  . 254
% identity
                 - 35
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
                   11290
Seq. No.
                   21171 2.R1040
Contig ID
                   fua701042933.h1
5'-most EST
                   11291
Seq. No.
                   21171 3.R1040
Contig ID
                   txt700736855.hl
5'-most EST
                   11292
Seq. No.
Contig ID
                   21174 1.R1040
5'-most EST
                   LIB3094-006-Q1-K1-G10
                   11293
Seq. No.
                   21174 2.R1040
Contig ID
5'-most EST
                   jC-gmro02910005a07a1
                   11294
Seq. No.
                   21174 3.R1040
Contig ID
                   leu701154556.h1
5'-most EST
                   11295
Seq. No.
```

Contig ID

21175 1.R1040 5'-most EST zpv700757458.h1

Method BLASTX g2194120 NCBI GI BLAST score 155 E value 7.0e-10 Match length 116 39 % identity

Contig ID

```
NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]
Seq. No.
                   11296
Contig ID
                   21175 2.R1040
                   zhf700964993.hl
5'-most EST
                   11297
Seq. No.
                   21178 1.R1040
Contig ID
5'-most EST
                   LIB3093-009-Q1-K1-F4
Method
                   BLASTX
NCBI GI
                   q1495804
BLAST score
                   3624
                   0.0e + 00
E value
                   926
Match length
% identity
                   75
                   (X96406) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
                   11298
Seq. No.
                   21178 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy126d02b1
                   11299
Seq. No.
Contig ID
                   21180_1.R1040
5'-most EST
                   LIB3050-003-Q1-E1-C4
Method
                   BLASTX
NCBI GI
                   q2245139
BLAST score
                   181
E value
                   3.0e-13
Match length
                   111
                   45
% identity
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
                   11300
Seq. No.
                   21197_1.R1040
Contig ID
                   LIB3050-003-Q1-E1-A8
5'-most EST
Method
                   BLASTN
NCBI GI .
                   q516102
BLAST score
                   218
E value
                   1.0e-119
Match length
                   425
                   95
% identity
NCBI Description
                   Soybean phytochrome B (phyB) gene exons 1-5, complete cds
                   11301
Seq. No.
                   21198 1.R1040
Contig ID
5'-most EST
                   fC-gmro700865957a4
Method
                   BLASTX
NCBI GI
                   g1871192
BLAST score
                   879
                   3.0e-94
E value
Match length
                   554
% identity
NCBI Description
                   (U90439) Cys3His zinc finger protein isolog [Arabidopsis
                   thaliana]
                   11302
Seq. No.
```

21198_2.R1040

Seq. No.

```
LIB3050-003-Q1-E1-A9
5'-most EST
                   11303
Seq. No.
                   21198_3.R1040
Contig ID
5'-most EST
                   jC-gmro02910064b03a1
                   BLASTX
Method
                   g1871192
NCBI GI
BLAST score
                   441
                   1.0e-43
E value
Match length
                   161
                   55
% identity
                   (U90439) Cys3His zinc finger protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   11304
Seq. No.
                   21198 5.R1040
Contig ID
                   LIB3139-006-P1-N1-D12
5'-most EST
                   11305
Seq. No.
                   21206 1.R1040
Contig ID
5'-most EST
                   LIB3050-002-Q1-E1-G6
                   11306
Seq. No.
                   21208 1.R1040
Contig ID
5'-most EST
                   jC-gmro02800032a08a1
                                                                  Method
                   BLASTX
                   g2664202
NCBI GI
                   370
BLAST score
                   1.0e-34
E value
                   399
Match length
                   33
% identity
NCBI Description
                  (AJ003217) GT2 [Arabidopsis thaliana]
                   11307
Seq. No.
                   21208 2.R1040
Contig ID
5'-most EST
                   LIB3170-044-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2664204
BLAST score
                   152
E value
                   7.0e-10
Match length
                   77
% identity
NCBI Description
                  (AJ003218) GTL1 [Arabidopsis thaliana]
                   11308
Seq. No.
                   21209 1.R1040
Contig ID
5'-most EST
                   LIB31\overline{3}8-125-Q1-N1-B4
Method
                   BLASTX
NCBI GI
                   q416639
BLAST score
                   282
E value
                   7.0e-25
Match length
                   87
% identity
                   68
                   INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG2
NCBI Description
                   >gi 287564 dbj BAA03307 (D14411) ORF [Vigna radiata]
```

5'-most EST

```
Contig ID
                   21210 1.R1040
5'-most EST
                   LIB3051-116-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   q3176686
BLAST score
                   807
                   2.0e-86
E value
Match length
                   267
                   58
% identity
                   (AC003671) Similar to high affinity potassium transporter,
NCBI Description
                   HAK1 protein gb U22945 from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
                   11310
Seq. No.
                   21212 1.R1040
Contig ID
5'-most EST
                   leu701146821.h1
                   11311
Seq. No.
                   21213 1.R1040
Contig ID
5'-most EST
                   LIB3050-002-Q1-E1-H12
                   11312
Seq. No.
                   21216 1.R1040
Contig ID
5'-most EST
                   eep700870341.hl
Method
                   BLASTX
                   q2467274
NCBI GI
BLAST score
                   337
                   2.0e-31
E value
                   148
Match length
% identity
                   53
                   (Z99759) rna binding protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                   11313
                   21217 1.R1040
Contig ID
5'-most EST
                   LIB3050-002-Q1-E1-H6
                   11314
Seq. No.
Contig ID
                   21218 1.R1040
5'-most EST
                   zsg70\overline{1}129457.h1
                   11315
Seq. No.
                   21223 1.R1040
Contig ID
5'-most EST
                   LIB3050-002-Q1-E1-F11
Seq. No.
                   11316
                   21224 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910075c09a1
Method
                   BLASTX
NCBI GI
                   q3927836
BLAST score
                   321
                   1.0e-37
E value
Match length
                   200
% identity
NCBI Description
                   (AC005727) unknown protein [Arabidopsis thaliana]
                   11317
Seq. No.
                   21224 2.R1040
Contig ID
```

jC-gmro02910004g02a1

BLAST score

```
Method
                   BLASTX
NCBI GI
                   q3927836
BLAST score
                   354
E value
                   1.0e-43
Match length
                   118
                   80
% identity
NCBI Description
                   (AC005727) unknown protein [Arabidopsis thaliana]
Seq. No.
                   11318
                   21244 1.R1040
Contig ID
5'-most EST
                   uC-gmronoir016h05b1
                   BLASTX
Method
NCBI GI
                   q2292988
BLAST score
                   191
E value
                   1.0e-13
Match length
                   366
                   26
% identity
NCBI Description
                   (Y11283) Inter-alpha-inhibitor H4 heavy chain [Rattus
                  norvegicus]
                   11319
Seq. No.
Contig ID
                   21244 3.R1040
5'-most EST
                   jC-gmf102220057a09d1
Seq. No.
                   11320
Contig ID
                   21248 1.R1040
5'-most EST
                   zsg701129729.h1
Seq. No.
                   11321
                   21252 1.R1040
Contig ID
5'-most EST
                   gsv701051533.hl
Method
                   BLASTX
                   g4218535
NCBI GI
BLAST score
                   626
E value
                   5.0e-65
Match length
                   201
% identity
                   59
                   (AJ010829) GRAB1 protein [Triticum sp.]
NCBI Description
                   11322
Seq. No.
                   21254 1.R1040
Contig ID
5'-most EST
                   gsv701045606.hl
Method.
                   BLASTX
                   g3970880
NCBI GI
BLAST score
                   448
E value
                   2.0e-44
Match length
                  179
% identity
                   49
NCBI Description
                   (AB015724) nuclear receptor binding factor-1 [Rattus
                  norvegicus]
Seq. No.
                   11323
Contig ID
                   21261 1.R1040
5'-most EST
                  uC-gmflminsoy053g04b1
Method
                  BLASTX
NCBI GI
                   g3522938
```

E value

```
E value
                   2.0e-96
Match length
                   401
                   49
% identity
                   (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
                   11324
Seq. No.
                   21263 1.R1040
Contig ID
                   zhf700963542.hl
5'-most EST
Method
                   BLASTX
                   q2760086
NCBI GI
BLAST score
                   425
                   3.0e-52
E value
Match length
                   178
                   19
% identity
NCBI Description
                   (Y16046) leucine-rich repeat protein [Arabidopsis thaliana]
Seq. No.
                   11325
                   21265 1.R1040
Contig ID
                   LIB30\overline{5}3-008-Q1-N1-G11
5'-most EST
Method
                   BLASTX
                   g1480347
NCBI GI
BLAST score
                   1788
E value
                   0.0e + 00
Match length
                   378
% identity
                   87
NCBI Description
                   (X99419) ferrodoxin NADP oxidoreductase [Pisum sativum]
Seq. No.
                   11326
Contig ID
                   21265 2.R1040
5'-most EST
                   asj700967432.h1
Method
                   BLASTN
NCBI GI
                   g1480346
BLAST score
                   57
E value
                   3.0e-23
Match length
                   129
                   86
% identity
                   P.sativum mRNA for ferrodoxin NADP oxidoreductase
NCBI Description
                   11327
Seq. No.
                   21265 3.R1040
Contig ID
5'-most EST
                   jC-gmst02400064a05d1
Seq. No.
                   11328
                   21267 1.R1040
Contig ID
                   crh70\overline{0}854281.h1
5'-most EST
                   11329
Seq. No.
Contig ID
                   21269 1.R1040
5'-most EST
                   LIB3050-002-Q1-E1-D10
                   11330
Seq. No.
                   21270 1.R1040
Contig ID
5'-most EST
                   rlr700901075.hl
Method
                   BLASTX
NCBI GI
                   g1742951
BLAST score
                   902
```

1.0e-97

Match length 201 % identity 83 NCBI Description (Y09817) Ca2+-ATPase [Arabidopsis thaliana] Seq. No. 11331

21272 1.R1040

5'-most EST LIB3139-013-P1-N1-G6
Method BLASTX
NCBI GI g3219273
BLAST score 585
E value 3.0e-60

E value 3.0e-60
Match length 242
% identity 48

Contig ID

NCBI Description (AB015316) MAP kinase kinase 5 [Arabidopsis thaliana]

Seq. No. 11332

Contig ID 21277_1.R1040

5'-most EST LIB3050-002-Q1-E1-A6

Seq. No. 11333

Contig ID 21279_1.R1040

5'-most EST LIB3050-002-Q1-E1-B1

Seq. No. 11334

Contig ID 21282 1.R1040

5'-most EST LIB3050-002-Q1-E1-B2

Method BLASTX
NCBI GI g1730796
BLAST score 347
E value 9.0e-33
Match length 146

% identity 46

NCBI Description HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC

REGION >gi_2132760_pir__S60964 probable membrane protein

YNL163c - yeast (Saccharomyces cerevisiae)

>gi_1050790_emb_CAA63276_ (X92517) N1718 [Saccharomyces
cerevisiae] >gi_1302132_emb_CAA96050_ (Z71439) ORF YNL163c

[Saccharomyces cerevisiae]

Seq. No. 11335

Contig ID 21286 1.R1040

5'-most EST LIB3170-067-Q1-K1-C8

Method BLASTX
NCBI GI 94008547
BLAST score 147
E value 4.0e-09
Match length 100
% identity 33

NCBI Description (AL022072) arginine n-methyltransferase

[Schizosaccharomyces pombe]

Seq. No. 11336

Contig ID 21288_1.R1040

5'-most EST LIB3051-079-Q1-K1-D4

Seq. No. 11337

Contig ID 21296_1.R1040

Seq. No.

```
5'-most EST
                      LIB3139-119-P1-N1-B6
Method
                      BLASTX
NCBI GI
                      q3641252
BLAST score
                       421
E value
                       2.0e-41
Match length
                       135
                       13
% identity
NCBI Description
                       (AF053127) leucine-rich receptor-like protein kinase [Malus
                       domestica]
Seq. No.
                       11338
                      21297 1.R1040
Contig ID
5'-most EST
                       q5126291
Method
                      BLASTX
NCBI GI
                       q122087
BLAST score
                       632
E value
                       4.0e-66
Match length
                       136
% identity
                       95
                      HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964 (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965 (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_
NCBI Description
                       (X00937) H3 histone [Triticum aestivum] >gi 488565 (U09459)
                      histone H3.1 [Medicago sativa] >gi_2565419 (AF026803)
                      histone H3 [Onobrychis viciifolia]
Seq. No.
                       11339
Contig ID
                       21298 1.R1040
5'-most EST
                      LIB3050-001-Q1-E1-F11
Seq. No.
                       11340
                       21298 2.R1040
Contig ID
5'-most EST
                      LIB3170-055-Q1-K1-A8
Seq. No.
                       11341
                       21300 1.R1040
Contig ID
5'-most EST
                       jsh701063920.hl
Seq. No.
                       11342
                       21304 1.R1040
Contig ID
5'-most EST
                      LIB3050-001-Q1-E1-F9
Seq. No.
                       11343
Contig ID
                       21305 1.R1040
5'-most EST
                      LIB3050-001-Q1-E1-G1
Method
                      BLASTX
NCBI GI
                      q282980
BLAST score
                       373
E value
                       8.0e-36
Match length
                       99
% identity
                       72
NCBI Description
                      helix-loop-helix protein DEL - garden snapdragon >gi 166428
                       (M84913) DEL [Antirrhinum majus]
```

Contig ID 5'-most EST

```
Contig ID
                   21306 1.R1040
                   LIB3051-001-Q1-E1-G11
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1169782
BLAST score
                   615
                   1.0e-129
E value
                   290
Match length
                   80
% identity
                  FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis
NCBI Description
                   thaliana]
                   11345
Seq. No.
Contig ID
                   21310 1.R1040
                   awf700840781.hl
5'-most EST
                   BLASTX
Method
                   g2388562
NCBI GI
BLAST score
                   166
                   2.0e-11
E value
                   73
Match length
                   47
% identity
                   (AC000098) EST gb ATTS0295 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   11346
Seq. No.
                   21314 1.R1040
Contig ID
5'-most EST
                   awf700842001.hl
                   BLASTX
Method
NCBI GI
                   g2392056
                   738
BLAST score
                   5.0e-78
E value
                   357
Match length
                   44
% identity
                  Chain A, Class 3 Aldehyde Dehydrogenase Complex With
NCBI Description
                   Nicotinamide-Adenine-Dinucleotide >gi 2392057_pdb_1AD3_B
                   Chain B, Class 3 Aldehyde Dehydrogenase Complex With
                   Nicotinamide-Adenine-Dinucleotide
Seq. No.
                   11347
                   21314 2.R1040
Contig ID
                   uC-gmrominsoy062b01b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455169
BLAST score
                   166
                   1.0e-11
E value
                   66
Match length
% identity
                   (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   11348
Seq. No.
                   21316 1.R1040
Contig ID
5'-most EST
                   LIB3050-001-Q1-E1-E11
                   11349
Seq. No.
                   21319 1.R1040
```

LIB3170-056-Q1-K1-D5

BLAST score

```
Seq. No.
                   11350
                   21319 2.R1040
Contig ID
5'-most EST
                   LIB3051-001-01-E1-E5
                   11351
Seq. No.
Contig ID
                   21323 1.R1040
5'-most EST
                   LIB3107-014-Q1-K1-C1
Seq. No.
                   11352
                   21325 1.R1040
Contig ID
5'-most EST
                   LIB3051-001-Q1-E1-C12
                   11353
Seq. No.
Contig ID
                   21327 1.R1040
5'-most EST
                   LIB3050-001-Q1-E1-C6
Method
                   BLASTX
NCBI GI
                   q4490702
BLAST score
                   143
E value
                   2.0e-13
Match length
                   109
                   52
% identity
NCBI Description
                   (AL035680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   11354
                   21333 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910040g04a1
                   11355
Seq. No.
                   21338 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-086-Q1-K1-E10
Seq. No.
                   11356
                   21341_1.R1040
Contig ID
5'-most EST
                   lus701015777.hl
Seq. No.
                   11357
Contig ID
                   21342 1.R1040
5'-most EST
                   bth700846441.h1
Method
                   BLASTX
                   q135535
NCBI GI
BLAST score
                   2385
E value
                   0.0e + 00
Match length
                   545
% identity
NCBI Description
                   T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
                   (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide
                   Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_
                   (D11351) t-complex polypeptide 1 homologue [Arabidopsis
                   thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
                   alpha/TCP-1 [Arabidopsis thaliana]
Seq. No.
                   11358
Contig ID
                   21345 1.R1040
5'-most EST
                   kl1701206501.hl
Method
                   BLASTX
NCBI GI
                   q116923
```

```
E value
                   1.0e-100
Match length
                   332
                   59
% identity
NCBI Description
                  COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
                   >gi_111414_pir__S13520 beta-COP protein - rat
                   >gi 55819 emb CAA40505 (X57228) beta COP [Rattus
                   norvegicus]
Seq. No.
                   11359
                   21349 1.R1040
Contig ID
5'-most EST
                  LIB3051-012-Q1-E1-H1
                   BLASTX
Method
                   q2134962
NCBI GI
BLAST score
                   321
E value
                   2.0e-29
Match length
                   119
% identity
                  cyclophilin-like protein CyP-60 - human >gi 1199598
NCBI Description
                   (U37219) cyclophilin-like protein CyP-60 [Homo sapiens]
                   >gi 1587642_prf__2207180A cyclophilin:ISOTYPE=CyP-60 [Homo
                   sapiens]
Seq. No.
                   11360
Contig ID
                   21350 1.R1040
                  LIB3050-001-Q1-E1-A9
5'-most EST
                   11361
Seq. No.
                   21351 1.R1040
Contig ID
5'-most EST
                  LIB3050-001-Q1-E1-B2
                   11362
Seq. No.
                   21354 1.R1040
Contig ID
                  LIB30\overline{5}0-001-Q1-E1-C1
5'-most EST
                   11363
Seq. No.
                   21355 1.R1040
Contig ID
5'-most EST
                  LIB3050-001-Q1-E1-C11
                   11364
Seq. No.
                   21358 1.R1040
Contig ID
                   cle70\overline{0}967790.h1
5'-most EST
Seq. No.
                   11365
                   21358 2.R1040
Contig ID
                  LIB3139-028-P1-N1-D3
5'-most EST
                   11366
Seq. No.
Contig ID
                   21359 1.R1040
5'-most EST
                  bth700843780.h1
Method
                  BLASTX
                   g3928869
NCBI GI
BLAST score
                   163
E value
                   4.0e-11
                   102
Match length
% identity
                   38
                   (AF093420) Hsp70 binding protein HspBP1 [Homo sapiens]
NCBI Description
```

```
Seq. No.
                   11367
                   21362 1.R1040
Contig ID
                   LIB30\overline{5}0-001-Q1-E1-E2
5'-most EST
Seq. No.
                   11368
                   21364 1.R1040
Contig ID
                   LIB3051-008-Q1-E1-F12
5'-most EST
                   11369
Seq. No.
                   21364 2.R1040
Contig ID
                   LIB3093-032-Q1-K1-E10
5'-most EST
Seq. No.
                   11370
                   21365 1.R1040
Contig ID
5'-most EST
                   zpv700763416.h1
Method
                   BLASTN
NCBI GI
                   g1065907
BLAST score
                   387
                   0.0e+00
E value
                   959
Match length
                   90
% identity
                   Pisum sativum chloroplast processing enzyme mRNA, nuclear
NCBI Description
                   gene encoding chloroplast protein, complete cds
                   11371
Seq. No.
                   21370 1:R1040
Contig ID
5'-most EST
                   gsv701048554.h1
Method
                   BLASTX
                   g1350548
NCBI GI
BLAST score
                   176
                   2.0e-12
E value
                   60
Match length
                   58
% identity
                   (L47609) heat shock-like protein [Picea glauca]
NCBI Description
                   11372
Seq. No.
                   21371_1.R1040
Contig ID
5'-most EST
                   LIB3050-001-Q1-E1-G5
Method
                   BLASTX
NCBI GI
                   g4336436
                   373
BLAST score
                   1.0e-35
E value
                   114
Match length
                   65
% identity
                   (AF092432) protein phosphatase type 2C [Lotus japonicus]
NCBI Description
                   11373
Seq. No.
                   21372 1.R1040
Contig ID
5'-most EST
                   LIB3050-001-Q1-E1-H11
                   BLASTX
Method
NCBI GI
                   g421955
                   155
BLAST score
                   2.0e-16
E value
                   106
Match length
                   54
% identity
                   hypothetical protein 4 - potato transposon Tst1
NCBI Description
```

>gi_21434_emb_CAA36616_ (X52387) ORF4 [Solanum tuberosum]

5'-most EST

```
. .
                   11374
Seq. No.
Contig ID
                   21373 1.R1040
5'-most EST
                   LIB3050-001-Q1-E1-H12
Method
                   BLASTX
NCBI GI
                   g2980806
BLAST score
                   588
                   7.0e-61
E value
Match length
                   176
                   48
% identity
NCBI Description
                   (AL022197) putative protein [Arabidopsis thaliana]
                   11375
Seq. No.
Contig ID
                   21375 1.R1040
5'-most EST
                   jC-gmf102220083a02a1
Method
                   BLASTX
NCBI GI
                   q3643598
BLAST score
                   325
E value
                   2.0e-29
Match length
                   89
% identity
                   62
                   (ACO05395) putative poly(A) polymerase [Arabidopsis
NCBI Description
                   thaliana]
                   11376
Seq. No.
Contig ID
                   21376 1.R1040
                   jC-gmro02800030a01d1
5'-most EST
Seq. No.
                   11377
                   21383 1.R1040
Contig ID
5'-most EST
                   LIB3107-029-Q1-K1-F7
Method
                   BLASTX
                   g2980767
NCBI GI
BLAST score
                   533
E value
                   3.0e-54
Match length
                   170
% identity
                   63
                   (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
                   11378
Seq. No.
                   21386 1.R1040
Contig ID
5'-most EST
                   94295843
                   11379
Seq. No.
                   21386 2.R1040
Contig ID
5'-most EST
                   q5606\overline{5}41
Method
                   BLASTX
NCBI GI
                   q1174199
BLAST score
                   216
E value
                   4.0e-17
Match length
                   130
% identity
                   45
NCBI Description
                   (U44760) S25-PR6 [Nicotiana tabacum]
                   11380
Seq. No.
                   21404 1.R1040
Contig ID
```

zsg701118990.h1

Match length

266

```
Seq. No.
                   11381
Contig ID
                   21410 1.R1040
5'-most EST
                   txt700734121.hl
Method
                   BLASTX
NCBI GI
                   q4580389
BLAST score
                   454
E value
                   6.0e-45
Match length
                   228
% identity
                   43
NCBI Description
                   (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                   11382
Contig ID
                   21410 2.R1040
5'-most EST
                   bth700849572.h1
Method
                   BLASTX
NCBI GI
                   g4580389
BLAST score
                   316
E value
                   9.0e-29
Match length
                   159
% identity
                   41
NCBI Description
                   (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                   11383
                   21414 1.R1040
Contig ID
5'-most EST
                   LIB3106-085-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   a4538973
BLAST score
                   553
                   1.0e-56
E value
Match length
                   218
% identity
                   51
NCBI Description
                   (AL049487) hypothetical protein [Arabidopsis thaliana]
                   11384
Seq. No.
Contig ID
                   21419 1.R1040
5'-most EST
                   LIB3050-024-Q1-K1-D11
Method
                   BLASTX
                   q1532167
NCBI GI
BLAST score
                   150
E value
                   1.0e-09
Match length
                   65
% identity
NCBI Description
                   (U63815) localized according to blastn similarity to EST
                   sequences; therefore, the coding span corresponds only to
                   an area of similarity since the initation codon and stop
                   codon could not be precisely determined [Arabidopsis
                   thaliana]
                   11385
Seq. No.
Contig ID
                   21423 1.R1040
5'-most EST
                   a5175463
Method
                   BLASTX
NCBI GI
                   g2191141
BLAST score
                   691
E value
                   1.0e-85
```

% identity

NCBI Description

76

```
% identity
                   (AF007269) A IG002N01.21 gene product [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   11386
                   21425 1.R1040
Contig ID
                   hrw701062017.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3386565
BLAST score
                   1028
E value
                   1.0e-112
Match length
                   307
% identity
                   66
                   (AF079588) 1-aminocyclopropane-1-carboxylate oxidase
NCBI Description
                   [Sorghum bicolor]
                   11387
Seq. No.
Contig ID
                   21425 2.R1040
5'-most EST
                   jC-gmst02400007d12d1
Method
                   BLASTX
                   g398994
NCBI GI
                   302
BLAST score
E value
                   3.0e-27
                   89
Match length
% identity
                   63
                   1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)
NCBI Description
                   (ETHYLENE-FORMING ENZYME) (EFE) >gi_166313 (M97961) tomato
                   and apple ACC oxidase homologue [Actinidia deliciosa]
                   11388
Seq. No.
                   21429 1.R1040
Contig ID
                   LIB3050-028-Q1-E1-B2
5'-most EST
                   11389
Seq. No.
                   21437_1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-010-Q1-E1-G8
Method
                   BLASTX
                   g3834302
NCBI GI
BLAST score
                   2334
E value
                   0.0e + 00
Match length
                   559
                   83
% identity
NCBI Description
                   (AC005679) Similar to gb D45384 vacuolar H+-pyrophosphatase
                   from Oryza sativa. ESTs gb F14272 and gb F14273 come from
                   this gene. [Arabidopsis thaliana]
                   11390
Seq. No.
Contig ID
                   21437 2.R1040
5'-most EST
                   ssr70\overline{0}558351.h1
Method
                   BLASTX
                   g3355717
NCBI GI
BLAST score
                   551
E value
                   2.0e-73
                   184
Match length
```

(Y13053) seryl-tRNA synthetase [Zea mays]

BLAST score

298

```
Seq. No.
                   11391
                   21439 1.R1040
Contig ID
5'-most EST
                   taw700655923.h1
Method
                   BLASTX
NCBI GI
                   g3334223
BLAST score
                   435
E value
                   5.0e-43
Match length
                   94
% identity
                   86
NCBI Description
                   4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)
                   >gi_2145039 (AF000228) p-hydroxyphenylpyruvate dioxygenase
[Arabidopsis thaliana] >gi_2392518 (U89267)
                   p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]
                   >gi 3098559 (AF047834) 4-hydroxyphenylpyruvate dioxygenase
                   [Arabidopsis thaliana]
Seq. No.
                   11392
Contig ID
                   21440 1.R1040
5'-most EST
                   zsg701123794.hl
Method
                   BLASTX
NCBI GI
                   q3334219
BLAST score
                   939
E value
                   1.0e-101
Match length
                   306
                   62
% identity
NCBI Description
                   4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)
                   >gi 2231615 (U87257) 4-hydroxyphenylpyruvate dioxygenase
                   [Daucus carota]
                   11393
Seq. No.
Contig ID
                   21447 1.R1040
5'-most EST
                   LIB3093-044-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   g3548818
BLAST score
                   1391
E value
                   1.0e-154
Match length
                   342
% identity
                   (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                   11394
Seq. No.
                   21447 2.R1040
Contig ID
5'-most EST
                   LIB3107-034-Q1-K1-E7
Method
                   BLASTX
NCBI GI
                   q3548818
BLAST score
                   332
E value
                   5.0e-31
Match length
                   94
% identity
                   71
NCBI Description
                   (AC005313) unknown protein [Arabidopsis thaliana]
                   11395
Seq. No.
Contig ID
                   21448 1.R1040
5'-most EST
                   zzp700834891.h1
Method
                   BLASTX
NCBI GI
                   q4457221
```

5'-most EST

```
E value
                   1.0e-26
Match length
                   130
                   53
% identity
NCBI Description
                   (AF127797) putative bZIP DNA-binding protein [Capsicum
                   chinense]
                   11396
Seq. No.
                   21449 1.R1040
Contig ID
5'-most EST
                  g5057953
                   BLASTX
Method
NCBI GI
                   q100226
BLAST score
                   635
E value
                   5.0e-66
Match length
                   212
% identity
                   57
NCBI Description
                  hypothetical protein - tomato >gi 19275 emb CAA78112
                   (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi 445619 prf 1909366A Leu zipper protein
                   [Lycopersicon esculentum]
                   11397
Seq. No.
                   21450 1.R1040
Contig ID
5'-most EST
                   LIB3051-041-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   q3790554
BLAST score
                   208
E value
                   2.0e-16
Match length
                   119
% identity
                   37
NCBI Description
                   (AF078683) RING-H2 finger protein RHA1a [Arabidopsis
                   thaliana]
                   11398
Seq. No.
Contig ID
                   21451 1.R1040
                   LIB3139-088-P1-N1-G10
5'-most EST
Method
                   BLASTX
                   q3451072
NCBI GI
BLAST score
                   616
E value
                   9.0e-64
Match length
                   158
                   70
% identity
NCBI Description
                   (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                   11399
                   21451 3.R1040
Contig ID
5'-most EST
                   uC-gmropic070g07b1
Method
                  BLASTX
NCBI GI
                  q3451072
BLAST score
                   253
                   1.0e-21
E value
Match length
                  73
% identity
NCBI Description
                   (AL031326) putative protein [Arabidopsis thaliana]
                   11400
Seq. No.
                   21451 4.R1040
Contig ID
```

uC-gmropic022a05b1

Contig ID

```
Method
                   BLASTX
                   g3451072
NCBI GI
BLAST score
                   350
E value
                   8.0e-37
Match length
                   99
                   75
% identity
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   11401
Seq. No.
                   21451 7.R1040
Contig ID
5'-most EST
                   seb700651120.h1
                   11402
Seq. No.
                   21453 1.R1040
Contig ID
5'-most EST
                   r1r70\overline{0}897774.h1
Method
                   BLASTX
                   q1872521
NCBI GI
BLAST score
                   585
E value
                   4.0e-60
Match length
                   178
% identity
                   54
                   (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
NCBI Description
                   >gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
                   thaliana]
                   11403
Seq. No.
Contig ID
                   21453 2.R1040
5'-most EST
                   LIB31\overline{0}9-001-Q1-K2-B12
Method
                   BLASTX
NCBI GI
                   g1872521
BLAST score
                   247
E value
                   6.0e-21
                   84
Match length
                   30
% identity
                   (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
NCBI Description
                   >gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
                   thaliana]
                   11404
Seq. No.
                   21453 3.R1040
Contig ID
5'-most EST
                   LIB3051-019-Q1-E1-H6
Method
                   BLASTX
                   g1872521
NCBI GI
BLAST score
                   500
E value
                   1.0e-62
Match length
                   178
                   50
% identity
NCBI Description
                   (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
                   >gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
                   thaliana]
                   11405
Seq. No.
Contig ID
                   21453 4.R1040
5'-most EST
                   LIB3109-043-Q1-K1-D3
                   11406
Seq. No.
```

21454 1.R1040

```
5'-most EST
                  bth700849155.h1
Method
                  BLASTX
NCBI GI
                  g2129575
BLAST score
                  557
E value
                  3.0e-57
                  142
Match length
                  77
% identity
                  DNA repair protein homolog XPBara - Arabidopsis thaliana
NCBI Description
                  11407
Seq. No.
Contig ID
                  21457 1.R1040
5'-most EST
                  wrg700789425.h2
                  BLASTX
Method
NCBI GI
                  g2914706
BLAST score
                  648
E value
                  7.0e-68
                  167
Match length
                  71
% identity
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]
                  11408
Seq. No.
                  21457 2.R1040
Contig ID
                  leu701147230.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2914706
BLAST score
                  - 592
E value
                  3.0e-61
Match length
                  152
% identity
                  72
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]
                  11409
Seq. No.
                  21460 1.R1040
Contig ID
5'-most EST
                  jC-gmf102220054g09a1
Method
                  BLASTX
NCBI GI
                  g1076660
BLAST score
                  1141
E value
                  1.0e-125
                  333
Match length
% identity
                  D13F(MYBST1) protein - potato >gi_786426_bbs_159122
NCBI Description
                   (S74753) MybSt1=Myb-related transcriptional activator
                  {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                  leaf, Peptide, 342 aa] [Solanum tuberosum] 😓
                  11410
Seq. No.
                  21460 3.R1040
Contig ID
5'-most EST
                  ek170\overline{0}968295.h1
Method
                  BLASTX
                  g1076660
NCBI GI
BLAST score
                  154
                  2.0e-10
E value
Match length
                  28
% identity
                  D13F(MYBST1) protein - potato >gi 786426_bbs_159122
NCBI Description
                   (S74753) MybSt1=Myb-related transcriptional activator
                  {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
```

E value

3.0e-14

```
leaf, Peptide, 342 aa] [Solanum tuberosum]:
                   11411
Seq. No.
                   21464 1.R1040
Contig ID
                   uxk70\overline{0}668564.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3152606
BLAST score
                   674
E value
                   1.0e-70
Match length
                   169
% identity
                   72
NCBI Description
                   (AC004482) putative ring zinc finger protein [Arabidopsis
                   thalianal
Seq. No.
                   11412
                   21464 3.R1040
Contig ID
                   LIB3051-002-Q1-E1-E5
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3152606
BLAST score
                   291
E value
                   4.0e-26
Match length
                   54
% identity
                   81
NCBI Description
                   (AC004482) putative ring zinc finger protein [Arabidopsis
                   thaliana]
                   11413
Seq. No.
                   21465 1.R1040
Contig ID
                   eep70\overline{0}868572.h1
5'-most EST
Method
                   BLASTX
                   g1871192
NCBI GI
BLAST score
                   213
                   6.0e-17
E value
Match length
                   92
% identity
                   48
NCBI Description
                   (U90439) Cys3His zinc finger protein isolog [Arabidopsis
                   thaliana]
                   11414
Seq. No.
                   21465 2.R1040
Contig ID
                   uC-qmflminsoy011d06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1871192
BLAST score
                   227
E value
                   1.0e-18
Match length
                   94
% identity
                   49
NCBI Description
                   (U90439) Cys3His zinc finger protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                   11415
                                                                      .
Contig ID
                   21466 1.R1040
5'-most EST
                   xpa700793076.hl
Method
                   BLASTX
NCBI GI
                   g1519680
BLAST score
                   193
```

-;-.

```
182
Match length
% identity
                   31
NCBI Description
                   (U67953) contains similarity to C3HC4-class zinc finger
                   (PS:PS00518) [Caenorhabditis elegans]
Seq. No.
                  11416
                  21469 1.R1040
Contig ID
5'-most EST
                  LIB3051-026-Q1-K1-B7
                  BLASTX
Method
NCBI GI
                  g3152598
                  389
BLAST score
E value
                  1.0e-37
Match length
                  113
% identity
                   (AC002986) Contains similarity to C2-HC type zinc finger
NCBI Description
                  protein C.e-MyT1 gb_U67079 from C. elegans and to
                  hypersensitivity-related gene 201 isolog T28M21.14 from A.
                  thaliana BAC gb AF002109. [Arabidopsis thaliana]
                  11417
Seq. No.
Contig ID
                  21472 1.R1040
5'-most EST
                  LIB3051-059-Q1-K2-E10
Method
                  BLASTX
NCBI GI
                  g2130078
BLAST score
                  251
                  2.0e-21
E value
Match length
                  136
% identity
                  46
                  MADS-box protein 3 - rice >gi 886405 (L37528) MADS box
NCBI Description
                  protein [Oryza sativa]
                  11418
Seq. No.
                  21472_2.R1040
Contig ID
5'-most EST
                  LIB3170-050-Q1-J1-C8
                  11419
Seq. No.
Contig ID
                  21475_1.R1040
                  jC-gmro02910060a03a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2865394
BLAST score
                  185
E value
                  2.0e-13
Match length
                  118
% identity
                   (AF036949) basic leucine zipper protein [Zea mays]
NCBI Description
                  11420
Seq. No.
Contig ID
                  21476_1.R1040
5'-most EST
                  awf700836445.hl
Method
                  BLASTX
NCBI GI
                  g2062176
BLAST score
                  859
E value
                  4.0e-92
Match length
                  356
% identity
                  55
NCBI Description
                   (AC001645) Myb-related transcription activator (MybSt1)
```

isolog [Arabidopsis thaliana]

NCBI GI

```
Seq. No.
                   11421
                   21476 2.R1040
Contig ID
5'-most EST
                   LIB3170-024-Q1-K1-G1
Method
                   BLASTX
                   g2062176
NCBI GI
BLAST score
                   314
                   1.0e-28
E value
Match length
                   117
% identity
                   56
NCBI Description
                   (AC001645) Myb-related transcription activator (MybSt1)
                   isolog [Arabidopsis thaliana]
                   11422
Seq. No.
                   21476 3.R1040
Contig ID
5'-most EST
                   g5752602
                   11423
Seq. No.
Contig ID
                   21478 1.R1040
5'-most EST
                   LIB3170-052-Q1-K1-C9
                   BLASTX
Method
NCBI GI
                   g1945281
BLAST score
                   247
E value
                   6.0e-21
Match length
                   45
% identity
                   91
NCBI Description (Y11352) myb factor [Oryza sativa]
                   11424
Seq. No.
                   21478 2.R1040
Contig ID
5'-most EST
                   LIB3051-084-Q1-K1-A12
Method
                   BLASTX
                   g3941528
NCBI GI
BLAST score
                   458
E value
                   3.0e-45
Match length
                   220
% identity
                   68
NCBI Description
                   (AF062918) putative transcription factor [Arabidopsis
                   thaliana]
                   11425
Seq. No.
                   21478 3.R1040
Contig ID
5'-most EST
                  uxk70\overline{0}673133.h1
Method
                   BLASTX
                   g3941528
NCBI GI
BLAST score
                   433
E value
                   1.0e-42
Match length
                   203
                   46
% identity
NCBI Description
                   (AF062918) putative transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   11426
                   21482 1.R1040
Contig ID
5'-most EST
                  LIB3106-010-Q1-K1-B6
Method
                   BLASTX
```

g2826884

```
BLAST score
                   393
E value
                   5.0e-38
Match length
                   169
                   54
% identity
                   (AJ223635) transcription factor IIA large subunit
NCBI Description
                   [Arabidopsis thaliana]
                   11427
Seq. No.
Contig ID
                   21485 1.R1040
                   awf700839210.h1
5'-most EST
Method
                   BLASTX
                   q3600059
NCBI GI
                   807
BLAST score
E value
                   2.0e-86
Match length
                   189
% identity
                   76
NCBI Description
                   (AF080120) contains similarity to WB domains, G-beta
                   repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03)
                   [Arabidopsis thaliana]
                   11428
Seq. No.
                   21488 1.R1040
Contig ID
                   gsv701046512.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4324495
BLAST score
                  414
E value
                   2.0e-40
Match length
                   140
                   68
% identity
                   (AF105221) glutamyl-tRNA reductase precursor [Glycine max]
NCBI Description
                   11429
Seq. No.
                   21490 1.R1040
Contig ID
5'-most EST
                   dpv701099817.h1
Method
                   BLASTX
NCBI GI
                   g4510377
BLAST score
                   309
E value
                   3.0e-28
                   140
Match length
% identity
                   (AC007017) putative RNA helicase A [Arabidopsis thaliana]
NCBI Description
                   11430
Seq. No.
Contig ID
                   21491 1.R1040
                  LIB3170-051-Q1-K1-B12
5'-most EST
                  BLASTX
Method
NCBI GI
                   g4415931
BLAST score
                   401
E value
                   5.0e-39
Match length
                  113
% identity
                   65
                   (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
                  11431
Seq. No.
```

21492 1.R1040

Contig ID

5'-most EST

```
5'-most EST
                  LIB3051-045-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                   q4128208
BLAST score
                  220
E value
                   7.0e-18
                  91
Match length
                   52
% identity
NCBI Description
                   (AF076277) ethylene response factor 1 [Arabidopsis
                   thaliana] >gi 4128210 (AF076278) ethylene response factor 1
                   [Arabidopsis thaliana]
                   11432
Seq. No.
                   21494 1.R1040
Contig ID
5'-most EST
                   kl1701213301.h1
                  BLASTX
Method
                   g2809251
NCBI GI
BLAST score
                   1185
E value
                   1.0e-130
Match length
                   351
% identity
                   61
NCBI Description
                   (AC002560) F21B7.20 [Arabidopsis thaliana]
Seq. No.
                   11433
                   21495 1.R1040
Contig ID
5'-most EST
                   jC-gmro02910040a03a1
Method
                   BLASTX
NCBI GI
                   a2462762
BLAST score
                   762
E value
                   5.0e-81
Match length
                   248
% identity
                   62
NCBI Description
                   (AC002292) Highly similar to auxin-induced protein
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                   11434
Contig ID
                   21496 1.R1040
5'-most EST
                   sat701012342.hl
Method
                   BLASTX
NCBI GI
                   a3193297
BLAST score
                   761
E value
                   5.0e-81
Match length
                   184
% identity
NCBI Description
                   (AF069298) similar to epoxide hydrolases [Arabidopsis
                   thalianal
Seq. No.
                   11435
Contig ID
                   21497 1.R1040
5'-most EST
                   uC-gmrominsoy057h04b1
Seq. No.
                   11436
Contig ID
                   21499 1.R1040
5'-most EST
                  LIB3051-082-01-K1-G3
Seq. No.
                   11437
                   21500 1.R1040
Contig ID
```

 $seb70\overline{0}652885.h1$

·

5'-most EST

```
BLASTX
Method
NCBI GI
                  g2827699.
BLAST score
                  167
E value
                   1.0e-11
                  57
Match length
                   53
% identity
                  (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   11438
Seq. No.
                   21500 2.R1040
Contig ID
                   kl1701212039.h1
5'-most EST
                  BLASTX
Method
                   g2827699
NCBI GI
BLAST score
                   167
                   8.0e-12
E value
                   57
Match length
% identity
                   (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11439
                   21501 1.R1040
Contig ID
5'-most EST
                   fC-gmse700752437a2
Method
                   BLASTX
NCBI GI
                   g3309084
BLAST score
                   469
                   8.0e-47
E value
Match length
                   114
% identity
                   82
                   (AF076252) calcineurin B-like protein 2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   11440
                   21501 3.R1040
Contig ID
5'-most EST
                   pcp700994873.h1
Method
                   BLASTX
NCBI GI
                   g3309084
BLAST score
                   195
E value
                   5.0e-15
Match length
                   55
% identity
                   (AF076252) calcineurin B-like protein 2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   11441
                   21502 1.R1040
Contig ID
5'-most EST
                   uC-gmropic090g04b1
Method
                   BLASTX
NCBI GI
                   g3287270
BLAST score
                   1044
E value
                   1.0e-114
                   274
Match length
% identity
                   73
                   (Y09533) involved in starch metabalism [Solanum tuberosum]
NCBI Description
                   11442
Seq. No.
                   21504_1.R1040
Contig ID
```

ncj700975676.h1

BLAST score

37

```
Method
                   BLASTX
NCBI GI
                   q3738306
BLAST score
                   160
E value
                   2.0e-10
                  76
Match length
% identity
                   42
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11443
                   21505 1.R1040
                                                              . .
Contig ID
5'-most EST
                   LIB3051-105-Q1-K1-G3
                   11444
Seq. No.
                   21505 2.R1040
Contig ID
                   taw700660105.hl
5'-most EST
Seq. No.
                   11445
                   21507 1.R1040
Contig ID
5'-most EST
                   LIB3051-020-Q1-E1-B12
Method
                   BLASTX
NCBI GI
                   q2465925
BLAST score
                   254
E value
                   8.0e-22
Match length
                   116
% identity
                   48
NCBI Description
                   (AF024649) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                   11446
Contig ID
                   21508 1.R1040
5'-most EST
                   LIB3051-107-Q1-K1-G11
Method
                   BLASTX
NCBI GI
                   q3298536
BLAST score
                   505
E value
                   3.0e-51
Match length
                   139
% identity
                   68
NCBI Description
                   (AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.
                   11447
Contig ID
                   21509 1.R1040
5'-most EST
                   LIB3051-070-Q1-K1-F1
Method
                   BLASTN
NCBI GI
                   q3241925
BLAST score
                   40
E value
                   4.0e-13
Match length
                   168
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOK9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   11448
Contig ID
                   21510 1.R1040
                   pxt700943472.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g2264312
```

5'-most EST

```
1.0e-10
E value
Match length
                   322
                   83
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOK16, complete sequence [Arabidopsis thaliana]
                   11449
Seq. No.
                   21510 2.R1040
Contig ID
5'-most EST
                   LIB3170-061-Q1-J1-C9
                   11450
Seq. No.
                   21511 1.R1040
Contig ID
                   LIB3051-111-Q1-K1-A2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3201627
BLAST score
                   639
E value
                   5.0e-67
Match length
                   139
                   88
% identity
NCBI Description
                   (AC004669) putative SWH1 protein [Arabidopsis thaliana]
Seq. No.
                   11451
                   21512_1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-112-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                  g2980788
BLAST score
                   434
                   2.0e-42
E value
Match length
                   278
                   43
% identity
                   (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   11452
Seq. No.
                   21514_1.R1040
Contig ID
                   k11701209925.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g598073
BLAST score
                   205
                   4.0e-16
E value
                   86
Match length
                   60
% identity
NCBI Description
                   (L36806) GT-1 [Arabidopsis thaliana]
Seq. No.
                   11453
                   21514 2.R1040
Contig ID
5'-most EST
                   awf700836550.hl
Method
                   BLASTX
                   g598073
NCBI GI
BLAST score
                   224
E value
                   3.0e-18
                   91
Match length
% identity
NCBI Description
                   (L36806) GT-1 [Arabidopsis thaliana]
                   11454
Seq. No.
                   21515 1.R1040
Contig ID
```

jC-gmro02910062b12a1

```
Method
                   BLASTX
NCBI GI
                   g2088651
BLAST score
                   295
E value
                   3.0e-26
Match length
                   158
% identity
                   42
NCBI Description
                   (AF002109) hypersensitivity-related gene 201 isolog
                   [Arabidopsis thaliana]
Seq. No.
                   11455
Contig ID
                   21518 1.R1040
5'-most EST
                  LIB3170-041-Q1-J1-F10
Method
                   BLASTX
NCBI GI
                   g4218141
BLAST score
                   240
E value
                   2.0e-19
Match length
                   331
                   30
% identity
NCBI Description (AJ236702) HMR1 protein [Antirrhinum majus]
Seq. No.
                   11456
                   21518 2.R1040
Contig ID
5'-most EST
                   k11701204524.h2
Method
                  BLASTX
NCBI GI
                  g555655
BLAST score
                   273
E value
                   1.0e-23
Match length
                   159
                   55
% identity
                  (U06712) DNA-binding protein [Nicotiana tabacum]
NCBI Description
Seq. No.
                   11457
                   21518 3.R1040
Contig ID
5'-most EST
                   jC-gmf102220051a02d1
                  11458
Seq. No.
Contig ID
                   21518 4.R1040
5'-most EST
                  ssr700556645.hl
                  11459
Seq. No.
Contig ID
                  21520 1.R1040
5'-most EST
                  asn701135640.h1
Method
                  BLASTX
NCBI GI
                  q4512667
BLAST score
                  939
                  1.0e-107
E value
Match length
                  311
% identity
NCBI Description
                   (AC006931) putative MAP kinase [Arabidopsis thaliana]
Seq. No.
                  11460
                  21520 2.R1040
Contig ID
                  ckk700605794.h2
5'-most EST
Method
                  BLASTX
                  g4512667
NCBI GI
BLAST score
                  171
```

5.0e-12

E value

```
97
Match length
% identity
                   56
NCBI Description
                   (AC006931) putative MAP kinase [Arabidopsis thaliana]
                   11461
Seq. No.
                   21521 1.R1040
Contig ID
5'-most EST
                   LIB3170-057-Q1-K1-E2
                   BLASTX
Method
NCBI GI
                   q3107903
BLAST score
                   186
E value
                   1.0e-13
Match length
                   61
                   59
% identity
NCBI Description
                   (D83719) polycomb-like protein [Daucus carota]
Seq. No.
                   11462
                   21522 1.R1040
Contig ID
5'-most EST
                   LIB3109-001-Q1-K2-A11
Method
                   BLASTX
NCBI GI
                   g3201618
                   798
BLAST score
                   2.0e-85
E value
Match length
                   166
                   85
% identity
                   (AC004669) Sop2p-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11463
                   21522 2.R1040
Contig ID
                   wvk70\overline{0}686490.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3201618
BLAST score
                   252
E value
                   1.0e-21
Match length
                   118
% identity
                   58
NCBI Description
                   (AC004669) Sop2p-like protein [Arabidopsis thaliana]
Seq. No.
                   11464
                   21523_1.R1040
Contig ID
                   LIB3051-027-Q1-K1-A6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1850546
BLAST score
                   562
                   9.0e-58
E value
Match length
                   141
% identity
                   (U88045) syntaxin related protein AtVam3p [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   11465
                   21524 1.R1040
Contig ID
5'-most EST
                   uC-gmflminsoy018e09b1
Method
                   BLASTX
NCBI GI
                   q4539418
BLAST score
                   477
                   7.0e-48
E value
```

Match length

```
% identity
                   (ALO49171) caffeoyl-CoA O-methyltransferase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   11466
Seq. No.
                   21525 1.R1040
Contig ID
                   LIB30\overline{5}1-026-Q1-K1-G11
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4006848
                   665
BLAST score
E value
                   6.0e-70
                   168
Match length
% identity
                   79
                   (AJ131433) selenocysteine methyltransferase [Astragalus
NCBI Description
                   bisulcatus]
                   11467
Seq. No.
                   21526 2.R1040
Contig ID
                   rca70\overline{0}999839.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3319342
BLAST score
                   537
E value
                   2.0e-54
Match length
                   252
% identity
                   45
                   (AF077407) similar to mitochondrial carrier proteins (Pfam:
NCBI Description
                   mit carr.hmm, score: 79.74 and 42.50) [Arabidopsis
                   thaliana)
                   11468
Seq. No.
                   21528 1.R1040
Contig ID
                   jC-gmle01810035d07a2
5'-most EST
Method
                   BLASTN
                   g1370155
NCBI GI
BLAST score
                   120
E value
                   8.0e-61
Match length
                   204
% identity
                   90
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB11H
                   11469
Seq. No.
                   21528 2.R1040
Contig ID
                   LIB30\overline{5}1-114-Q1-K1-F1
5'-most EST
Method
                   BLASTN
                   g1370155
NCBI GI
BLAST score
                   201
E value
                   1.0e-109
Match length
                   333
                   90
% identity
                   L.japonicus mRNA for small GTP-binding protein, RAB11H
NCBI Description
                   11470
Seq. No.
Contig ID
                   21529 1.R1040
                   LIB3093-042-Q1-K1-A10
5'-most EST
                   BLASTX
Method
                   g3395938
NCBI GI
```

BLAST score

NCBI GI

```
E value
                   6.0e-65
Match length
                   167
% identity
                   37
NCBI Description
                   (AF076924) polypyrimidine tract-binding protein homolog
                   [Arabidopsis thaliana]
                   11471
Seq. No.
                   21529 2.R1040
Contig ID
5'-most EST
                   LIB3138-094-Q1-N1-A6
                   BLASTX
Method
                   g3395938
NCBI GI
BLAST score
                   781
E value
                   2.0e-83
Match length
                   203
% identity
                   50
NCBI Description
                   (AF076924) polypyrimidine tract-binding protein homolog
                   [Arabidopsis thaliana]
Seq. No.
                   11472
Contig ID
                   21531 1.R1040
                   LIB30\overline{5}1-032-Q1-K1-G2
5'-most EST
Method
                   BLASTX
                   g688423
NCBI GI
BLAST score
                   292
                   2.0e-26
E value
Match length
                   102
% identity
                   50
NCBI Description
                   (D26453) tumor-related protein [Nicotiana glauca X
                   Nicotiana langsdorffii]
Seq. No.
                   11473
                   21533 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy188e03b1
Method
                   BLASTX
                   g3461820
NCBI GI
BLAST score
                   286
E value
                   2.0e-25
Match length
                   62
% identity
                   77
NCBI Description
                   (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   11474
                   21533 2.R1040
Contig ID
                   epx701106943.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3461820
BLAST score
                   211
E value
                   1.0e-16
Match length
                   49
% identity
NCBI Description
                   (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   11475
                   21534 1.R1040
Contig ID
                   jC-gmle01810068f02a1
5'-most EST
Method
                   BLASTX
```

g3522943

```
BLAST score
                   1300
E value
                   1.0e-144
Match length
                   441
% identity
                   36
NCBI Description
                   (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
                   11476
Seq. No.
                   21536 1.R1040
Contig ID
5'-most EST
                   LIB3109-043-Q1-K1-F1
                   11477
Seq. No.
Contig ID
                   21537 1.R1040
5'-most EST
                   LIB3051-108-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   q2498565
BLAST score
                   245
                   8.0e-21
E value
                   111
Match length
                   41
% identity
                   C-MYC BINDING PROTEIN MM-1 >qi 1731809 dbj BAA14006
NCBI Description
                   (D89667) c-myc binding protein [Homo sapiens]
                   >gi_4505743_ref_NP_002615.1_pPFDN5_ prefoldin
                   11478
Seq. No.
                   21537 2.R1040
Contig ID
5'-most EST
                   pcp700993248.hl
Method
                   BLASTX
NCBI GI
                   g2498565
BLAST score
                   232
                   3.0e-19
E value
Match length
                   111
                   39
% identity
NCBI Description
                   C-MYC BINDING PROTEIN MM-1 >gi 1731809 dbj BAA14006
                   (D89667) c-myc binding protein [Homo sapiens]
                   >gi_4505743_ref_NP_002615.1_pPFDN5_ prefoldin
                   11479
Seq. No.
Contig ID
                   21538 1.R1040
5'-most EST
                   LIB3051-110-Q1-K1-G7
                   BLASTX
Method
                   g4063751
NCBI GI
                   395
BLAST score
                   4.0e-38
E value
                   204
Match length
                   43
% identity
                   (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
                   protein [Arabidopsis thaliana]
                   11480
Seq. No.
                   21539_1.R1040
Contig ID
5'-most EST
                   asn701138037.hl
                   {\tt BLASTX}
Method
NCBI GI
                   q3894387
BLAST score
                   292
                   8.0e-26
E value
```

Match length

NCBI GI

```
% identity
                  (AF053995) Hcr2-OB [Lycopersicon esculentum]
NCBI Description
                  11481
Seq. No.
                  21540 1.R1040
Contig ID
                  LIB3167-004-P1-K1-H7
5'-most EST
                  BLASTN
Method
                  g510931
NCBI GI
                  292
BLAST score
                  1.0e-163
E value
                  448
Match length
                  92
% identity
NCBI Description V.faba mRNA for alpha 1,4-glucan phosphorylase type H
                  11482
Seq. No.
                  21541 1.R1040
Contig ID
5'-most EST
                  crh700855575.h1
                  BLASTN
Method
                  g18662
NCBI GI
BLAST score
                  535
                  0.0e + 00
E value
Match length
                  579
                  98
% identity
                  Glycine max hsp 70 gene
NCBI Description
Seq. No.
                  11483
                  21542 1.R1040
Contig ID
5'-most EST
                  LIB3109-032-Q1-K1-A5
Method
                  BLASTX
                  g1172555
NCBI GI
BLAST score
                  342
                  4.0e-32
E value
                  136
Match length
% identity
                  47
                  34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
NCBI Description
                  (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                  (POM 34) >gi_629720_pir__S46936 34K porin - potato
                  >gi 1076682 pir A55364 porin (clone pPOM-34) - potato
                  mitochondrion >gi 516166 emb CAA56599 (X80386) 34 kDA
                  porin [Solanum tuberosum]
                  11484
Seq. No.
Contig ID
                  21543 1.R1040
5'-most EST
                  LIB3051-006-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1743354
BLAST score
                  274
                  2.0e-53
E value
Match length
                  201
% identity
NCBI Description
                  (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
                  11485
Seq. No.
                  21544 1.R1040
Contig ID
5'-most EST
                  dpv701099148.hl
Method
                  BLASTX
```

g4539301

```
751
BLAST score
E value
                   1.0e-79
Match length
                   297
% identity
NCBI Description
                   (AL049480) putative mitochondrial protein [Arabidopsis
                   thaliana]
                   11486
Seq. No.
Contig ID
                  21544 2.R1040
5'-most EST
                  uC-qmflminsoy011c06b1
Method
                  BLASTX
NCBI GI
                  q4539301
BLAST score
                   121
                   4.0e-11
E value
Match length
                   97
                   48
% identity
NCBI Description
                   (AL049480) putative mitochondrial protein [Arabidopsis
                   thaliana]
Seq. No.
                   11487
                   21545 1.R1040
Contig ID
                  uC-gmflminsoy008g01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2723391
BLAST score
                  240.
E value
                   8.0e-20
                  197
Match length
% identity
                   36
NCBI Description
                   (AB007042) EXTR1 [Homo sapiens] >gi 2897905 (AF001690) EXT
                   like protein 3 [Homo sapiens] >gi_3043562_dbj_BAA25445_
                   (AB011091) KIAA0519 protein [Homo sapiens] >gi 4103884
                   (AF029231) EXT homolog [Homo sapiens]
                  >gi_4503617_ref_NP_001431.1_pEXTL3_ exostoses
                   (multiple) -like
                  11488
Seq. No.
Contig ID
                  21546_1.R1040
                  LIB3170-059-Q1-K1-E5
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2213594
BLAST score
                  868
E value
                   2.0e-93
Match length
                  257
% identity
NCBI Description
                   (AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                  11489
Contig ID
                  21572 1.R1040
5'-most EST
                  LIB3093-052-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q1354466
BLAST score
                   419
E value
                   6.0e-41
Match length
                  143
                  59
% identity
                   (U52910) U1 snRNP 70K truncated protein [Arabidopsis
NCBI Description
                  thaliana] >gi_1354468 (U52909) U1 snRNP 70K truncated
```

protein [Arabidopsis thaliana] No. 11490

 Seq. No.
 11490

 Contig ID
 21572_2.R1040

 5'-most EST
 trc700563627.h1

Method BLASTX
NCBI GI g1354466
BLAST score 179
E value 2.0e-13
Match length 48
% identity 75

NCBI Description (U52910) U1 snRNP 70K truncated protein [Arabidopsis thaliana] >gi_1354468 (U52909) U1 snRNP 70K truncated

protein [Arabidopsis thaliana]

Seq. No. 11491

Contig ID 21574 1.R1040

5'-most EST uC-gmrominsoy194e08b1

Method BLASTX
NCBI GI g452593
BLAST score 210
E value 1.0e-16
Match length 129
% identity 43

NCBI Description (D21814) ORF [Lilium longiflorum]

Seq. No. 11492

Contig ID 21575 1.R1040

5'-most EST LIB30 $\overline{5}1$ -017-Q1-E1-C10

Method BLASTX
NCBI GI g3184283
BLAST score 837
E value 6.0e-90
Match length 239
% identity 71

NCBI Description (AC004136) putative TBP-binding protein [Arabidopsis

thaliana]

Seq. No. 11493

Contig ID 21576_1.R1040 5'-most EST asn701136909.h1

Method BLASTX
NCBI GI g3063698
BLAST score 333
E value 1.0e-30
Match length 253
% identity 36

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 11494

Contig ID 21576_2.R1040

5'-most EST LIB3051-026-Q1-K1-C2

Method BLASTX
NCBI GI g3063698
BLAST score 181
E value 3.0e-13
Match length 79

```
% identity
NCBI Description
                   (AL022537) putative protein [Arabidopsis thaliana]
                   11495
Seq. No.
                   21577 1.R1040
Contig ID
                   g4396502
5'-most EST
Method
                   BLASTX
NCBI GI
                   g320556
BLAST score
                   507
                   7.0e-51
E value
                   252
Match length
                   40
% identity
                   chitinase (EC 3.2.1.14) precursor, basic - Arabidopsis
NCBI Description
                   thaliana >qi 166666 (M38240) basic chitinase [Arabidopsis
                   thaliana]
Seq. No.
                   11496
                   21577 2.R1040
Contig ID
                   leu701148149.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2980793
BLAST score
                   421
E value
                   6.0e-41
Match length
                   164
% identity
                   47
                   (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   11497
Seq. No.
                   21578 1.R1040
Contig ID
5'-most EST
                   k1170\overline{1}202926.h1
Method
                   BLASTX
NCBI GI
                   g4406784
BLAST score
                   203
E value
                   6.0e-16
Match length
                   95
% identity
                    (AC006532) putative oligopeptide transport protein
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   11498
                   21581 1.R1040
Contig ID
                   seb70\overline{0}654218.h1
5'-most EST
Method
                   BLASTX
                   g2829912
NCBI GI
BLAST score
                   486
E value
                   1.0e-64
Match length
                   158
% identity
                    (AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   11499
                   21582 1.R1040
Contiq ID
                   LIB30\overline{9}3-057-Q1-K1-F9
5'-most EST
Method
                   BLASTX
                   g3297816
NCBI GI
```

BLAST score

```
1.0e-106
E value
Match length
                   306
% identity
                   69
NCBI Description
                   (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                   11500
                   21582 3.R1040
Contiq ID
5'-most EST
                   uC-qmronoir006h07b1
Method
                   BLASTX
NCBI GI
                   q3297816
BLAST score
                   508
E value
                   2.0e-51
Match length
                   149
% identity
NCBI Description
                   (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                   11501
                   21586 1.R1040
Contig ID
5'-most EST
                   jC-gmle01810012e02a1
Method
                   BLASTX
NCBI GI
                   q1549249
BLAST score
                   315
E value
                   5.0e-30
Match length
                   176
                   43
% identity
NCBI Description
                   (U66620) SWI/SNF complex 60 KDa subunit [Mus musculus]
Seq. No.
                   11502
                   21587 1.R1040
Contig ID
5'-most EST
                   ek170\overline{0}968247.h1
Method
                   BLASTX
NCBI GI
                   q1431629
BLAST score
                   1396
E value
                   1.0e-155
Match length
                   398
% identity
                   63
NCBI Description
                   (X99348) pectinacetylesterase precursor [Vigna radiata]
                   11503
Seq. No.
                   21587 2.R1040
Contig ID
5'-most EST
                   k1170\overline{1}211669.h1
Method
                   BLASTN
NCBI GI
                   q1431628
BLAST score
                   35
E value
                   3.0e-10
Match length
                   43
% identity
                   95
NCBI Description
                   V.radiata mRNA for pectinacetylesterase
Seq. No.
                   11504
Contig ID
                   21589 1.R1040
5'-most EST
                   LIB3093-023-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   g2160144
BLAST score
                   267
E value
                   5.0e-23
Match length
                   169
```

Match length

427

```
% identity
NCBI Description
                   (AC000375) Strong similarity to Arabidopsis oligopeptide
                   transporter (gb X77503). [Arabidopsis thaliana]
Seq. No.
                   11505
Contig ID
                   21591 1.R1040
5'-most EST
                   k11701208328.h1
                   BLASTX
Method
NCBI GI
                   q4262226
BLAST score
                   347
E value
                   1.0e-32
Match length
                   90
% identity
                   71
NCBI Description
                   (AC006200) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   11506
Contig ID
                   21593 1.R1040
5'-most EST
                   fua701037592.h1
Method
                   BLASTX
NCBI GI
                   q4006917
BLAST score
                   640
E value
                   1.0e-66
Match length
                   204
% identity
                   58
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   11507
Seq. No.
                   21609 1.R1040
Contig ID
5'-most EST
                   crh700850349.h1
Method
                   BLASTN
NCBI GI
                   q1113940
BLAST score
                   233
E value
                   1.0e-128
Match length
                   391
                   90
% identity
NCBI Description
                  Phaseolus vulgaris Pv42p mRNA, complete cds
Seq. No.
                   11508
                   21612 1.R1040
Contig ID
5'-most EST
                   hrw701058417.hl
Method
                   BLASTX
NCBI GI
                   q3540199
BLAST score
                   1196
E value
                   1.0e-132
Match length
                   336
% identity
NCBI Description
                   (AC004260) Putative monosaccharide transport protein
                   [Arabidopsis thaliana]
                   11509
Seq. No.
                   21613 1.R1040
Contig ID
5'-most EST
                   LIB3051-009-Q1-E1-C10
Method
                   BLASTN
NCBI GI
                   g3941321
BLAST score
                   246
E value
                   1.0e-136
```

NCBI GI

BLAST score

```
% identity
                     91
  NCBI Description
                    Medicago truncatula gamma-glutamylcysteine synthetase mRNA,
                     nuclear gene encoding putative plastid protein, complete
                     11510
  Seq. No.
                     21614 1.R1040
  Contig ID
  5'-most EST
                     epx701110007.h1
                     BLASTX
  Method
                     g1946359
  NCBI GI
  BLAST score
                     999
  E value
                     1.0e-113
  Match length
                     433
                     51
  % identity
                    (U93215) unknown protein [Arabidopsis thaliana]
  NCBI Description
                     11511
  Seq. No.
                     21615 1.R1040
  Contig ID
                     LIB30\overline{5}1-004-Q1-E1-A12
  5'-most EST
  Method
                     BLASTX
                     g2330739
  NCBI GI
  BLAST score
                     203
                     2.0e-15
  E value
                     120
  Match length
                     42
  % identity
                     (Z98598) putative transcriptional regulator
  NCBI Description
                     [Schizosaccharomyces pombe]
                     11512
  Seq. No.
                     21616 1.R1040
  Contig ID
                     jC-gmf102220126b02a1
  5'-most EST
  Method
                     BLASTX
                     g3983665
  NCBI GI
  BLAST score
                     1551
                     1.0e-173
  E value
                     365
  Match length
                     82
  % identity
  NCBI Description
                     (AB011271) importin-beta2 [Oryza sativa]
                     11513
  Seq. No.
                     21617 1.R1040
  Contig ID
  5'-most EST
                     LIB3051-006-Q1-E1-A8
                     BLASTX
  Method
  NCBI GI
                     g2739168
  BLAST score
                     162
  E value
                     4.0e-11
  Match length
                     102
  % identity
  NCBI Description
                     (AF032386) aldose-1-epimerase-like protein [Nicotiana
                     tabacum]
                     11514
  Seq. No.
  Contig ID
                     21618 1.R1040
                     uC-gmrominsoy199c07b1
  5'-most EST
  Method
                     BLASTX
```

g4314401 1345

Method

BLASTX

```
1.0e-149
E value
Match length
                   342
% identity
                   70
NCBI Description
                   (ACO06232) putative beta-1,3-glucanase [Arabidopsis
                   thaliana]
                   11515
Seq. No.
Contig ID
                   21621 1.R1040
5'-most EST
                   uaw700660737.hl
                   BLASTX
Method
NCBI GI
                   g2464914
BLAST score
                   343
E value
                   3.0e-32
Match length
                   101
% identity
                   67
NCBI Description
                   (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   11516
                   21624 1.R1040
Contig ID
5'-most EST
                   LIB3052-009-Q1-N1-D6
Method
                   BLASTX
NCBI GI
                   q82051
BLAST score
                   108
E value
                   8.0e-11
Match length
                   132
% identity
                   lipid body-associated membrane protein - carrot
NCBI Description
                   >gi_259453_bbs_117620 (S47635) lipid body membrane
                   protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
                   180 aa] [Daucus carota]
Seq. No.
                   11517
                   21624 2.R1040
Contig ID
                   crh70\overline{0}852419.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q3097320
BLAST score
                   38
E value
                   6.0e-12
Match length
                   58
                   91
% identity
                  Glycine max gene for Bd 30K, complete cds
NCBI Description
Seq. No.
                   11518
                   21626_1.R1040
Contig ID
                   uC-gmrominsoy062c01b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2911052
BLAST score
                   1021
E value
                   1.0e-111
Match length
                   284
% identity
NCBI Description
                   (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                   11519
                   21627 1.R1040
Contig ID
5'-most EST
                   LIB3051-042-Q1-K1-D2
```

```
NCBI GI
                   g2072393 -
BLAST score
                   830
E value
                   3.0e-89
Match length
                   174
% identity
                   92
NCBI Description
                   (U29168) similar to human Xeroderma pigmentosum group B DNA
                   repair protein, Swiss-Prot Accession Number P19447
                   [Arabidopsis thaliana]
Seq. No.
                   11520
                   21628 1.R1040
Contig ID
5'-most EST
                   ncj700988180.hl
Method
                   BLASTX
NCBI GI
                   q3201635
BLAST score
                   413
E value
                   2.0e-40
Match length
                   132
                   59
% identity
                   (AC004669) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   11521
Seq. No.
                   21629 1.R1040
Contig ID
5'-most EST
                   LIB30\overline{5}1-011-Q1-E1-H5
Method
                   BLASTX
NCBI GI
                   q3540181
BLAST score
                   497
E value
                   2.0e-50
Match length
                   135
% identity
                   74
                   (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11522
                   21635_1.R1040
Contig ID
5'-most EST
                   LIB3051-002-Q1-E1-E10
Method
                   BLASTX
NCBI GI
                   g728906
BLAST score
                   266
                   3.0e-23
E value
Match length
                   90
% identity
                   PROBABLE CALCIUM-TRANSPORTING ATPASE 5
NCBI Description
                   >gi_1077722_pir__S50669 hypothetical protein YER166w -
                   yeast (Saccharomyces cerevisiae) >gi_603407 (U18922)
                   Yer166wp [Saccharomyces cerevisiae]
Seq. No.
                   11523
Contig ID
                   21637 1.R1040
5'-most EST
                   LIB3051-034-Q1-K1-E2
Method
                   BLASTX
NCBI GI
                   g1532171
BLAST score
                   496
E value
                   3.0e-50
Match length
                   132
% identity
                   (U63815) AT.I.24-9 gene product [Arabidopsis thaliana]
NCBI Description
```

11524

Seq. No.

```
21638 1.R1040
Contig ID
5'-most EST
                   LIB3138-024-Q1-N1-D7
Method
                   BLASTX
NCBI GI
                   q2213591
BLAST score
                   225
                   3.0e-18
E value
                   135
Match length
                   41
% identity
NCBI Description
                   (AC000348) T7N9.11 [Arabidopsis thaliana]
Seq. No.
                   11525
                   21638 2.R1040
Contig ID
5'-most EST
                   LIB3106-031-Q1-K1-H1
Method
                   BLASTX
NCBI GI
                   q2213591
BLAST score
                   149
E value
                   1.0e-09
Match length
                   64
% identity
                   48
NCBI Description
                   (AC000348) T7N9.11 [Arabidopsis thaliana]
                   11526
Seq. No.
                   21639_1.R1040
Contig ID
5'-most EST
                   hrw701062732.hl
Method
                   BLASTX
NCBI GI
                   q2911072
                   213
BLAST score
                   5.0e-17
E value
                   88
Match length
                   55
% identity
NCBI Description
                   (AL021960) putative protein [Arabidopsis thaliana]
                   11527
Seq. No.
                   21640_1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy167h12b1
Method
                   BLASTX
                   g3738325
NCBI GI
                   779
BLAST score
E value
                   2.0e-91
Match length
                   188
% identity
                   90
NCBI Description
                   (AC005170) putative CaMB-channel protein [Arabidopsis
                   thaliana]
                   11528
Seq. No.
                   21641 1.R1040
Contig ID
5'-most EST
                   pxt700943810.hl
Method
                   BLASTX
NCBI GI
                   g3451411
BLAST score
                   1083
                   1.0e-126
E value
Match length
                   254
% identity
                   86
NCBI Description
                   (Z98761) seryl-tRNA synthetase [Helianthus annuus]
                   11529
Seq. No.
```

....

21642_1.R1040

Contig ID

```
5'-most EST
                  bth700846162.hl
Method
                   BLASTX
NCBI GI
                   a2576361
BLAST score
                   517
E value
                   2.0e-52
Match length
                   144
% identity
                   66
                   (U39782) lysine and histidine specific transporter
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   11530
                   21645 1.R1040
Contig ID
                   eep700868213.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   a4008006
BLAST score
                   501
                  1.0e-50
E value
Match length
                   152
% identity
                   64
NCBI Description
                   (AF084034) receptor-like protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   11531
                   21646_1.R1040
Contig ID
5'-most EST
                   seb700650524.hl
Method
                   BLASTX
                   g115473
NCBI GI
BLAST score
                   947
E value
                   1.0e-102
Match length
                   253
                   71
% identity
NCBI Description
                  CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                   DEHYDRATASE) >gi_170219 (M94135) chloroplast carbonic
                   anhydrase [Nicotiana tabacum] >gi_445610_prf__1909357A
                   carbonic anhydrase [Nicotiana tabacum]
Seq. No.
                   11532
                   21646 2.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy247g12b1
                   BLASTX
Method
NCBI GI
                   q1168740
BLAST score
                   581
E value
                   5.0e-60
Match length
                   140
                   77
% identity
                  CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi 882244
NCBI Description
                   (U19740) carbonic anhydrase 2 [Flaveria linearis]
                   11533
Seq. No.
                   21646_3.R1040
Contig ID
5'-most EST
                   jsh701065528.h1
Method
                   BLASTX
NCBI GI
                  g1168740
BLAST score
                   310
                   6.0e-35
E value
```

60

Match length

% identity

NCBI Description CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >qi 882244 (U19740) carbonic anhydrase 2 [Flaveria linearis] Seq. No. 11534 21649 1.R1040 Contig ID LIB3051-064-Q1-K1-D8 5'-most EST Method BLASTX q4510339 NCBI GI BLAST score 525 2.0e-57 E value Match length 142 % identity (AC006921) putative ABC transporter protein [Arabidopsis NCBI Description thalianal 11535 Seq. No. 21651 1.R1040 Contig ID $LIB30\overline{5}1-104-Q1-K1-A8$ 5'-most EST Method BLASTX NCBI GI q3482933 BLAST score 436 5.0e-43 E value Match length 118 % identity NCBI Description (AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana] 11536 Seq. No. Contig ID 21652 1.R1040 5'-most EST $uxk70\overline{0}672746.h1$ Method BLASTX NCBI GI g461812 BLAST score 506 E value 4.0e-51 Match length 216 % identity 47 NCBI Description CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi 445604_prf__1909351A cytochrome P450 [Catharanthus roseus] Seq. No. 11537 21654 1.R1040 Contig ID 5'-most EST zpv700757258.h1 Method BLASTX NCBI GI q4406780 BLAST score 1759 E value 0.0e + 00Match length 498 % identity 80

Seq. No. 11538

NCBI Description

Contig ID 21654_2.R1040 5'-most EST dpv701098741.h2

[Arabidopsis thaliana]

(AC006532) putative multispanning membrane protein

Method

BLASTX

```
Method
                   BLASTX
NCBI GI
                   a4406780
BLAST score
                   509
E value
                   2.0e-51
                   128
Match length
                   75
% identity
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   11539
Contig ID
                   21655 1.R1040
5'-most EST
                   LIB3051-035-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   g2739386
BLAST score
                   475
                   1.0e-47
E value
Match length
                   168
                   59
% identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   11540
                   21656_1.R1040
Contig ID
5'-most EST
                   LIB3051-037-Q1-K1-C4
Method
                   BLASTX
                   g2224901
NCBI GI
BLAST score
                   263
                   7.0e-23
E value
Match length
                   136
                   49
% identity
NCBI Description
                   (U67134) PcMYB1 protein [Petroselinum crispum]
                   11541
Seq. No.
Contig ID
                   21656 2.R1040
5'-most EST
                   LIB3087-004-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   g2224899
BLAST score
                   377
                   5.0e-36
E value
                   203
Match length
                   47
% identity
                   (U67133) DNA-binding protein PcMYB1 [Petroselinum crispum]
NCBI Description
                   11542
Seq. No.
                   21657 1.R1040
Contig ID
                   dpv70\overline{1}103216.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1786134
BLAST score
                   207
E value
                   1.0e-16
                   97
Match length
% identity
                   51
NCBI Description
                   (AB000451) PEThy; ZPT2-5 [Petunia x hybrida]
Seq. No.
                   11543
                   21658 1.R1040
Contig ID
5'-most EST
                   zsg701129482.h1
```

```
NCBI GI
                  q4519417
BLAST score
                  382
E value
                  2.0e-36
Match length
                  109
% identity
                  62
NCBI Description
                  (AB024327) WD-40 repeat protein [Homo sapiens]
Seq. No.
                  11544
Contig ID
                  21661 1.R1040
5'-most EST
                  fua701041663.hl
Method
                  BLASTX
NCBI GI
                  q3935138
BLAST score
                  969
E value
                  1.0e-105
Match length
                  358
% identity
NCBI Description
                  (AC005106) T25N20.2 [Arabidopsis thaliana]
                  11545
Seq. No.
Contig ID
                  21662 1.R1040
                  LIB3051-039-Q1-K1-B10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2642450
BLAST score
                  669
                  2.0e-70
E value
Match length
                  168
% identity
                  77
NCBI Description
                   (AC002391) putative metal ion transporter (Nramp)
                  [Arabidopsis thaliana] >gi 3169188 (AC004401) putative
                  metal ion transporter (Nramp) [Arabidopsis thaliana]
Seq. No.
                  11546
Contig ID
                  21665_1.R1040
                  jC-gmst02400031f11a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4521322
BLAST score
                  402
                  8.0e-39
E value
                  156
Match length
% identity
NCBI Description
                  (U11790) mitotic centromere-associated kinesin [Cricetulus
                  griseus]
                  11547
Seq. No.
                  21665 3.R1040
Contig ID
5'-most EST
                  LIB3170-049-Q1-K2-E3
Method
                  BLASTX
NCBI GI
                  g2497528
BLAST score
                  467
E value
                  1.0e-46
Match length
                  199
% identity
NCBI Description
                  KINESIN-LIKE PROTEIN KIF2 (KINESIN-RELATED PROTEIN XKIF2)
                  >gi 1171151 (U36486) kinesin-related protein XKIF2 [Xenopus
                  laevis]
```

Seq. No.

```
Contig ID
                   21665 4.R1040
5'-most EST
                   uC-gmflminsoy016g07b1
Method
                   BLASTN
NCBI GI
                   q4159706
BLAST score
                   43
E value
                   5.0e-15
                   207
Match length
                   80
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MGL6, complete sequence [Arabidopsis thaliana]
Seq. No.
                   11549
                   21666 1.R1040
Contig ID
5'-most EST
                   hyd70\overline{0}728575.h1
Method
                   BLASTX
                   q2864624
NCBI GI
BLAST score
                   558
E value
                   1.0e-90
                   437
Match length
% identity
                   25
NCBI Description
                   (AL021811) putative protein [Arabidopsis thaliana]
                   11550
Seq. No.
Contig ID
                   21672 1.R1040
5'-most EST
                   LIB3051-111-Q1-K1-E2
Seq. No.
                   11551
                   21674 1.R1040
Contig ID
5'-most EST
                   uC-gmrominsoy069a01b1
Method
                   BLASTX
NCBI GI
                   g1717871
BLAST score
                   577
E value
                   2.0e-59
Match length
                   259
                   45
% identity
NCBI Description
                   UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (UBIQUITIN
                   THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE
                   15) (DEUBIQUITINATING ENZYME 15) >gi_1078006_pir__$53974
                   hypothetical protein YMR304w - yeast (Saccharomyces
                   cerevisiae) >gi_798946_emb_CAA89137_ (Z49212) unknown
                   [Saccharomyces cerevisiae]
Seq. No.
                   11552
Contig ID
                   21675 1.R1040
5'-most EST
                   LIB3170-011-Q1-K1-B10
Method
                   BLASTX
NCBI GI
                   g2244993
BLAST score
                   316
E value
                   6.0e-29
Match length
                   91
                   66
% identity
NCBI Description
                   (Z97341) similarity to AMP-activated protein kinase beta
                   [Arabidopsis thaliana]
Seq. No.
                   11553
```

21677 1.R1040

 $jex70\overline{0}905308.h1$

Contig ID 5'-most EST

NCBI GI

E value

BLAST score





Method BLASTX NCBI GI q2498512 BLAST score 310 E value 4.0e-28 Match length 229 33 % identity LDLC PROTEIN >gi_1082264_pir__A53542 brefeldin A-sensitive NCBI Description Golgi protein LDLC - human >gi_575654_emb_CAA84427_ (Z34975) ldlCp [Homo sapiens] Seq. No. 11554 21687 1.R1040 Contig ID 5'-most EST LIB3051-112-Q1-K1-E6 BLASTX Method NCBI GI q3776559 BLAST score 440 E value 4.0e-43 Match length 165 % identity NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana] 11555 Seq. No. Contig ID 21688 1.R1040 5'-most EST LIB3051-114-Q1-K1-E10 Method BLASTN NCBI GI g2760167 BLAST score 43 E value 7.0e-15 Match length 179 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MCO15, complete sequence [Arabidopsis thaliana] Seq. No. 11556 21689 1.R1040 Contig ID 5'-most EST asn701134480.hl Method BLASTX NCBI GI q3776559 BLAST score 639 E value 1.0e-66 Match length 160 % identity NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana] Seq. No. 11557 Contig ID 21691 1.R1040 5'-most EST LIB3109-021-Q1-K2-F8 Method BLASTX

2000

g2632106

1.0e-166

1493